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(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR  
QQKKKIERQEEKLNNDLSMVRMKSMAIGFCFTALMGFMNSIFDGRVVAKLPTPLSYIQ  
GLSHRNLLGDDTTDCSFIFLYILCTMSIRONIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

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## SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

### FIELD OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

### BACKGROUND OF THE INVENTION

Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

#### SUMMARY OF THE INVENTION

In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%

nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid

sequence identity, alternatively at least about 82 % amino acid sequence identity, alternatively at least about 83 % amino acid sequence identity, alternatively at least about 84 % amino acid sequence identity, alternatively at least about 85 % amino acid sequence identity, alternatively at least about 86 % amino acid sequence identity, alternatively at least about 87 % amino acid sequence identity, alternatively at least about 88 % amino acid sequence identity, alternatively at least about 89 % amino acid sequence identity, alternatively at least about 90 % amino acid sequence identity, alternatively at least about 91 % amino acid sequence identity, alternatively at least about 92 % amino acid sequence identity, alternatively at least about 93 % amino acid sequence identity, alternatively at least about 94 % amino acid sequence identity, alternatively at least about 95 % amino acid sequence identity, alternatively at least about 96 % amino acid sequence identity, alternatively at least about 97 % amino acid sequence identity, alternatively at least about 98 % amino acid sequence identity and alternatively at least about 99 % amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

5 In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

10 In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

15 In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

#### 20 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO177 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16438-1387".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

25 Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO3574 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA19360-2552".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

30 Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO1280 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA33455-1548".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO4984 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA37155-2651".

35 Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO4988 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA38269-2654".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

5 Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO305 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA40619-1220".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO1866 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA44174-2513".

10 Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO4996 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA44675-2662".

15 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO4406 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA45408-2615".

Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

20 Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO1120 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA48606-1479".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

25 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO4990 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA52753-2656".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO738 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA53915-1258".

30 Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO3577 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA53991-2553".

35 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO1879 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA54009-2517".

Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO1471 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA56055-1643".

5 Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO1114 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA57033-1403".

Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

10 Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO1076 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA57252-1453".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

15 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO1483 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA58799-1652".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO4985 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA59770-2652".

20 Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO5000 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA59774-2665".

25 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO1881 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA60281-2518".

Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

30 Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO4314 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA60736-2559".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

35 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO4987 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA61875-2653".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.



Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO4313 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA62312-2558".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

5 Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO4799 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA62849-1604".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO4995 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA66307-2661".

10 Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO1341 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA66677-2535".

15 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO1777 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA71235-1706".

Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

20 Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO3580 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA71289-2547".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

25 Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO1779 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA73775-1707".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1754 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA76385-1692".

30 Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO1906 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA76395-2527".

35 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1870 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA77622-2516".

Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO4329 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA77629-2573".

5 Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO4979 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA77645-2648".

Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

10 Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO1885 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA79302-2521".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

15 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO1882 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA79865-2519".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO4989 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA80135-2655".

20 Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO4323 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA80794-2568".

25 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO1886 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA80796-2523".

Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

30 Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO4395 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA80840-2605".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

35 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO1782 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA80899-2501".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO4338 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA81228-2580".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

5 Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO4341 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA81761-2583".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO5990 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA96042-2682".

10 Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO3438 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA82364-2538".

15 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO4321 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA82424-2566".

Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

20 Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO4304 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA82430-2557".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

25 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA83500-2506".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO4403 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA83509-2612".

30 Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO4324 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA83560-2569".

35 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO4303 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA84139-2555".

Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO4305 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA84141-2556".

5 Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO4404 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA84142-2613".

Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

10 Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1884 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA84318-2520".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

15 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO4349 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA84909-2590".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO4401 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA84912-2610".

20 Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1867 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA84925-2514".

25 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO4319 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA84928-2564".

Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

30 Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO4991 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA84932-2657".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

35 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO4398 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA86592-2607".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO4346 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA86594-2587".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO4350 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA86647-2591".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO4318 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA87185-2563".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO4340 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA87656-2582".

Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO4400 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA87974-2609".

Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO4320 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA88001-2565".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO4409 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA88004-2575".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO4399 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA89220-2608".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO4418 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA89947-2618".

Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO4330 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA90842-2574".

Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO4339 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA91775-2581".

5 Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO4326 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA91779-2571".

Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

10 Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO6014 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA92217-2697".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

15 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO3446 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA92219-2541".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4322 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA92223-2567".

20 Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO4381 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA92225-2603".

25 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO4348 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA92232-2589".

Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

30 Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO4371 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA92233-2599".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

35 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO3742 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA92243-2549".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO5773 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA92253-2671".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

5 Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO5774 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA92254-2672".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO4343 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA92255-2584".

10 Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO4325 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA92269-2570".

15 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO4347 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA92288-2588".

Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

20 Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO3743 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA92290-2550".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

25 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO4426 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA93012-2622".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO4500 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA93020-2642".

30 Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO4389 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA94830-2604".

35 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO4337 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA94833-2579".

Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO4992 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA94838-2658".

5 Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO5996 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA94844-2686".

Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

10 Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO4345 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA94854-2586".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

15 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA95930".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO5780 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA96868-2677".

20 Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO5992 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA96871-2683".

25 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO4428 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA96880-2624".

Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

30 Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO4994 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA96986-2660".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

35 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO5995 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA96988-2685".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.



Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO6094 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA96995-2709".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

5 Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO4317 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA97004-2562".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO5997 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA97005-2687".

10 Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO5005 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA97009-2668".

15 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO5004 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA97013-2667".

Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

20 Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO6001 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA98380-2690".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

25 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO6013 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA98561-2696".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO4502 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA98575-2644".

30 Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO6007 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA98593-2694".

35 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO6028 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA98600-2703".

Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO100 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA99333".

5 Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO4327 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA99391-2572".

Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

10 Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO4315 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA99393-2560".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

15 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO5993 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA100276-2684".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO4503 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA100312-2645".

20 Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO4976 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA100902-2646".

25 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO5798 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA102899-2679".

Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

30 Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO6242 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA104875-2720".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

35 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO6095 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA105680-2710".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO6093 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA105779-2708".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO6012 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA105794-2695".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO6027 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA105838-2702".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO6181 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA107698-2715".

Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO6097 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA107701-2711".

Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO6090 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA107781-2707".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO7171 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA108670-2744".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO6258 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA108688-2725".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO9820 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA108769-2765".

Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO6243 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA108935-2721".

Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO6182 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA110700-2716".

5 Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO6079 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA111750-2706".

Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

10 Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO7434 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA123430-2755".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

15 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO9865 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA125154-2785".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO9828 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA142238-2768".

20 Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO196 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA22779-1130".

25 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO197 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA22780-1078".

Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

30 Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO195 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA26847-1395".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

35 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO187 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA27864-1155".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO182 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA27865-1091".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

5 Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO188 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA28497-1130".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO183 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA28498".

10 Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO184 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA28500".

15 Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO185 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA28503".

Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

20 Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO200 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA29101-1122".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

25 Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO202 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA30869".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

Figure 289 shows a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO214 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA32286-1191".

30 Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figure 289.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO215 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA32288-1132".

35 Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO219 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA32290-1164".

Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO211 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA32292-1131".

5 Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO220 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA32298-1132".

Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

10 Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO366 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA33085-1110".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

15 Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO216 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA33087-1158".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO221 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA33089-1132".

20 Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO228 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA33092-1202".

25 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO217 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA33094-1131".

Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

30 Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO222 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA33107-1135".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

35 Figure 311 shows a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO224 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA33221-1133".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figure 311.

Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO230 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA33223-1136".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

5 Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO198 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA33457-1078".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO226 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA33460-1166".

10 Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO261 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA33473-1176".

15 Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO242 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA33785-1143".

Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

20 Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO227 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA33786-1132".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

25 Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO237 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA34353-1428".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO241 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA34392-1170".

30 Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO231 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA34434-1139".

35 Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO235 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA35558-1167".

Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO323 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA35595-1228".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO245 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA35638-1216".

Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO246 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA35639-1172".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO288 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA35663-1129".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO248 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA35674-1142".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO257 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA35841-1173".

Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO172 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA35916-1161".

Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO258 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA35918-1174".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO265 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA36350-1158".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.



Figure 351 shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO326 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA37140-1234".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figure 351.

5 Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO266 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA37150-1178".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO269 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA38260-1180".

10 Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO285 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA40021-1154".

15 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO328 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA40587-1231".

Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

20 Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO344 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA40592-1242".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

25 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO272 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA40620-1183".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO301 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA40628-1216".

30 Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO331 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA40981-1234".

35 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO332 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA40982-1235".

Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO353 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA41234-1242".

5 Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO310 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA43046-1225".

Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

10 Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO337 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA43316-1237".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

15 Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO346 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA44167-1243".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO350 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA44175-1314".

20 Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO526 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA44184-1319".

25 Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO381 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA44194-1317".

Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

30 Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO846 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA44196-1353".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

35 Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO363 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA45419-1252".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO365 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA46777-1253".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

5 Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO1310 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA47394-1572".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO731 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA48331-1329".

10 Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO322 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA48336-1309".

15 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO536 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA49142-1430".

Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

20 Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO719 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA49646-1327".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

25 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO619 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA49821-1562".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO771 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA49829-1346".

30 Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA50921-1458".

35 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO862 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA52187-1354".

Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO733 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA52196-1348".

5 Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO1188 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA52598-1518".

Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

10 Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO770 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA54228-1366".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

15 Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO1080 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA56047-1456".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO1017 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA56112-1379".

20 Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO1016 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA56113-1378".

25 Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO792 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56352-1358".

Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

30 Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO938 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56433-1406".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

35 Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO1012 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA56439-1376".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO1008 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57530-1375".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

5 Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO1075 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57689-1385".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1007 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57690-1374".

10 Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO1056 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA57693-1424".

15 Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO791 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA57838-1337".

Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

20 Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1111 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA58721-1475".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

25 Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO812 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59205-1421".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO1066 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59215-1425".

30 Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1185 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59220-1514".

35 Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1031 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA59294-1381".

Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1360 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA59488-1603".

5 Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1309 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA59588-1571".

Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

10 Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1107 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA59606-1471".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

15 Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO836 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA59620-1463".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO1132 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA59767-1489".

20 Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA59777-1480".

25 Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1130 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA59814-1486".

Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

30 Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO844 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA59839-1461".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

35 Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1154 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA59846-1503".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1181 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA59847-1511".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

5 Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1126 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA60615-1483".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1186 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA60621-1516".

10 Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO1198 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA60622-1525".

15 Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO1159 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA60627-1508".

Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

20 Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO1265 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA60764-1533".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

25 Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO1250 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA60775-1532".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO1475 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA61185-1646".

30 Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO1312 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA61873-1574".

35 Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO1308 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA62306-1570".

Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO1326 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA62808-1582".

5 Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO1192 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA62814-1521".

Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

10 Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO1246 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA64885-1529".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

15 Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO1356 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA64886-1601".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO1275 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA64888-1542".

20 Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO1274 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA64889-1541".

25 Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO1358 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA64890-1612".

Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

30 Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO1286 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA64903-1553".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

35 Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO1294 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA64905-1558".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.



Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO1273 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA65402-1540".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

5 Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO1279 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA65405-1547".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO1195 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA65412-1523".

10 Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO1271 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA66309-1538".

15 Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO1338 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA66667-1596".

Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

20 Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA66675-1587".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

25 Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO1434 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA68818-2536".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO1418 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA68864-1629".

30 Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO1387 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA68872-1620".

35 Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO1384 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA71159-1617".

Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO1565 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA73727-1673".

5 Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figure 525 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO1474 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA73739-1645".

Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figure 525.

10 Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO1917 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA76400-2528".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

15 Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO1787 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA76510-2504".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO1556 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA76529-1666".

20 Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO1561 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA76538-1670".

25 Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO1693 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA77301-1708".

Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

30 Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO1868 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA77624-2515".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

35 Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO1890 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA79230-2525".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO1887 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA79862-2522".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO4353 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA80145-2594".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA83500-2506".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO4357 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA84917-2597".

Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO4302 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA92218-2554".

Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

## DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

### I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be

isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (*e.g.*, Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for

instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly

available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence

comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

5 In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

10 
$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

15 "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-

length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic



acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, %  
5 nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value  
10 is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides  
15 of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected  
25 occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid  
30 sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will  
35 be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to

C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

5 "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 10 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

15 An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

25 The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

30 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not

substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')<sub>2</sub>, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')<sub>2</sub> fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V<sub>H</sub>-V<sub>L</sub> dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')<sub>2</sub> antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and

IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the  $V_H$  and  $V_L$  domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the  $V_H$  and  $V_L$  domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) in the same polypeptide chain ( $V_H$ - $V_L$ ). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The

components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and  
5 in a routine manner, in relation to the stated purpose.

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

10  int  _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ { -2, -4, 15, -5, -5, -4, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15  /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ { -4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ { -1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20  /* I */ { -1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ { -1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ { -2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ { -1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25  /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ { -2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30  /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
35  /* W */ { -6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ { -3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};
40

45

50

55

```



Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0        8      /* penalty for a gap */
15
#define DINS1        1      /* penalty per base */
#define PINS0        8      /* penalty for a gap */
#define PINS1        4      /* penalty per residue */

struct jmp {
20
    short            n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short   x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int              score;      /* score at last jmp */
    long             offset;     /* offset of prev block */
    short            jmp;        /* current jmp index */
    struct jmp        jp;        /* list of jmps */
};

30
struct path {
    int              spc;        /* number of leading spaces */
    short            n[JMPS]; /* size of jmp (gap) */
    int              x[JMPS]; /* loc of jmp (last elem before gap) */
};

35
char              *ofile;      /* output file name */
char              *namex[2];   /* seq names: getseqs() */
char              *prog;       /* prog name for err msgs */
40
char              *seqx[2];     /* seqs: getseqs() */
int               dmax;         /* best diag: nw() */
int               dmax0;        /* final diag */
int               dna;          /* set if dna: main() */
int               endgaps;      /* set if penalizing end gaps */
45
int               gapx, gapy;    /* total gaps in seqs */
int               len0, len1;    /* seq lens */
int               ngapx, ngapy;  /* total size of gaps */
int               smax;         /* max score: nw() */
int               *xbm;         /* bitmap for matching */
50
long             offset;        /* current offset in jmp file */
struct diag       *dx;          /* holds diagonals */
struct path       pp[2];        /* holds path for seqs */

char              *calloc(), *malloc(), *index(), *strcpy();
55
char              *getseq(), *g_calloc();

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
* The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static _pbval[26] = {
    1,2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
    int    ac;
    char    *av[];
{
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                /* 1 to penalize endgaps */
    ofile = "align.out";        /* output file */

    nw();                        /* fill in the matrix, get the possible jmps */
    readjmps();                 /* get the actual jmps */
    print();                     /* print stats, alignment */

    cleanup();                  /* unlink any tmp files */
}

```

Table 1 (cont')

/\* do the alignment, return best score: main()

\* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983

\* pro: PAM 250 values

\* When scores are equal, we prefer mismatches to any gap, prefer

\* a new gap to extending an ongoing gap, and prefer a gap in seqx

\* to a gap in seq y.

\*/

nw()

nw

{

```

char      *px, *py;           /* seqs and ptrs */
int        *ndely, *dely;      /* keep track of dely */
int        ndelx, delx;        /* keep track of delx */
int        *tmp;              /* for swapping row0, row1 */
int        mis;               /* score for each type */
int        ins0, ins1;         /* insertion penalties */
register    id;                /* diagonal index */
register    ij;                /* jmp index */
register    *col0, *col1;       /* score for curr, last row */
register    xx, yy;            /* index into seqs */

```

dx = (struct diag \*)g\_calloc("to get diags", len0 + len1 + 1, sizeof(struct diag));

ndely = (int \*)g\_calloc("to get ndely", len1 + 1, sizeof(int));

dely = (int \*)g\_calloc("to get dely", len1 + 1, sizeof(int));

col0 = (int \*)g\_calloc("to get col0", len1 + 1, sizeof(int));

col1 = (int \*)g\_calloc("to get col1", len1 + 1, sizeof(int));

ins0 = (dna)? DINS0 : PINS0;

ins1 = (dna)? DINS1 : PINS1;

smax = -10000;

if (endgaps) {

```

    for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
        col0[yy] = dely[yy] = col0[yy-1] - ins1;
        ndely[yy] = yy;
    }

```

col0[0] = 0; /\* Waterman Bull Math Biol 84 \*/

}

else

```

    for (yy = 1; yy <= len1; yy++)
        dely[yy] = -ins0;

```

/\* fill in match matrix

\*/

for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {

/\* initialize first entry in col

\*/

if (endgaps) {

if (xx == 1)

col1[0] = delx = -(ins0 + ins1);

else

col1[0] = delx = col0[0] - ins1;

ndelx = xx;

}

else {

col1[0] = 0;

delx = -ins0;

ndelx = 0;

}

Table 1 (cont')

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */

```

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
5   else if (delx >= dely[yy]) {
        coll[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10   && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejmps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
15   offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
20   dx[id].score = delx;
    }
    else {
        coll[yy] = dely[yy];
        ij = dx[id].ijmp;
25   if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejmps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
30   offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = -ndely[yy];
        dx[id].jp.x[ij] = xx;
35   dx[id].score = dely[yy];
    }
    if (xx == len0 && yy < len1) {
        /* last col
        */
        if (endgaps)
            coll[yy] -= ins0+ins1*(len1-yy);
40   if (coll[yy] > smax) {
            smax = coll[yy];
            dmax = id;
45   }
    }
}
50   if (endgaps && xx < len0)
        coll[yy-1] -= ins0+ins1*(len0-xx);
    if (coll[yy-1] > smax) {
        smax = coll[yy-1];
        dmax = id;
55   }
    tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
60   (void) free((char *)col0);
    (void) free((char *)coll);
}

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
10 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256    /* maximum output line */
#define P_SPC    3      /* space between name or num and seq */

20 extern _day[26][26];
int      olen;          /* set output line length */
FILE     *fx;           /* output file */

25 print()
{
    int      lx, ly, firstgap, lastgap;    /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "< first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "< second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50         lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
55         lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}
60

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)                                getmat
    int    lx, ly;                                /* "core" (minus endgaps) */
    int    firstgap, lastgap;                      /* leading trailing overlap */
{
    int    nm, i0, i1, siz0, siz1;
10    char    outx[32];
    double    pct;
    register    n0, n1;
    register char    *p0, *p1;

15    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
25        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
30            p0++;
            n0++;
            siz1--;
        }
        else {
35            if (xbm[*p0-'A'] & xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
40            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
45    }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
50    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
55    pct = 100.*((double)nm)/((double)lx);
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
60

```

Table 1 (cont')

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        gapx, (dna)? "base": "residue", (gapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%s)",
            gapy, (dna)? "base": "residue", (gapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "< endgaps not penalized\n");
}

static nm; /* matches in core -- for checking */
static lmax; /* lengths of stripped file names */
static ij[2]; /* jmp index for a path */
static nc[2]; /* number at start of current line */
static ni[2]; /* current elem number -- for gapping */
static siz[2];
static char *ps[2]; /* ptr to current element */
static char *po[2]; /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int nn; /* char count */
    int more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr\_align



Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25            po[i]++;
            ps[i]++;

            /*
            * are we at next gap for this seq?
            */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                * we need to merge all gaps
                * at this location
                */
35                siz[i] = pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
            }
            ni[i]++;
40        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
45    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
55 static
dumpblock()
{
    register i;

60    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';

```

...pr\_align

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10         putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15     }
    }
}

/*
20  * put out a number line: dumpblock()
  */
static
nums(ix)
25  {
    int    ix;      /* index in out[] holding seq line */

    char    nline[P_LINE];
    register i, j;
    register char *pn, *px, *py;

30    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
35        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
40                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
45                i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
50    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

55  /*
    * put out a line (name, [num], seq, [num]): dumpblock()
    */
static
putline(ix)
60  {
    int    ix;
    {

```

nums

putline

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */

15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
   static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(p0[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(p0[1]) == ' '))
          return;
      px = star;
      for (i = lmax+P_SPC; i--;)
35         *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {
40             if (xbm[*p0-'A']&xbm[*p1-'A']) {
                 cx = '*';
                 nm++;
             }
             else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                 cx = '.';
             else
                 cx = ' ';
          }
          else
50             cx = ' ';
          *px++ = cx;
      }
      *px++ = '\n';
      *px = '\0';
55  }

```

stars

60

Table 1 (cont')

```
/*  
 * strip path or prefix from pn, return len: pr_align()  
 */  
static  
stripname(pn)  
{  
    char    *pn;    /* file name (may be path) */  
    register char    *px, *py;  
    py = 0;  
    for (px = pn; *px; px++)  
        if (*px == '/')  
            py = px + 1;  
    if (py)  
        (void) strcpy(pn, py);  
    return(strlen(pn));  
}
```

stripname

**Table 1 (cont')**

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>
10
char    *jname = "/tmp/homgXXXXXX";      /* tmp file for jumps */
FILE    *fj;

int      cleanup();                      /* cleanup tmp file */
15 long    lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)                                cleanup
    int    i;
    {
        if (fj)
            (void) unlink(jname);
25        exit(i);
    }

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30
char    *
getseq(file, len)                                getseq
35     char    *file;    /* file name */
     int      *len;     /* seq len */
    {
        char    line[1024], *pseq;
        register char    *px, *py;
        int      natgc, tlen;
        FILE     *fp;

        if ((fp = fopen(file, "r")) == 0) {
            fprintf(stderr, "%s: can't read %s\n", prog, file);
            exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
            if (*line == ';' || *line == '<' || *line == '>')
                continue;
            for (px = line; *px != '\n'; px++)
                if (isupper(*px) || islower(*px))
                    tlen++;
        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
            fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
            exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

Table 1 (cont')

```

py = pseq + 4;
*len = tlen;
rewind(fp);
5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
15
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

25
char *
g_alloc(msg, nx, sz)
    char *msg;          /* program, calling routine */
    int nx, sz;          /* number and size of elements */
    {
30
        char *px, *calloc();

        if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
            if (*msg) {
35
                fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                exit(1);
            }
        }
        return(px);
    }
}

40
/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjumps()
45
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50
    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
60
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)

```

...getseq

g\_alloc

readjumps

Table 1 (cont')

...readjumps

```

5      if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
      }
      else
10         break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1 */
            /*
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
35            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
    }
    else
40        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
        offset = 0;
60    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */

```

**writejumps**

```

5  writejumps(ix)
    int    ix;
    {
10     char    *mktemp();
        if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
                fprintf(stderr, "%s: can't write %s\n", prog, jname);
                exit(1);
            }
20         }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }

```



**Table 2**

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYY	(Length = 12 amino acids)

5    % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10    5 divided by 15 = 33.3%

**Table 3**

15    PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20    (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

**Table 4**

PRO-DNA	NNNNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLLLL	(Length = 16 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 6 divided by 14 = 42.9%

**Table 5**

15 PRO-DNA	NNNNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

20 (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

4 divided by 12 = 33.3%

## II. Compositions and Methods of the Invention

### A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

### B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
20	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
25	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
	Gln (Q)	asn	asn
	Glu (E)	asp	asp
30	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe; norleucine	leu
	Leu (L)	norleucine; ile; val; met; ala; phe	ile
35	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
40	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
45	Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- (3) acidic: asp, glu;
- (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., **13**:4331 (1986); Zoller et al., Nucl. Acids Res., **10**:6487 (1987)], cassette mutagenesis [Wells et al., Gene, **34**:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, **317**:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, **244**: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., **150**:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

### C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-

octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to

be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an  $\alpha$ -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

#### D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

##### 1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

## 2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl<sub>2</sub>, CaPO<sub>4</sub>, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the



method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

5           Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include  
10   Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant  
15   DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli*  
20   W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan'*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

25           In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces*  
30   such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al.,

Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotrophic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

### 3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces*  $\alpha$ -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 $\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

5 Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

10 An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

15 Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

25 Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

30 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

35 PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July

1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

#### 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

### 5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

5 It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns  
10 to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

### 15 E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO  
20 polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50  
25 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels,  
30 including radionucleotides such as  $^{32}\text{P}$  or  $^{35}\text{S}$ , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

35 Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means.

The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increase affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example,  $\text{CaPO}_4$ -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of

the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral



(typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN<sup>TM</sup>, PLURONICS<sup>TM</sup> or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

5 Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling  
10 in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to  
15 particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-  
20 (rhIFN- ), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit and Adjuvant Approach*, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation  
30 products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), *Biodegradable Polymers as Drug Delivery Systems* (Marcel Dekker: New York, 1990), pp. 1-41.

35 This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides

encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

5 All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

10 In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

20 If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for  $\beta$ -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein

domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

5 F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

10 1. Polyclonal Antibodies

The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

20 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of

HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent

heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

*In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

### 3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and



Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, Bio/Technology 10, 779-783 (1992); Lonberg *et al.*, Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild *et al.*, Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

#### 4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain.

In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

5 Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g.  $F(ab')_2$  bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

10 Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

20 Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the  $V_H$  and  $V_L$  domains of one fragment are forced to pair with the complementary  $V_L$  and  $V_H$  domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

25 Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. 35 Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule

on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

#### 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.*, Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).

#### 7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins

(PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, croton, saponaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionucleotide).

#### 8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

#### 9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that

specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and  $\gamma$  ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT<sup>TM</sup> (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

#### G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC

Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

## EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

### EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g., LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were

often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to Sall hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

#### EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

##### 1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the Sall/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

##### 2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

### 3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, *ura3-52*, *leu2-3*, *leu2-112*, *his3-11*, *his3-15*, *MAL*<sup>+</sup>, *SUC*<sup>+</sup>, *GAL*<sup>+</sup>. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., *SEC61p*, *SEC72p*, *SEC62p*, *SEC63p*, *TDJ1p* or *SSA1p-4p*) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz et al., Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about  $2 \times 10^6$  cells/ml (approx.  $OD_{600}=0.1$ ) into fresh YEPD broth (500 ml) and regrown to  $1 \times 10^7$  cells/ml (approx.  $OD_{600}=0.4-0.5$ ).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM  $Li_2OOCCH_3$ ), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100  $\mu$ l) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1  $\mu$ g, vol. < 10  $\mu$ l) in microfuge tubes. The mixture was mixed briefly by vortexing; then 40% PEG/TE (600  $\mu$ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM  $Li_2OOCCH_3$ , pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500  $\mu$ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells



were then diluted into TE (1 ml) and aliquots (200  $\mu$ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al., Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

#### 4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30  $\mu$ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5  $\mu$ l) was used as a template for the PCR reaction in a 25  $\mu$ l volume containing: 0.5  $\mu$ l Klentaq (Clontech, Palo Alto, CA); 4.0  $\mu$ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5  $\mu$ l Kentaq buffer (Clontech); 0.25  $\mu$ l forward oligo 1; 0.25  $\mu$ l reverse oligo 2; 12.5  $\mu$ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:553)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:554)

PCR was then performed as follows:

a.	Denature	92°C, 5 minutes
b.	3 cycles of:	
	Denature	92°C, 30 seconds
	Anneal	59°C, 30 seconds
	Extend	72°C, 60 seconds
c.	3 cycles of:	
	Denature	92°C, 30 seconds
	Anneal	57°C, 30 seconds
	Extend	72°C, 60 seconds
d.	25 cycles of:	
	Denature	92°C, 30 seconds
	Anneal	55°C, 30 seconds
	Extend	72°C, 60 seconds

e. Hold 4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 µl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

#### EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

#### EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
DNA16438-1387	209771	April 14, 1998
DNA19360-2552	203654	February 9, 1999
DNA33455-1548	PTA-127	May 25, 1999
DNA37155-2651	PTA-429	July 27, 1999
DNA38269-2654	PTA-432	July 27, 1999
DNA40619-1220	209525	December 10, 1997

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA44174-2513	203577	January 12, 1999
	DNA44675-2662	PTA-430	July 27, 1999
	DNA45408-2615	PTA-203	June 8, 1999
5	DNA48606-1479	203040	July 1, 1998
	DNA52753-2656	PTA-611	August 31, 1999
	DNA53915-1258	209593	January 21, 1998
	DNA53991-2553	203649	February 9, 1999
	DNA54009-2517	203574	January 12, 1999
10	DNA56055-1643	PTA-129	May 25, 1999
	DNA57033-1403	209905	May 27, 1998
	DNA57252-1453	203585	January 12, 1999
	DNA58799-1652	203665	February 9, 1999
	DNA59770-2652	PTA-427	July 27, 1999
15	DNA59774-2665	PTA-615	August 31, 1999
	DNA60281-2518	203582	January 12, 1999
	DNA60736-2559	203838	March 9, 1999
	DNA61875-2653	PTA-428	July 27, 1999
	DNA62312-2558	203836	March 9, 1999
20	DNA62849-1604	PTA-205	June 8, 1999
	DNA66307-2661	PTA-431	July 27, 1999
	DNA66677-2535	203659	February 9, 1999
	DNA71235-1706	203584	January 12, 1999
	DNA71289-2547	PTA-126	May 25, 1999
25	DNA73775-1707	PTA-128	May 25, 1999
	DNA76385-1692	203664	February 9, 1999
	DNA76395-2527	203578	January 12, 1999
	DNA77622-2516	203554	December 22, 1998
	DNA77629-2573	203850	March 16, 1999
30	DNA77645-2648	PTA-45	May 11, 1999
	DNA79302-2521	203545	December 22, 1998
	DNA79865-2519	203544	December 22, 1998
	DNA80135-2655	PTA-234	June 15, 1999
	DNA80794-2568	203848	March 16, 1999
35	DNA80796-2523	203555	December 22, 1998
	DNA80840-2605	203949	April 20, 1999
	DNA80899-2501	203539	December 15, 1998
	DNA81228-2580	203871	March 23, 1999
	DNA81761-2583	203862	March 23, 1999
40	DNA82358-2738	PTA-510	August 10, 1999
	DNA82364-2538	203603	January 20, 1999
	DNA82424-2566	203813	March 2, 1999
	DNA82430-2557	203812	March 2, 1999
	DNA83500-2506	203391	October 29, 1998
45	DNA83509-2612	203965	April 27, 1999
	DNA83560-2569	203816	March 2, 1999
	DNA84139-2555	203814	March 2, 1999
	DNA84141-2556	203810	March 2, 1999
	DNA84142-2613	PTA-22	May 4, 1999
50	DNA84318-2520	203580	January 12, 1999
	DNA84909-2590	203889	March 30, 1999
	DNA84912-2610	203964	April 27, 1999
	DNA84925-2514	203548	December 22, 1998
	DNA84928-2564	203817	March 2, 1999
55	DNA84932-2657	PTA-235	June 15, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA86592-2607	203968	April 27, 1999
	DNA86594-2587	203894	March 30, 1999
	DNA86647-2591	203893	March 30, 1999
5	DNA87185-2563	203811	March 2, 1999
	DNA87656-2582	203867	March 23, 1999
	DNA87974-2609	203963	April 27, 1999
	DNA88001-2565	203815	March 2, 1999
	DNA88004-2575	203890	March 30, 1999
10	DNA89220-2608	PTA-130	May 25, 1999
	DNA89947-2618	203970	April 27, 1999
	DNA90842-2574	203845	March 16, 1999
	DNA91775-2581	203861	March 23, 1999
	DNA91779-2571	203844	March 16, 1999
15	DNA92217-2697	PTA-513	August 10, 1999
	DNA92219-2541	203663	February 9, 1999
	DNA92223-2567	203851	March 16, 1999
	DNA92225-2603	203950	April 20, 1999
	DNA92232-2589	203895	March 30, 1999
20	DNA92233-2599	PTA-134	May 25, 1999
	DNA92243-2549	203852	March 16, 1999
	DNA92253-2671	PTA-258	June 22, 1999
	DNA92254-2672	PTA-259	June 22, 1999
	DNA92255-2584	203866	March 23, 1999
25	DNA92269-2570	203853	March 16, 1999
	DNA92288-2588	203892	March 30, 1999
	DNA92290-2550	203847	March 16, 1999
	DNA93012-2622	PTA-21	May 4, 1999
	DNA93020-2642	PTA-121	May 25, 1999
30	DNA94830-2604	203951	April 20, 1999
	DNA94833-2579	203869	March 23, 1999
	DNA94838-2658	PTA-232	June 15, 1999
	DNA94844-2686	PTA-385	July 20, 1999
	DNA94854-2586	203864	March 23, 1999
35	DNA96868-2677	PTA-262	June 22, 1999
	DNA96871-2683	PTA-381	July 20, 1999
	DNA96880-2624	PTA-15	May 4, 1999
	DNA96986-2660	PTA-239	June 15, 1999
	DNA96988-2685	PTA-384	July 20, 1999
40	DNA96995-2709	PTA-475	August 3, 1999
	DNA97004-2562	203854	March 16, 1999
	DNA97005-2687	PTA-378	July 20, 1999
	DNA97009-2668	PTA-257	June 22, 1999
	DNA97013-2667	PTA-231	June 15, 1999
45	DNA98380-2690	PTA-388	July 20, 1999
	DNA98561-2696	PTA-620	August 31, 1999
	DNA98575-2644	PTA-118	May 25, 1999
	DNA98593-2694	PTA-477	August 3, 1999
	DNA98600-2703	PTA-488	August 3, 1999
50	DNA99391-2572	203849	March 16, 1999
	DNA99393-2560	203837	March 9, 1999
	DNA100276-2684	PTA-380	July 20, 1999
	DNA100312-2645	PTA-44	May 11, 1999
	DNA100902-2646	PTA-42	May 11, 1999
55	DNA102899-2679	PTA-123	May 25, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA104875-2720	PTA-482	August 3, 1999
	DNA105680-2710	PTA-483	August 3, 1999
	DNA105779-2708	PTA-485	August 3, 1999
5	DNA105794-2695	PTA-480	August 3, 1999
	DNA105838-2702	PTA-476	August 3, 1999
	DNA107698-2715	PTA-472	August 3, 1999
	DNA107701-2711	PTA-487	August 3, 1999
	DNA107781-2707	PTA-484	August 3, 1999
10	DNA108670-2744	PTA-546	August 17, 1999
	DNA108688-2725	PTA-515	August 10, 1999
	DNA108769-2765	PTA-861	October 19, 1999
	DNA108935-2721	PTA-518	August 10, 1999
	DNA110700-2716	PTA-512	August 10, 1999
15	DNA111750-2706	PTA-489	August 3, 1999
	DNA123430-2755	PTA-614	August 31, 1999
	DNA125154-2785	PTA-957	November 16, 1999
	DNA142238-2768	PTA-819	October 5, 1999
	DNA22779-1130	209280	September 18, 1997
20	DNA26847-1395	209772	April 14, 1998
	DNA27864-1155	209375	October 16, 1997
	DNA27865-1091	209296	September 23, 1997
	DNA28497-1130	209279	September 18, 1997
	DNA29101-1122	209653	March 5, 1998
25	DNA32286-1191	209385	October 16, 1997
	DNA32288-1132	209261	September 16, 1997
	DNA32290-1164	209384	October 16, 1997
	DNA32292-1131	209258	September 16, 1997
	DNA32298-1132	209257	September 16, 1997
30	DNA33085-1110	209087	May 30, 1997
	DNA33087-1158	209381	October 16, 1997
	DNA33089-1132	209262	September 16, 1997
	DNA33092-1202	209420	October 28, 1997
	DNA33094-1131	209256	September 16, 1997
35	DNA33107-1135	209251	September 16, 1997
	DNA33221-1133	209263	September 16, 1997
	DNA33223-1136	209264	September 16, 1997
	DNA33460-1166	209376	October 16, 1997
	DNA33473-1176	209391	October 17, 1997
40	DNA33785-1143	209417	October 28, 1997
	DNA33786-1132	209253	September 16, 1997
	DNA34353-1428	209855	May 12, 1998
	DNA34392-1170	209526	December 10, 1997
	DNA34434-1139	209252	September 16, 1997
45	DNA35558-1167	209374	October 16, 1997
	DNA35595-1228	209528	December 10, 1997
	DNA35638-1216	209265	September 16, 1997
	DNA35639-1172	209396	October 17, 1997
	DNA35663-1129	209201	August 18, 1997
50	DNA35674-1142	209416	October 28, 1997
	DNA35841-1173	209403	October 17, 1997
	DNA35916-1161	209419	October 28, 1997
	DNA35918-1174	209402	October 17, 1997
	DNA36350-1158	209378	October 16, 1997
55	DNA37140-1234	209489	November 21, 1997

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA37150-1178	209401	October 17, 1997
	DNA38260-1180	209397	October 17, 1997
	DNA40021-1154	209389	October 17, 1997
5	DNA40587-1231	209438	November 7, 1997
	DNA40592-1242	209492	November 21, 1997
	DNA40620-1183	209388	October 17, 1997
	DNA40628-1216	209432	November 7, 1997
	DNA40981-1234	209439	November 7, 1997
10	DNA40982-1235	209433	November 7, 1997
	DNA41234-1242	209618	February 5, 1998
	DNA43046-1225	209484	November 21, 1997
	DNA43316-1237	209487	November 21, 1997
	DNA44167-1243	209434	November 7, 1997
15	DNA44184-1319	209704	March 26, 1998
	DNA44194-1317	209808	April 28, 1998
	DNA44196-1353	209847	May 6, 1998
	DNA45419-1252	209616	February 5, 1998
	DNA46777-1253	209619	February 5, 1998
20	DNA47394-1572	203109	August 11, 1998
	DNA48331-1329	209715	March 31, 1998
	DNA48336-1309	209669	March 11, 1998
	DNA49142-1430	203002	June 23, 1998
	DNA49646-1327	209705	March 26, 1998
25	DNA49821-1562	209981	June 16, 1998
	DNA49829-1346	209749	April 7, 1998
	DNA50921-1458	209859	May 12, 1998
	DNA52187-1354	209845	May 6, 1998
	DNA52196-1348	209748	April 7, 1998
30	DNA52598-1518	203107	August 11, 1998
	DNA54228-1366	209801	April 23, 1998
	DNA56047-1456	209948	June 9, 1998
	DNA56112-1379	209883	May 20, 1998
	DNA56113-1378	203049	July 1, 1998
35	DNA56352-1358	209846	May 6, 1998
	DNA56433-1406	209857	May 12, 1998
	DNA56439-1376	209864	May 14, 1998
	DNA57530-1375	209880	May 20, 1998
	DNA57689-1385	209869	May 14, 1998
40	DNA57690-1374	209950	June 9, 1998
	DNA57693-1424	203008	June 23, 1998
	DNA57838-1337	203014	June 23, 1998
	DNA58721-1475	203110	August 11, 1998
	DNA59205-1421	203009	June 23, 1998
45	DNA59215-1425	209961	June 9, 1998
	DNA59220-1514	209962	June 9, 1998
	DNA59294-1381	209866	May 14, 1998
	DNA59488-1603	203157	August 25, 1998
	DNA59588-1571	203106	August 11, 1998
50	DNA59606-1471	209945	June 9, 1998
	DNA59620-1463	209989	June 16, 1998
	DNA59767-1489	203108	August 11, 1998
	DNA59777-1480	203111	August 11, 1998
	DNA59814-1486	203359	October 20, 1998
55	DNA59839-1461	209988	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA59846-1503	209978	June 16, 1998
	DNA59847-1511	203098	August 4, 1998
	DNA60615-1483	209980	June 16, 1998
5	DNA60621-1516	203091	August 4, 1998
	DNA60622-1525	203090	August 4, 1998
	DNA60627-1508	203092	August 4, 1998
	DNA60764-1533	203452	November 10, 1998
	DNA60775-1532	203173	September 1, 1998
10	DNA61185-1646	203464	November 17, 1998
	DNA61873-1574	203132	August 18, 1998
	DNA62306-1570	203254	September 9, 1998
	DNA62808-1582	203358	October 20, 1998
	DNA62814-1521	203093	August 4, 1998
15	DNA64885-1529	203457	November 3, 1998
	DNA64886-1601	203241	September 9, 1998
	DNA64888-1542	203249	September 9, 1998
	DNA64889-1541	203250	September 9, 1998
	DNA64890-1612	203131	August 18, 1998
20	DNA64903-1553	203223	September 15, 1998
	DNA64905-1558	203233	September 15, 1998
	DNA65402-1540	203252	September 9, 1998
	DNA65405-1547	203476	November 17, 1998
	DNA65412-1523	203094	August 4, 1998
25	DNA66309-1538	203235	September 15, 1998
	DNA66667-1596	203267	September 22, 1998
	DNA66675-1587	203282	September 22, 1998
	DNA68818-2536	203657	February 9, 1999
	DNA68864-1629	203276	September 22, 1998
30	DNA68872-1620	203160	August 25, 1998
	DNA71159-1617	203135	August 18, 1998
	DNA73727-1673	203459	November 3, 1998
	DNA73739-1645	203270	September 22, 1998
	DNA76400-2528	203573	January 12, 1999
35	DNA76510-2504	203477	November 17, 1998
	DNA76529-1666	203315	October 6, 1998
	DNA76538-1670	203313	October 6, 1998
	DNA77301-1708	203407	October 27, 1998
	DNA77624-2515	203553	December 22, 1998
40	DNA79230-2525	203549	December 22, 1998
	DNA79862-2522	203550	December 22, 1998
	DNA80145-2594	PTA-204	June 8, 1999
	DNA83500-2506	203391	October 29, 1998
	DNA84917-2597	203863	March 23, 1999
45	DNA92218-2554	203834	March 9, 1999
	DNA96042-2682	PTA-382	July 20, 1999

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of

the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

5 The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

10 EXAMPLE 5: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

15 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

20 DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 6: Expression of PRO in *E. coli*

25 This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

35 The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant



colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

5 After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

10 PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110  
15 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate•2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO<sub>4</sub>) and grown for approximately 20-30 hours at 30°C with shaking. Samples are  
20 removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

*E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results  
25 in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the  
30 desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA.  
35 Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the

solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 7: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10  $\mu$ g pRK5-PRO DNA is mixed with about 1  $\mu$ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500  $\mu$ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M  $\text{CaCl}_2$ . To this mixture is added, dropwise, 500  $\mu$ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM  $\text{NaPO}_4$ , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200  $\mu$ Ci/ml  $^{35}\text{S}$ -cysteine and 200  $\mu$ Ci/ml  $^{35}\text{S}$ -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO<sub>4</sub> or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as <sup>35</sup>S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni<sup>2+</sup>-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect<sup>®</sup> (Quiagen), Dosper<sup>®</sup> or Fugene<sup>®</sup> (Boehringer

Mannheim). The cells are grown as described in Lucas et al., *supra*. Approximately  $3 \times 10^7$  cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2  $\mu$ m filtered PS20 with 5% 0.2  $\mu$ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with  $3 \times 10^5$  cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at  $1.2 \times 10^6$  cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22  $\mu$ m filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275  $\mu$ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme

sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM

phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching  $A_{280}$  baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with  $Ni^{2+}$ -NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 10: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

**EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies**

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

**EXAMPLE 12: Drug Screening**

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment

and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

#### EXAMPLE 13: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then



be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

**EXAMPLE 14: Identification of PRO Polypeptides That Stimulate TNF- $\alpha$  Release In Human Blood (Assay 128)**

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- $\alpha$  in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- $\alpha$  would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- $\alpha$  release would be beneficial. Specifically, 200  $\mu$ l of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 $\mu$ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50 $\mu$ l of plasma is collected from each well and tested for the presence of TNF- $\alpha$  by ELISA assay. A positive in the assay is a higher amount of TNF- $\alpha$  in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay: PRO195, PRO202, PRO215, PRO221, PRO217, PRO222, PRO198, PRO245, PRO172, PRO265, PRO266, PRO344, PRO337, PRO322, PRO1286, PRO1279, PRO1338 and PRO1343.

**EXAMPLE 15: Detection of Polypeptides That Affect Glucose or FFA Uptake in Skeletal Muscle (Assay 106)**

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as being capable of affecting glucose and/or FFA uptake by skeletal muscle in this assay: PRO182, PRO366, PRO198, PRO172 and PRO719.

**EXAMPLE 16: Chondrocyte Re-differentiation Assay (Assay 110)**

This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100 µl of the same media without serum and 100 µl of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 µl/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

The following polypeptide tested positive in this assay: PRO182, PRO366, PRO198 and PRO1868.

**EXAMPLE 17: Chondrocyte Proliferation Assay (Assay 111)**

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are reseeded to 25,000 cells/cm<sup>2</sup> every five days. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37°C, 20 µl of Alamar blue is added to each well and the plates are incubated for an additional 3 hours at 37°C. The fluorescence is then measured in each well (Ex: 530 nm; Em: 590 nm). The fluorescence of a plate containing 200 µl of the serum-free medium is measured to obtain the background. A positive result in the assay is obtained when the fluorescence of the PRO polypeptide treated sample is more like that of the positive control than the negative control.

The following PRO polypeptides tested positive in this assay: PRO202, PRO224, PRO172 and PRO1312.

**EXAMPLE 18: Detection of PRO Polypeptides That Affect Glucose or FFA Uptake by Primary Rat Adipocytes (Assay 94)**

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by adipocyte cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by adipocytes

would be beneficial including, for example, obesity, diabetes or hyper- or hypo-insulinemia.

In a 96 well format, PRO polypeptides to be assayed are added to primary rat adipocytes, and allowed to incubate overnight. Samples are taken at 4 and 16 hours and assayed for glycerol, glucose and FFA uptake. After the 16 hour incubation, insulin is added to the media and allowed to incubate for 4 hours. At this time, a sample is taken and glycerol, glucose and FFA uptake is measured. Media containing insulin without the PRO polypeptide is used as a positive reference control. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as being capable of affecting glucose and/or FFA uptake in this assay: PRO202, PRO211, PRO344 and PRO1338.

#### EXAMPLE 19: Gene Expression in Bovine Pericytes (Assay 105)

This assay is designed to identify PRO polypeptides which activate gene expression in pericytes. Such polypeptides would be expected to be useful as growth factors and/or for situations where the activation of gene expression is desired or beneficial. Bovine pericytes are plated on 60mm culture dishes in growth media for 1 week. On day 1, various PRO polypeptides are diluted (1%) and incubated with the pericytes for 1, 4 and 24 hr. timepoints. The cells are harvested and the RNA isolated using TRI-Reagent following the included instructions. The RNA is then quantified by reading the 260/280 OD using a spectrophotometer. The gene expression analysis is done by TaqMan reactions using Perkin Elmer reagents and specially designed bovine probes and primers. Expression of the following genes is analyzed: GAPDH, beta-integrin, connective tissue growth factor (CTGF), ICAM-1, monocyte chemoattractant protein-1 (MCP-1), osteopontin, transforming growth factor-beta (TGF-beta), TGF-beta receptor, tissue inhibitor of metalloproteinase (TIMP), tissue factor (TF), VEGF- $\alpha$ , thrombospondin, VEGF- $\beta$ , angiopoietin-2, and collagenase. Replicates are then averaged and the SD determined. The gene expression levels are then normalized to GAPDH. These are then normalized to the expression levels obtained with a protein (PIN32) which does not significantly induce gene expression in bovine pericytes when compared to untreated controls. Any PRO polypeptide that gives a gene expression level 2-fold or higher over the PIN32 control is considered a positive hit.

The following PRO polypeptides tested positive in this assay: PRO366.

#### EXAMPLE 20: Identification of PRO Polypeptides That Activate Pericytes (Assay 125)

This assay shows that certain polypeptides of the invention act to activate proliferation of pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Such PRO polypeptides also would be expected to be useful as growth factors and/or for situations where the induction of cell proliferation is desired or beneficial. Activation of pericyte proliferation also correlates with the induction of angiogenesis and, as such, PRO polypeptides capable of inducing pericyte proliferation would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received

from VEC Technologies, and all but 5 ml media is removed from the flask. On day 2, the pericytes are trypsinized, washed, spun and plated on 96 well plates. On day 7, the media is removed and the pericytes are treated with 100  $\mu$ l of either the specific PRO polypeptide or control treatments (positive control = DME+5% +/- PDGF @ 500ng/ $\mu$ l; negative control=PIN32, a polypeptide determined to have no significant effect on pericyte proliferation). C-fos and GAPDH gene expression levels are then determined and the replicates are averaged and the SD is determined. The c-fos values are normalized to GAPDH and the results are expressed as fold increase over PIN32. Anything providing at least a 2-fold or higher response as compared to the negative control is considered positive for the assay.

The following polypeptides tested positive in this assay: PRO366.

10 **EXAMPLE 21: Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)**

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

15 The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO<sub>2</sub> in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100U/ml penicillin and 100 $\mu$ g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 20 18 ng/ml interleukin-1 $\alpha$ , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, *Biochem. Biophys. Acta* 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

25 When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 $\alpha$  and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The polypeptides testing positive in this assay are : PRO216.

30 **EXAMPLE 22: Proliferation of Rat Utricular Supporting Cells (Assay 54)**

35 This assay shows that certain polypeptides of the invention act as potent mitogens for inner ear supporting cells which are auditory hair cell progenitors and, therefore, are useful for inducing the regeneration of auditory hair cells and treating hearing loss in mammals. The assay is performed as follows. Rat UEC-4 utricular epithelial cells are aliquoted into 96 well plates with a density of 3000 cells/well in 200  $\mu$ l of serum-containing medium at 33°C. The cells are cultured overnight and are then switched to serum-free medium at

37°C. Various dilutions of PRO polypeptides (or nothing for a control) are then added to the cultures and the cells are incubated for 24 hours. After the 24 hour incubation, <sup>3</sup>H-thymidine (1 µCi/well) is added and the cells are then cultured for an additional 24 hours. The cultures are then washed to remove unincorporated radiolabel, the cells harvested and Cpm per well determined. Cpm of at least 30% or greater in the PRO polypeptide treated cultures as compared to the control cultures is considered a positive in the assay.

5 The following polypeptides tested positive in this assay: PRO172.

**EXAMPLE 23: Stimulatory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 24)**

10 This example shows that certain polypeptides of the invention are active as a stimulator of the proliferation of stimulated T-lymphocytes. Compounds which stimulate proliferation of lymphocytes are useful therapeutically where enhancement of an immune response is beneficial. A therapeutic agent may take the form of antagonists of the polypeptide of the invention, for example, murine-human chimeric, humanized or human antibodies against the polypeptide.

15 The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc.

20 More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37°C, 5% CO<sub>2</sub>) and then washed and resuspended to 3x10<sup>6</sup> cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

The assay is prepared by plating in triplicate wells a mixture of:

100:1 of test sample diluted to 1% or to 0.1%,

25 50 :1 of irradiated stimulator cells, and

50 :1 of responder PBMC cells.

100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37°C, 5% CO<sub>2</sub> for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mCi/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

30 In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to 1x10<sup>7</sup> cells/ml of assay media. The assay is then conducted as described above.

35 Positive increases over control are considered positive with increases of greater than or equal to 180% being preferred. However, any value greater than control indicates a stimulatory effect for the test protein.

The following PRO polypeptides tested positive in this assay: PRO344.

**EXAMPLE 24: Pericyte c-Fos Induction (Assay 93)**

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100  $\mu$ l of PRO polypeptide test samples and controls (positive control = DME+5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM +5% FBS.

The following polypeptides tested positive in this assay: PRO301, PRO619, PRO1066 and PRO1265.

**EXAMPLE 25: Cytokine Release Assay (Assay 120)**

This assay is designed to determine whether PRO polypeptides of the present invention are capable of inducing the release of cytokines from peripheral blood mononuclear cells (PBMCs). PRO polypeptides capable of inducing the release of cytokines from PBMCs are useful from the treatment of conditions which would benefit from enhanced cytokine release and will be readily evident to those of ordinary skill in the art. Specifically,  $1 \times 10^6$  cells/ml of peripheral blood mononuclear cells (PBMC) are cultured with 1% of a PRO polypeptide for 3 days in complete RPMI media. The supernatant is then harvested and tested for increased concentrations of various cytokines by ELISA as compared to a human IgG treated control. A positive in the assay is a 10-fold or greater increase in cytokine concentration in the PRO polypeptide treated sample as compared to the human IgG treated control.

The following polypeptides tested positive in this assay: PRO526 and PRO1343.

**EXAMPLE 26: Inhibition of A-Peptide Binding to Factor VIIA (Assay 118)**

This assay is designed to identify PRO polypeptides which are capable of inhibiting the binding of A-peptide to factor VIIA, thereby affecting the blood coagulation cascade. PRO polypeptides testing positive in this assay are expected to be useful for the treatment of conditions where alteration of the blood coagulation cascade would be beneficial including, for example, stroke, heart attack and various coagulation disorders. These PRO polypeptides are also useful for the identification of agonist and antagonist molecules which would

also be useful for treatment of those conditions.

Specifically, 384 well plates are coated with soluble factor VIIA and are incubated overnight at 4°C. The wells are then decanted and are blocked by the addition of 0.5% BSA for 1 hour. The wells are then washed and 20µl of biotinylated A-peptide and either various concentration of the PRO polypeptide (test) or nothing (negative control) are added to each well. The plates are then incubated for 1 hour at room temperature. The wells are again washed and then 40µl of streptavidin-europium is added to each well. The plates are then incubated for 30 minutes at room temperature and then washed. 40µl of a fluorescence enhancement solution is then added to each well, the plates incubated for 5 minutes at room temperature and each well is then read on Wallac Victor reader under europium delayed fluorescence settings. Percent inhibition of binding of the A-peptide to the factor VIIA is then determined (as compared to the negative control), wherein a positive in the assay is a percent inhibition of 30% or greater.

The following PRO polypeptides tested positive in this assay: PRO182.

EXAMPLE 27: Inhibition of Adipocyte Differentiation Assay (Assay 66)

This assay is designed to identify PRO polypeptides which are capable of inhibiting insulin-induced differentiation of adipocytes. PRO polypeptides testing positive in this assay would be expected to be useful for the treatment of conditions associated with obesity, diabetes, etc.

Specifically, 3T3-L1 cells are seeded into the wells of 96 well plates at  $6 \times 10^4$  cells/well and allowed to grow to confluency for 7 days. At day 7, the cells are treated with various concentrations of the PRO polypeptide (or nothing for the negative control) in the presence of 1µg/ml insulin,  $0.25 \times 10^{-6}$  M dexamethasone and 0.5mM IBMX. The samples are then incubated at 37°C in 7% CO<sub>2</sub> for 2 days. After the incubation, the media is removed by aspiration and the cells are washed with PBS and re-exposed to the PRO polypeptide (or nothing for the negative control) and 1µg/ml insulin. After 5 days, the media is removed and replaced with fresh PRO polypeptide (or nothing for the negative control) and insulin. After 5 days, the cells are lysed and the cell lysate is assayed using Sigma's Triglyceride [INT] kit (Sigma procedure #336). A positive in the assay is 20% greater inhibition of adipocyte differentiation in the PRO polypeptide treated samples as compared to the negative control.

The following PRO polypeptides tested positive in this assay: PRO185 and PRO198.

EXAMPLE 28: HUVEC Stimulation by PRO Polypeptides (Assay 131)

This assay is designed to identify PRO polypeptides which are capable of stimulating the proliferation of HUVEC cells. PRO polypeptides testing positive in this assay would be expected to be useful for inducing angiogenesis for the treatment of conditions where angiogenesis would be beneficial including, for example, wound healing, and the like. Antagonists of these PRO polypeptides would be expected to be useful for inhibiting angiogenesis for the treatment of, for example, tumors, and the like.

Specifically, COSTAR® flat bottom black plates are treated with fibronectin for 20 minutes and then washed twice with PBS. HUVEC cells are then plated at 2000 cells/well in an appropriate growth medium. The plates are then incubated overnight and then the PRO polypeptide (1% final concentration), nothing (negative

control) or IL1 $\beta$  (3.3 ng/ml final concentration; positive control) is added. The plates are again incubated overnight, stained with ICAM1-Cy5 and read on FMAT. A positive in the assay is a 2-fold or greater increase in fluorescence as compared to the positive control.

The following PRO polypeptides tested positive in this assay: PRO222.

5 **EXAMPLE 29: Promotion of Chondrocyte Redifferentiation (Assay 129)**

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

10 Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4  $\mu$ g/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 $\mu$ l of the same media without serum and 100  $\mu$ l of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200  $\mu$ l/well. After 5 days at 37°C, 22  $\mu$ l of media containing 100 $\mu$ g/ml Hoechst 33342 and 50  $\mu$ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the > 50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

20 The following PRO polypeptides tested positive in this assay: PRO301.

**EXAMPLE 30: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors**

25 Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

35 The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and



hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

Table 8

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO177	breast tumor	universal normal control
PRO177	liver tumor	universal normal control
PRO177	lung tumor	universal normal control
PRO3574	breast tumor	universal normal control
PRO3574	colon tumor	matched normal colon control
PRO1280	breast tumor	universal normal control
PRO1280	lung tumor	universal normal control
PRO4984	lung tumor	universal normal control
PRO4988	colon tumor	universal normal control
PRO4988	lung tumor	universal normal control
PRO305	lung tumor	universal normal control
PRO305	colon tumor	universal normal control
PRO1866	prostate tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1866	lung tumor	universal normal control
	PRO1866	colon tumor	universal normal control
	PRO4996	breast tumor	universal normal control
5	PRO4996	lung tumor	universal normal control
	PRO4406	lung tumor	universal normal control
	PRO4406	colon tumor	universal normal control
	PRO1120	colon tumor	universal normal control
	PRO1120	breast tumor	universal normal control
10	PRO1120	rectal tumor	universal normal control
	PRO4990	lung tumor	universal normal control
	PRO738	cervical tumor	universal normal control
	PRO738	lung tumor	universal normal control
	PRO738	breast tumor	universal normal control
15	PRO3577	lung tumor	universal normal control
	PRO1879	breast tumor	universal normal control
	PRO1879	lung tumor	universal normal control
	PRO1879	colon tumor	universal normal control
	PRO1471	lung tumor	universal normal control
20	PRO1076	prostate tumor	universal normal control
	PRO1483	lung tumor	universal normal control
	PRO4985	rectal tumor	universal normal control
	PRO4985	colon tumor	universal normal control
	PRO4985	breast tumor	universal normal control
25	PRO4985	lung tumor	universal normal control
	PRO5000	lung tumor	universal normal control
	PRO1881	liver tumor	universal normal control
	PRO1881	lung tumor	universal normal control
	PRO1881	breast tumor	universal normal control
30	PRO4314	lung tumor	universal normal control
	PRO4314	breast tumor	universal normal control
	PRO4987	lung tumor	universal normal control
	PRO4313	lung tumor	universal normal control
	PRO4313	breast tumor	universal normal control
35	PRO4799	colon tumor	universal normal control
	PRO4995	liver tumor	universal normal control
	PRO4995	colon tumor	universal normal control
	PRO4995	colon tumor	matched normal colon control
40	PRO1341	prostate tumor	universal normal control
	PRO1341	lung tumor	universal normal control
	PRO1341	colon tumor	universal normal control
	PRO1341	colon tumor	matched normal colon control
	PRO1777	lung tumor	universal normal control
	PRO1777	colon tumor	matched normal colon control
45	PRO3580	lung tumor	universal normal control
	PRO3580	prostate tumor	universal normal control
	PRO1779	lung tumor	universal normal control
	PRO1779	colon tumor	universal normal control
	PRO1779	cervical tumor	universal normal control
50	PRO1754	breast tumor	universal normal control
	PRO1754	lung tumor	universal normal control
	PRO1906	breast tumor	universal normal control
	PRO1906	colon tumor	universal normal control
55	PRO1906	prostate tumor	universal normal control
	PRO1870	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4329	lung tumor	universal normal control
	PRO4979	colon tumor	universal normal control
	PRO1885	rectal tumor	universal normal control
5	PRO1885	colon tumor	universal normal control
	PRO1885	colon tumor	matched normal colon control
	PRO1882	prostate tumor	universal normal control
	PRO1882	lung tumor	universal normal control
	PRO1882	colon tumor	universal normal control
10	PRO1882	breast tumor	universal normal control
	PRO1882	cervical tumor	universal normal control
	PRO4989	rectal tumor	universal normal control
	PRO4989	breast tumor	universal normal control
	PRO4989	colon tumor	matched normal colon control
15	PRO4989	colon tumor	universal normal control
	PRO4323	lung tumor	universal normal control
	PRO4323	liver tumor	universal normal control
	PRO1886	breast tumor	universal normal control
	PRO1886	lung tumor	universal normal control
20	PRO1886	rectal tumor	universal normal control
	PRO4395	colon tumor	universal normal control
	PRO4395	prostate tumor	universal normal control
	PRO4395	lung tumor	universal normal control
	PRO4395	cervical tumor	universal normal control
25	PRO1782	colon tumor	universal normal control
	PRO1782	lung tumor	universal normal control
	PRO4388	lung tumor	universal normal control
	PRO4341	breast tumor	universal normal control
	PRO4341	lung tumor	universal normal control
30	PRO3438	lung tumor	universal normal control
	PRO4321	breast tumor	universal normal control
	PRO4321	lung tumor	universal normal control
	PRO4321	colon tumor	universal normal control
	PRO4304	breast tumor	universal normal control
35	PRO4304	lung tumor	universal normal control
	PRO4403	colon tumor	universal normal control
	PRO4403	breast tumor	universal normal control
	PRO4403	lung tumor	universal normal control
	PRO4324	lung tumor	universal normal control
40	PRO4324	breast tumor	universal normal control
	PRO4303	cervical tumor	universal normal control
	PRO4303	lung tumor	universal normal control
	PRO4303	breast tumor	universal normal control
	PRO4303	colon tumor	universal normal control
45	PRO4303	prostate tumor	universal normal control
	PRO4305	breast tumor	universal normal control
	PRO4305	lung tumor	universal normal control
	PRO4305	colon tumor	universal normal control
	PRO4305	liver tumor	universal normal control
50	PRO4404	lung tumor	universal normal control
	PRO4404	breast tumor	universal normal control
	PRO4404	rectal tumor	universal normal control
	PRO1884	lung tumor	universal normal control
	PRO4349	colon tumor	universal normal control
55	PRO4349	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4401	colon tumor	universal normal control
	PRO4401	lung tumor	universal normal control
	PRO1867	lung tumor	universal normal control
5	PRO1867	liver tumor	universal normal control
	PRO4319	breast tumor	universal normal control
	PRO4319	lung tumor	universal normal control
	PRO4991	lung tumor	universal normal control
	PRO4991	colon tumor	universal normal control
10	PRO4398	lung tumor	universal normal control
	PRO4346	lung tumor	universal normal control
	PRO4350	colon tumor	universal normal control
	PRO4350	prostate tumor	universal normal control
	PRO4350	lung tumor	universal normal control
15	PRO4318	prostate tumor	universal normal control
	PRO4318	lung tumor	universal normal control
	PRO4340	breast tumor	universal normal control
	PRO4340	lung tumor	universal normal control
	PRO4400	breast tumor	universal normal control
20	PRO4400	lung tumor	universal normal control
	PRO4320	lung tumor	universal normal control
	PRO4409	lung tumor	universal normal control
	PRO4409	cervical tumor	universal normal control
	PRO4409	colon tumor	universal normal control
25	PRO4399	lung tumor	universal normal control
	PRO4399	breast tumor	universal normal control
	PRO4418	lung tumor	universal normal control
	PRO4418	breast tumor	universal normal control
	PRO4330	cervical tumor	universal normal control
30	PRO4330	colon tumor	matched normal colon control
	PRO4339	breast tumor	universal normal control
	PRO4339	colon tumor	universal normal control
	PRO4326	lung tumor	universal normal control
	PRO4326	colon tumor	universal normal control
35	PRO6014	breast tumor	universal normal control
	PRO3446	colon tumor	universal normal control
	PRO3446	lung tumor	universal normal control
	PRO4322	lung tumor	universal normal control
	PRO4322	rectal tumor	universal normal control
40	PRO4322	colon tumor	matched normal colon control
	PRO4381	breast tumor	universal normal control
	PRO4381	lung tumor	universal normal control
	PRO4381	colon tumor	universal normal control
	PRO4348	lung tumor	universal normal control
45	PRO4348	prostate tumor	universal normal control
	PRO4371	breast tumor	universal normal control
	PRO3742	colon tumor	universal normal control
	PRO3742	lung tumor	universal normal control
	PRO5773	lung tumor	universal normal control
50	PRO5773	colon tumor	universal normal control
	PRO5773	prostate tumor	universal normal control
	PRO5774	colon tumor	universal normal control
	PRO4343	colon tumor	universal normal control
	PRO4325	lung tumor	universal normal control
55	PRO4347	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4347	colon tumor	universal normal control
	PRO4347	rectal tumor	universal normal control
	PRO3743	colon tumor	universal normal control
5	PRO3743	lung tumor	universal normal control
	PRO3743	prostate tumor	universal normal control
	PRO4426	colon tumor	universal normal control
	PRO4500	colon tumor	universal normal control
	PRO4389	breast tumor	universal normal control
10	PRO4389	lung tumor	universal normal control
	PRO4337	colon tumor	universal normal control
	PRO4337	breast tumor	universal normal control
	PRO4337	lung tumor	universal normal control
	PRO4992	lung tumor	universal normal control
15	PRO5996	lung tumor	universal normal control
	PRO4345	lung tumor	universal normal control
	PRO4345	colon tumor	universal normal control
	PRO5780	lung tumor	universal normal control
	PRO5780	breast tumor	universal normal control
20	PRO5992	lung tumor	universal normal control
	PRO5992	colon tumor	universal normal control
	PRO5992	breast tumor	universal normal control
	PRO4428	prostate tumor	universal normal control
	PRO4994	lung tumor	universal normal control
25	PRO5995	lung tumor	universal normal control
	PRO5995	colon tumor	universal normal control
	PRO6094	lung tumor	universal normal control
	PRO6094	colon tumor	universal normal control
	PRO4317	lung tumor	universal normal control
30	PRO4317	colon tumor	universal normal control
	PRO4317	liver tumor	universal normal control
	PRO4317	colon tumor	matched normal colon control
	PRO5997	colon tumor	universal normal control
	PRO5997	lung tumor	universal normal control
35	PRO5005	lung tumor	universal normal control
	PRO5005	colon tumor	universal normal control
	PRO5004	colon tumor	universal normal control
	PRO6001	breast tumor	universal normal control
	PRO6013	colon tumor	universal normal control
40	PRO4502	lung tumor	universal normal control
	PRO4502	colon tumor	universal normal control
	PRO6007	breast tumor	universal normal control
	PRO6028	breast tumor	universal normal control
	PRO6028	colon tumor	universal normal control
45	PRO4327	prostate tumor	universal normal control
	PRO4315	colon tumor	universal normal control
	PRO5993	lung tumor	universal normal control
	PRO5993	colon tumor	universal normal control
	PRO4503	colon tumor	universal normal control
50	PRO4976	lung tumor	universal normal control
	PRO5798	lung tumor	universal normal control
	PRO5798	colon tumor	universal normal control
	PRO6242	colon tumor	universal normal control
	PRO6242	colon tumor	matched normal colon control
55	PRO6242	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO6242	liver tumor	universal normal control
	PRO6242	rectal tumor	universal normal control
	PRO6095	breast tumor	universal normal control
5	PRO6095	lung tumor	universal normal control
	PRO6093	colon tumor	universal normal control
	PRO6093	breast tumor	universal normal control
	PRO6093	lung tumor	universal normal control
	PRO6093	colon tumor	universal normal control
10	PRO6012	colon tumor	matched normal colon control
	PRO6027	lung tumor	universal normal control
	PRO6027	colon tumor	universal normal control
	PRO6027	rectal tumor	universal normal control
	PRO6181	prostate tumor	universal normal control
15	PRO6181	lung tumor	universal normal control
	PRO6181	colon tumor	universal normal control
	PRO6097	colon tumor	universal normal control
	PRO6097	lung tumor	universal normal control
	PRO6090	lung tumor	universal normal control
20	PRO7171	lung tumor	universal normal control
	PRO7171	colon tumor	universal normal control
	PRO7171	breast tumor	universal normal control
	PRO6258	prostate tumor	universal normal control
	PRO6258	breast tumor	universal normal control
25	PRO6258	cervical tumor	universal normal control
	PRO6258	liver tumor	universal normal control
	PRO6258	colon tumor	universal normal control
	PRO9820	prostate tumor	universal normal control
	PRO6243	lung tumor	universal normal control
30	PRO6182	lung tumor	universal normal control
	PRO6079	lung tumor	universal normal control
	PRO6079	colon tumor	universal normal control
	PRO6079	breast tumor	universal normal control
	PRO6079	prostate tumor	universal normal control
35	PRO7434	lung tumor	universal normal control
	PRO9865	colon tumor	universal normal control
	PRO9828	colon tumor	universal normal control
	PRO196	colon tumor	universal normal control
	PRO196	lung tumor	universal normal control
40	PRO196	breast tumor	universal normal control
	PRO197	colon tumor	universal normal control
	PRO197	lung tumor	universal normal control
	PRO197	breast tumor	universal normal control
	PRO195	colon tumor	universal normal control
45	PRO195	lung tumor	universal normal control
	PRO195	breast tumor	universal normal control
	PRO187	lung tumor	universal normal control
	PRO187	liver tumor	universal normal control
	PRO182	colon tumor	universal normal control
50	PRO182	lung tumor	universal normal control
	PRO182	breast tumor	universal normal control
	PRO188	rectal tumor	universal normal control
	PRO183	colon tumor	universal normal control
	PRO183	lung tumor	universal normal control
55	PRO183	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO183	rectal tumor	universal normal control
	PRO184	lung tumor	universal normal control
	PRO184	breast tumor	universal normal control
5	PRO185	lung tumor	universal normal control
	PRO200	colon tumor	universal normal control
	PRO200	lung tumor	universal normal control
	PRO200	breast tumor	universal normal control
	PRO200	rectal tumor	universal normal control
10	PRO202	colon tumor	universal normal control
	PRO202	lung tumor	universal normal control
	PRO202	breast tumor	universal normal control
	PRO202	rectal tumor	universal normal control
	PRO202	liver tumor	universal normal control
15	PRO214	colon tumor	universal normal control
	PRO214	lung tumor	universal normal control
	PRO215	colon tumor	universal normal control
	PRO215	lung tumor	universal normal control
	PRO215	breast tumor	universal normal control
20	PRO219	colon tumor	universal normal control
	PRO219	lung tumor	universal normal control
	PRO219	breast tumor	universal normal control
	PRO219	liver tumor	universal normal control
	PRO211	lung tumor	universal normal control
25	PRO211	breast tumor	universal normal control
	PRO220	colon tumor	universal normal control
	PRO220	lung tumor	universal normal control
	PRO220	breast tumor	universal normal control
	PRO366	colon tumor	universal normal control
30	PRO366	lung tumor	universal normal control
	PRO366	breast tumor	universal normal control
	PRO216	lung tumor	universal normal control
	PRO221	colon tumor	universal normal control
	PRO221	lung tumor	universal normal control
35	PRO221	breast tumor	universal normal control
	PRO228	lung tumor	universal normal control
	PRO228	breast tumor	universal normal control
	PRO217	lung tumor	universal normal control
	PRO217	breast tumor	universal normal control
40	PRO222	colon tumor	universal normal control
	PRO222	lung tumor	universal normal control
	PRO222	breast tumor	universal normal control
	PRO224	colon tumor	universal normal control
	PRO224	lung tumor	universal normal control
45	PRO224	breast tumor	universal normal control
	PRO224	prostate tumor	universal normal control
	PRO224	rectal tumor	universal normal control
	PRO230	colon tumor	universal normal control
	PRO230	lung tumor	universal normal control
50	PRO230	breast tumor	universal normal control
	PRO230	prostate tumor	universal normal control
	PRO198	colon tumor	universal normal control
	PRO198	lung tumor	universal normal control
	PRO198	breast tumor	universal normal control
55	PRO198	liver tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO226	lung tumor	universal normal control
	PRO226	breast tumor	universal normal control
5	PRO261	lung tumor	universal normal control
	PRO242	colon tumor	universal normal control
	PRO242	lung tumor	universal normal control
	PRO242	breast tumor	universal normal control
	PRO227	colon tumor	universal normal control
	PRO227	lung tumor	universal normal control
10	PRO237	colon tumor	universal normal control
	PRO237	lung tumor	universal normal control
	PRO237	breast tumor	universal normal control
	PRO237	prostate tumor	universal normal control
	PRO241	colon tumor	universal normal control
15	PRO241	lung tumor	universal normal control
	PRO241	breast tumor	universal normal control
	PRO231	colon tumor	universal normal control
	PRO231	lung tumor	universal normal control
	PRO231	breast tumor	universal normal control
20	PRO231	rectal tumor	universal normal control
	PRO235	colon tumor	universal normal control
	PRO235	lung tumor	universal normal control
	PRO235	breast tumor	universal normal control
	PRO235	liver tumor	universal normal control
25	PRO323	lung tumor	universal normal control
	PRO323	breast tumor	universal normal control
	PRO323	rectal tumor	universal normal control
	PRO245	colon tumor	universal normal control
	PRO245	lung tumor	universal normal control
30	PRO245	breast tumor	universal normal control
	PRO245	cervical tumor	universal normal control
	PRO245	liver tumor	universal normal control
	PRO246	colon tumor	universal normal control
	PRO246	lung tumor	universal normal control
35	PRO246	breast tumor	universal normal control
	PRO288	lung tumor	universal normal control
	PRO288	breast tumor	universal normal control
	PRO248	lung tumor	universal normal control
	PRO248	rectal tumor	universal normal control
40	PRO257	colon tumor	universal normal control
	PRO257	lung tumor	universal normal control
	PRO257	prostate tumor	universal normal control
	PRO172	colon tumor	universal normal control
	PRO172	lung tumor	universal normal control
45	PRO172	breast tumor	universal normal control
	PRO258	colon tumor	universal normal control
	PRO258	lung tumor	universal normal control
	PRO258	breast tumor	universal normal control
	PRO265	lung tumor	universal normal control
50	PRO265	breast tumor	universal normal control
	PRO265	rectal tumor	universal normal control
	PRO326	colon tumor	universal normal control
	PRO326	lung tumor	universal normal control
	PRO326	breast tumor	universal normal control
55	PRO326	liver tumor	universal normal control



Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO266	colon tumor	universal normal control
	PRO266	lung tumor	universal normal control
	PRO266	breast tumor	universal normal control
5	PRO269	lung tumor	universal normal control
	PRO269	rectal tumor	universal normal control
	PRO285	colon tumor	universal normal control
	PRO285	lung tumor	universal normal control
	PRO285	breast tumor	universal normal control
10	PRO328	colon tumor	universal normal control
	PRO328	lung tumor	universal normal control
	PRO328	breast tumor	universal normal control
	PRO344	breast tumor	universal normal control
	PRO272	lung tumor	universal normal control
15	PRO301	colon tumor	universal normal control
	PRO301	lung tumor	universal normal control
	PRO301	breast tumor	universal normal control
	PRO331	colon tumor	universal normal control
	PRO331	lung tumor	universal normal control
20	PRO331	breast tumor	universal normal control
	PRO332	colon tumor	universal normal control
	PRO332	lung tumor	universal normal control
	PRO332	breast tumor	universal normal control
	PRO353	colon tumor	universal normal control
25	PRO353	lung tumor	universal normal control
	PRO353	breast tumor	universal normal control
	PRO310	colon tumor	universal normal control
	PRO310	lung tumor	universal normal control
	PRO310	breast tumor	universal normal control
30	PRO310	rectal tumor	universal normal control
	PRO337	colon tumor	universal normal control
	PRO337	lung tumor	universal normal control
	PRO337	breast tumor	universal normal control
	PRO346	lung tumor	universal normal control
35	PRO350	lung tumor	universal normal control
	PRO350	breast tumor	universal normal control
	PRO526	colon tumor	universal normal control
	PRO526	lung tumor	universal normal control
	PRO526	breast tumor	universal normal control
40	PRO381	colon tumor	universal normal control
	PRO381	lung tumor	universal normal control
	PRO381	breast tumor	universal normal control
	PRO381	prostate tumor	universal normal control
	PRO846	colon tumor	universal normal control
45	PRO846	lung tumor	universal normal control
	PRO363	colon tumor	universal normal control
	PRO363	lung tumor	universal normal control
	PRO365	lung tumor	universal normal control
	PRO365	breast tumor	universal normal control
50	PRO1310	breast tumor	universal normal control
	PRO731	colon tumor	universal normal control
	PRO731	lung tumor	universal normal control
	PRO731	breast tumor	universal normal control
	PRO322	colon tumor	universal normal control
55	PRO322	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO322	breast tumor	universal normal control
	PRO322	rectal tumor	universal normal control
	PRO322	liver tumor	universal normal control
5	PRO536	lung tumor	universal normal control
	PRO536	breast tumor	universal normal control
	PRO536	liver tumor	universal normal control
	PRO719	colon tumor	universal normal control
	PRO719	lung tumor	universal normal control
10	PRO719	breast tumor	universal normal control
	PRO619	colon tumor	universal normal control
	PRO619	lung tumor	universal normal control
	PRO619	breast tumor	universal normal control
	PRO771	colon tumor	universal normal control
15	PRO771	lung tumor	universal normal control
	PRO771	breast tumor	universal normal control
	PRO1083	colon tumor	universal normal control
	PRO1083	lung tumor	universal normal control
	PRO1083	breast tumor	universal normal control
20	PRO1083	prostate tumor	universal normal control
	PRO862	colon tumor	universal normal control
	PRO862	lung tumor	universal normal control
	PRO862	breast tumor	universal normal control
	PRO733	colon tumor	universal normal control
25	PRO733	lung tumor	universal normal control
	PRO733	breast tumor	universal normal control
	PRO733	liver tumor	universal normal control
	PRO1188	lung tumor	universal normal control
	PRO1188	breast tumor	universal normal control
30	PRO1188	rectal tumor	universal normal control
	PRO770	lung tumor	universal normal control
	PRO770	breast tumor	universal normal control
	PRO1080	colon tumor	universal normal control
	PRO1080	lung tumor	universal normal control
35	PRO1080	breast tumor	universal normal control
	PRO1017	colon tumor	universal normal control
	PRO1017	lung tumor	universal normal control
	PRO1017	breast tumor	universal normal control
	PRO1016	colon tumor	universal normal control
40	PRO1016	lung tumor	universal normal control
	PRO1016	breast tumor	universal normal control
	PRO1016	rectal tumor	universal normal control
	PRO792	lung tumor	universal normal control
	PRO938	colon tumor	universal normal control
45	PRO938	lung tumor	universal normal control
	PRO938	breast tumor	universal normal control
	PRO1012	colon tumor	universal normal control
	PRO1012	lung tumor	universal normal control
	PRO1012	rectal tumor	universal normal control
50	PRO1012	liver tumor	universal normal control
	PRO1008	lung tumor	universal normal control
	PRO1075	colon tumor	universal normal control
	PRO1075	lung tumor	universal normal control
	PRO1007	colon tumor	universal normal control
55	PRO1007	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1007	breast tumor	universal normal control
	PRO1007	rectal tumor	universal normal control
	PRO1056	colon tumor	universal normal control
5	PRO1056	lung tumor	universal normal control
	PRO1056	breast tumor	universal normal control
	PRO791	colon tumor	universal normal control
	PRO791	lung tumor	universal normal control
	PRO791	breast tumor	universal normal control
10	PRO791	rectal tumor	universal normal control
	PRO1111	colon tumor	universal normal control
	PRO1111	lung tumor	universal normal control
	PRO1111	breast tumor	universal normal control
	PRO812	lung tumor	universal normal control
15	PRO812	breast tumor	universal normal control
	PRO812	rectal tumor	universal normal control
	PRO1066	lung tumor	universal normal control
	PRO1185	colon tumor	universal normal control
	PRO1185	lung tumor	universal normal control
20	PRO1185	breast tumor	universal normal control
	PRO1031	lung tumor	universal normal control
	PRO1360	lung tumor	universal normal control
	PRO1360	breast tumor	universal normal control
	PRO1309	lung tumor	universal normal control
25	PRO1309	breast tumor	universal normal control
	PRO1107	lung tumor	universal normal control
	PRO1107	breast tumor	universal normal control
	PRO836	colon tumor	universal normal control
	PRO836	lung tumor	universal normal control
30	PRO1132	lung tumor	universal normal control
	PRO1132	breast tumor	universal normal control
	PRO1131	colon tumor	universal normal control
	PRO1131	lung tumor	universal normal control
	PRO1131	breast tumor	universal normal control
35	PRO1131	liver tumor	universal normal control
	PRO1130	colon tumor	universal normal control
	PRO1130	lung tumor	universal normal control
	PRO1130	breast tumor	universal normal control
	PRO844	colon tumor	universal normal control
40	PRO844	lung tumor	universal normal control
	PRO844	breast tumor	universal normal control
	PRO844	rectal tumor	universal normal control
	PRO1154	colon tumor	universal normal control
	PRO1154	lung tumor	universal normal control
45	PRO1154	rectal tumor	universal normal control
	PRO1154	liver tumor	universal normal control
	PRO1181	lung tumor	universal normal control
	PRO1181	breast tumor	universal normal control
	PRO1126	colon tumor	universal normal control
50	PRO1126	lung tumor	universal normal control
	PRO1126	breast tumor	universal normal control
	PRO1126	adrenal tumor	universal normal control
	PRO1186	colon tumor	universal normal control
	PRO1186	lung tumor	universal normal control
55	PRO1186	breast tumor	universal normal control

Table 8 (cont')

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO1186	liver tumor	universal normal control
PRO1198	colon tumor	universal normal control
PRO1198	lung tumor	universal normal control
5 PRO1159	lung tumor	universal normal control
PRO1159	breast tumor	universal normal control
PRO1159	liver tumor	universal normal control
PRO1265	colon tumor	universal normal control
PRO1265	breast tumor	universal normal control
10 PRO1250	colon tumor	universal normal control
PRO1250	lung tumor	universal normal control
PRO1250	breast tumor	universal normal control
PRO1475	colon tumor	universal normal control
PRO1475	breast tumor	universal normal control
15 PRO1312	colon tumor	universal normal control
PRO1312	lung tumor	universal normal control
PRO1312	breast tumor	universal normal control
PRO1308	colon tumor	universal normal control
PRO1308	lung tumor	universal normal control
20 PRO1308	liver tumor	universal normal control
PRO1326	colon tumor	universal normal control
PRO1325	lung tumor	universal normal control
PRO1326	breast tumor	universal normal control
PRO1192	colon tumor	universal normal control
25 PRO1192	lung tumor	universal normal control
PRO1192	breast tumor	universal normal control
PRO1246	colon tumor	universal normal control
PRO1246	lung tumor	universal normal control
PRO1246	breast tumor	universal normal control
30 PRO1246	prostate tumor	universal normal control
PRO1356	colon tumor	universal normal control
PRO1356	lung tumor	universal normal control
PRO1356	breast tumor	universal normal control
PRO1275	lung tumor	universal normal control
35 PRO1275	breast tumor	universal normal control
PRO1274	lung tumor	universal normal control
PRO1358	colon tumor	universal normal control
PRO1358	lung tumor	universal normal control
PRO1358	prostate tumor	universal normal control
40 PRO1286	colon tumor	universal normal control
PRO1286	lung tumor	universal normal control
PRO1286	prostate tumor	universal normal control
PRO1286	rectal tumor	universal normal control
PRO1294	colon tumor	universal normal control
45 PRO1294	lung tumor	universal normal control
PRO1294	breast tumor	universal normal control
PRO1294	rectal tumor	universal normal control
PRO1273	lung tumor	universal normal control
PRO1273	rectal tumor	universal normal control
50 PRO1279	colon tumor	universal normal control
PRO1279	lung tumor	universal normal control
PRO1195	lung tumor	universal normal control
PRO1195	breast tumor	universal normal control
PRO1271	lung tumor	universal normal control
55 PRO1271	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1271	liver tumor	universal normal control
	PRO1338	colon tumor	universal normal control
	PRO1338	lung tumor	universal normal control
5	PRO1338	breast tumor	universal normal control
	PRO1343	colon tumor	universal normal control
	PRO1343	lung tumor	universal normal control
	PRO1343	breast tumor	universal normal control
	PRO1343	rectal tumor	universal normal control
10	PRO1434	lung tumor	universal normal control
	PRO1418	lung tumor	universal normal control
	PRO1418	liver tumor	universal normal control
	PRO1387	colon tumor	universal normal control
	PRO1387	lung tumor	universal normal control
15	PRO1387	prostate tumor	universal normal control
	PRO1387	rectal tumor	universal normal control
	PRO1384	colon tumor	universal normal control
	PRO1384	lung tumor	universal normal control
	PRO1565	colon tumor	universal normal control
20	PRO1565	lung tumor	universal normal control
	PRO1565	prostate tumor	universal normal control
	PRO1474	colon tumor	universal normal control
	PRO1474	lung tumor	universal normal control
	PRO1474	breast tumor	universal normal control
25	PRO1474	rectal tumor	universal normal control
	PRO1917	colon tumor	universal normal control
	PRO1917	lung tumor	universal normal control
	PRO1917	breast tumor	universal normal control
	PRO1787	colon tumor	universal normal control
30	PRO1787	lung tumor	universal normal control
	PRO1787	breast tumor	universal normal control
	PRO1556	lung tumor	universal normal control
	PRO1556	breast tumor	universal normal control
	PRO1561	colon tumor	universal normal control
35	PRO1561	lung tumor	universal normal control
	PRO1561	rectal tumor	universal normal control
	PRO1693	colon tumor	universal normal control
	PRO1693	lung tumor	universal normal control
	PRO1693	breast tumor	universal normal control
40	PRO1868	lung tumor	universal normal control
	PRO1868	breast tumor	universal normal control
	PRO1890	colon tumor	universal normal control
	PRO1890	lung tumor	universal normal control
	PRO1890	breast tumor	universal normal control
45	PRO1890	prostate tumor	universal normal control
	PRO1887	colon tumor	universal normal control
	PRO1887	breast tumor	universal normal control
	PRO4353	lung tumor	universal normal control
	PRO4353	breast tumor	universal normal control
50	PRO1801	colon tumor	universal normal control
	PRO1801	lung tumor	universal normal control
	PRO4357	lung tumor	universal normal control
	PRO4357	breast tumor	universal normal control
	PRO4302	colon tumor	universal normal control
55	PRO4302	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4302	breast tumor	universal normal control
	PRO4302	prostate tumor	universal normal control
	PRO5990	colon tumor	universal normal control
5	PRO5990	lung tumor	universal normal control
	PRO5990	breast tumor	universal normal control

EXAMPLE 31: Identification of Receptor/Ligand Interactions

10 In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor or ligand molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise 15 cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a biological or immunological activity of a cell expressing the receptor or ligand, and various other indications 20 which will be readily apparent to the ordinarily skilled artisan.

The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound 25 immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible receptor binding. The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with 30 fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of 35 cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is "broken down") to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine "His" tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have

been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel of potential receptors.

Using these assays, the following receptor/ligand interactions have been herein identified:

- (1) PRO1801 binds to PRO1114 and PRO4978.
- (2) PRO100 binds to PRO1114.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

PCT

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P3330R1

0-1	Form - PCT/RO/134 (EASY) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis)	
0-1-1	Prepared using	PCT-EASY Version 2.91 (updated 10.10.2000)
0-2	International Application No.	
0-3	Applicant's or agent's file reference	P3330R1
1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	page	98
1-2	line	34
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	American Type Culture Collection
1-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
1-3-3	Date of deposit	14 April 1998 (14.04.1998)
1-3-4	Accession Number	ATCC 209771
1-4	Additional Indications	NONE
1-5	Designated States for Which Indications are Made	all designated States
1-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
2	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
2-1	page	98
2-2	line	35
2-3	Identification of Deposit	
2-3-1	Name of depositary institution	American Type Culture Collection
2-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
2-3-3	Date of deposit	09 February 1999 (09.02.1999)
2-3-4	Accession Number	ATCC 203654
2-4	Additional Indications	NONE
2-5	Designated States for Which Indications are Made	all designated States
2-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
3	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
3-1	page	98
3-2	line	36



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P3330R1

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3-3	Identification of Deposit	
3-3-1	Name of depositary institution	American Type Culture Collection
3-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
3-3-3	Date of deposit	25 May 1999 (25.05.1999)
3-3-4	Accession Number	ATCC PTA-127
3-4	Additional Indications	NONE
3-5	Designated States for Which Indications are Made	all designated States
3-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
4	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
4-1	page	98
4-2	line	37
4-3	Identification of Deposit	
4-3-1	Name of depositary institution	American Type Culture Collection
4-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
4-3-3	Date of deposit	27 July 1999 (27.07.1999)
4-3-4	Accession Number	ATCC PTA-429
4-4	Additional Indications	NONE
4-5	Designated States for Which Indications are Made	all designated States
4-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
5	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
5-1	page	98
5-2	line	38
5-3	Identification of Deposit	
5-3-1	Name of depositary institution	American Type Culture Collection
5-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
5-3-3	Date of deposit	27 July 1999 (27.07.1999)
5-3-4	Accession Number	ATCC PTA-432
5-4	Additional Indications	NONE
5-5	Designated States for Which Indications are Made	all designated States
5-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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6	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
6-1	page	98
6-2	line	39
6-3	Identification of Deposit	
6-3-1	Name of depositary institution	American Type Culture Collection
6-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
6-3-3	Date of deposit	10 December 1997 (10.12.1997)
6-3-4	Accession Number	ATCC 209525
6-4	Additional Indications	NONE
6-5	Designated States for Which Indications are Made	all designated States
6-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
7	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
7-1	page	99
7-2	line	2
7-3	Identification of Deposit	
7-3-1	Name of depositary institution	American Type Culture Collection
7-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
7-3-3	Date of deposit	12 January 1999 (12.01.1999)
7-3-4	Accession Number	ATCC 203577
7-4	Additional Indications	NONE
7-5	Designated States for Which Indications are Made	all designated States
7-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
8	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
8-1	page	99
8-2	line	3
8-3	Identification of Deposit	
8-3-1	Name of depositary institution	American Type Culture Collection
8-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
8-3-3	Date of deposit	27 July 1999 (27.07.1999)
8-3-4	Accession Number	ATCC PTA-430
8-4	Additional Indications	NONE
8-5	Designated States for Which Indications are Made	all designated States

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8-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
9	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
9-1	page	99
9-2	line	4
9-3	Identification of Deposit	
9-3-1	Name of depositary institution	American Type Culture Collection
9-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
9-3-3	Date of deposit	08 June 1999 (08.06.1999)
9-3-4	Accession Number	ATCC PTA-203
9-4	Additional Indications	NONE
9-5	Designated States for Which Indications are Made	all designated States
9-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
10	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
10-1	page	99
10-2	line	5
10-3	Identification of Deposit	
10-3-1	Name of depositary institution	American Type Culture Collection
10-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
10-3-3	Date of deposit	01 July 1998 (01.07.1998)
10-3-4	Accession Number	ATCC 203040
10-4	Additional Indications	NONE
10-5	Designated States for Which Indications are Made	all designated States
10-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
11	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
11-1	page	99
11-2	line	6
11-3	Identification of Deposit	
11-3-1	Name of depositary institution	American Type Culture Collection
11-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
11-3-3	Date of deposit	31 August 1999 (31.08.1999)
11-3-4	Accession Number	ATCC PTA-611

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11-4	Additional Indications	NONE
11-5	Designated States for Which Indications are Made	all designated States
11-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
12	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
12-1	page	99
12-2	line	7
12-3	Identification of Deposit	
12-3-1	Name of depositary institution	American Type Culture Collection
12-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
12-3-3	Date of deposit	21 January 1998 (21.01.1998)
12-3-4	Accession Number	ATCC 209593
12-4	Additional Indications	NONE
12-5	Designated States for Which Indications are Made	all designated States
12-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
13	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
13-1	page	99
13-2	line	8
13-3	Identification of Deposit	
13-3-1	Name of depositary institution	American Type Culture Collection
13-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
13-3-3	Date of deposit	09 February 1999 (09.02.1999)
13-3-4	Accession Number	ATCC 203649
13-4	Additional Indications	NONE
13-5	Designated States for Which Indications are Made	all designated States
13-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
14	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
14-1	page	99
14-2	line	9

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14-3	Identification of Deposit	
14-3-1	Name of depositary institution	American Type Culture Collection
14-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
14-3-3	Date of deposit	12 January 1999 (12.01.1999)
14-3-4	Accession Number	ATCC 203574
14-4	Additional Indications	NONE
14-5	Designated States for Which Indications are Made	all designated States
14-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
15	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
15-1	page	99
15-2	line	10
15-3	Identification of Deposit	
15-3-1	Name of depositary institution	American Type Culture Collection
15-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
15-3-3	Date of deposit	25 May 1999 (25.05.1999)
15-3-4	Accession Number	ATCC PTA-129
15-4	Additional Indications	NONE
15-5	Designated States for Which Indications are Made	all designated States
15-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
16	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
16-1	page	99
16-2	line	11
16-3	Identification of Deposit	
16-3-1	Name of depositary institution	American Type Culture Collection
16-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
16-3-3	Date of deposit	27 May 1998 (27.05.1998)
16-3-4	Accession Number	ATCC 209905
16-4	Additional Indications	NONE
16-5	Designated States for Which Indications are Made	all designated States
16-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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17	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
17-1	page	99
17-2	line	12
17-3	Identification of Deposit	
17-3-1	Name of depositary institution	American Type Culture Collection
17-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
17-3-3	Date of deposit	12 January 1999 (12.01.1999)
17-3-4	Accession Number	ATCC 203585
17-4	Additional Indications	NONE
17-5	Designated States for Which Indications are Made	all designated States
17-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
18	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
18-1	page	99
18-2	line	13
18-3	Identification of Deposit	
18-3-1	Name of depositary institution	American Type Culture Collection
18-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
18-3-3	Date of deposit	09 February 1999 (09.02.1999)
18-3-4	Accession Number	ATCC 203665
18-4	Additional Indications	NONE
18-5	Designated States for Which Indications are Made	all designated States
18-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
19	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
19-1	page	99
19-2	line	14
19-3	Identification of Deposit	
19-3-1	Name of depositary institution	American Type Culture Collection
19-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
19-3-3	Date of deposit	27 July 1999 (27.07.1999)
19-3-4	Accession Number	ATCC PTA-427
19-4	Additional Indications	NONE
19-5	Designated States for Which Indications are Made	all designated States

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19-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
20	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
20-1	page	99
20-2	line	15
20-3	Identification of Deposit	
20-3-1	Name of depositary institution	American Type Culture Collection
20-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
20-3-3	Date of deposit	31 August 1999 (31.08.1999)
20-3-4	Accession Number	ATCC PTA-615
20-4	Additional Indications	NONE
20-5	Designated States for Which Indications are Made	all designated States
20-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
21	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
21-1	page	99
21-2	line	16
21-3	Identification of Deposit	
21-3-1	Name of depositary institution	American Type Culture Collection
21-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
21-3-3	Date of deposit	12 January 1999 (12.01.1999)
21-3-4	Accession Number	ATCC 203582
21-4	Additional Indications	NONE
21-5	Designated States for Which Indications are Made	all designated States
21-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
22	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
22-1	page	99
22-2	line	17
22-3	Identification of Deposit	
22-3-1	Name of depositary institution	American Type Culture Collection
22-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
22-3-3	Date of deposit	09 March 1999 (09.03.1999)
22-3-4	Accession Number	ATCC 203838

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22-4	Additional Indications	NONE
22-5	Designated States for Which Indications are Made	all designated States
22-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
23	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
23-1	page	99
23-2	line	18
23-3	Identification of Deposit	
23-3-1	Name of depositary institution	American Type Culture Collection
23-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
23-3-3	Date of deposit	27 July 1999 (27.07.1999)
23-3-4	Accession Number	ATCC PTA-428
23-4	Additional Indications	NONE
23-5	Designated States for Which Indications are Made	all designated States
23-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
24	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
24-1	page	99
24-2	line	19
24-3	Identification of Deposit	
24-3-1	Name of depositary institution	American Type Culture Collection
24-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
24-3-3	Date of deposit	09 March 1999 (09.03.1999)
24-3-4	Accession Number	ATCC 203836
24-4	Additional Indications	NONE
24-5	Designated States for Which Indications are Made	all designated States
24-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
25	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
25-1	page	99
25-2	line	20



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25-3	Identification of Deposit	
25-3-1	Name of depositary institution	American Type Culture Collection
25-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
25-3-3	Date of deposit	08 June 1999 (08.06.1999)
25-3-4	Accession Number	ATCC PTA-205
25-4	Additional Indications	NONE
25-5	Designated States for Which Indications are Made	all designated States
25-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
26	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
26-1	page	99
26-2	line	21
26-3	Identification of Deposit	
26-3-1	Name of depositary institution	American Type Culture Collection
26-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
26-3-3	Date of deposit	27 July 1999 (27.07.1999)
26-3-4	Accession Number	ATCC PTA-431
26-4	Additional Indications	NONE
26-5	Designated States for Which Indications are Made	all designated States
26-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
27	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
27-1	page	99
27-2	line	22
27-3	Identification of Deposit	
27-3-1	Name of depositary institution	American Type Culture Collection
27-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
27-3-3	Date of deposit	09 February 1999 (09.02.1999)
27-3-4	Accession Number	ATCC 203659
27-4	Additional Indications	NONE
27-5	Designated States for Which Indications are Made	all designated States
27-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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28	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
28-1	page	99
28-2	line	23
28-3	Identification of Deposit	
28-3-1	Name of depositary institution	American Type Culture Collection
28-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
28-3-3	Date of deposit	12 January 1999 (12.01.1999)
28-3-4	Accession Number	ATCC 203584
28-4	Additional Indications	NONE
28-5	Designated States for Which Indications are Made	all designated States
28-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
29	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
29-1	page	99
29-2	line	24
29-3	Identification of Deposit	
29-3-1	Name of depositary institution	American Type Culture Collection
29-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
29-3-3	Date of deposit	25 May 1999 (25.05.1999)
29-3-4	Accession Number	ATCC PTA-126
29-4	Additional Indications	NONE
29-5	Designated States for Which Indications are Made	all designated States
29-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
30	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
30-1	page	99
30-2	line	25
30-3	Identification of Deposit	
30-3-1	Name of depositary institution	American Type Culture Collection
30-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
30-3-3	Date of deposit	25 May 1999 (25.05.1999)
30-3-4	Accession Number	ATCC PTA-128
30-4	Additional Indications	NONE
30-5	Designated States for Which Indications are Made	all designated States

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30-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
31	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
31-1	page	99
31-2	line	26
31-3	Identification of Deposit	
31-3-1	Name of depositary institution	American Type Culture Collection
31-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
31-3-3	Date of deposit	09 February 1999 (09.02.1999)
31-3-4	Accession Number	ATCC 203664
31-4	Additional Indications	NONE
31-5	Designated States for Which Indications are Made	all designated States
31-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
32	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
32-1	page	99
32-2	line	27
32-3	Identification of Deposit	
32-3-1	Name of depositary institution	American Type Culture Collection
32-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
32-3-3	Date of deposit	12 January 1999 (12.01.1999)
32-3-4	Accession Number	ATCC 203578
32-4	Additional Indications	NONE
32-5	Designated States for Which Indications are Made	all designated States
32-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
33	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
33-1	page	99
33-2	line	28
33-3	Identification of Deposit	
33-3-1	Name of depositary institution	American Type Culture Collection
33-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
33-3-3	Date of deposit	22 December 1998 (22.12.1998)
33-3-4	Accession Number	ATCC 203554

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33-4	Additional Indications	NONE
33-5	Designated States for Which Indications are Made	all designated States
33-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
34	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
34-1	page	99
34-2	line	29
34-3	Identification of Deposit	
34-3-1	Name of depositary institution	American Type Culture Collection
34-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
34-3-3	Date of deposit	16 March 1999 (16.03.1999)
34-3-4	Accession Number	ATCC 203850
34-4	Additional Indications	NONE
34-5	Designated States for Which Indications are Made	all designated States
34-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
35	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
35-1	page	99
35-2	line	30
35-3	Identification of Deposit	
35-3-1	Name of depositary institution	American Type Culture Collection
35-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
35-3-3	Date of deposit	11 May 1999 (11.05.1999)
35-3-4	Accession Number	ATCC PTA-45
35-4	Additional Indications	NONE
35-5	Designated States for Which Indications are Made	all designated States
35-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
36	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
36-1	page	99
36-2	line	31

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36-3	Identification of Deposit	
36-3-1	Name of depositary institution	American Type Culture Collection
36-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
36-3-3	Date of deposit	22 December 1998 (22.12.1998)
36-3-4	Accession Number	ATCC 203545
36-4	Additional Indications	NONE
36-5	Designated States for Which Indications are Made	all designated States
36-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
37	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
37-1	page	99
37-2	line	32
37-3	Identification of Deposit	
37-3-1	Name of depositary institution	American Type Culture Collection
37-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
37-3-3	Date of deposit	22 December 1998 (22.12.1998)
37-3-4	Accession Number	ATCC 203544
37-4	Additional Indications	NONE
37-5	Designated States for Which Indications are Made	all designated States
37-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
38	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
38-1	page	99
38-2	line	33
38-3	Identification of Deposit	
38-3-1	Name of depositary institution	American Type Culture Collection
38-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
38-3-3	Date of deposit	15 June 1999 (15.06.1999)
38-3-4	Accession Number	ATCC PTA-234
38-4	Additional Indications	NONE
38-5	Designated States for Which Indications are Made	all designated States
38-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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39	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
39-1	page	99
39-2	line	34
39-3	Identification of Deposit	
39-3-1	Name of depositary institution	American Type Culture Collection
39-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
39-3-3	Date of deposit	16 March 1999 (16.03.1999)
39-3-4	Accession Number	ATCC 203848
39-4	Additional Indications	NONE
39-5	Designated States for Which Indications are Made	all designated States
39-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
40	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
40-1	page	99
40-2	line	35
40-3	Identification of Deposit	
40-3-1	Name of depositary institution	American Type Culture Collection
40-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
40-3-3	Date of deposit	22 December 1998 (22.12.1998)
40-3-4	Accession Number	ATCC 203555
40-4	Additional Indications	NONE
40-5	Designated States for Which Indications are Made	all designated States
40-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
41	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
41-1	page	99
41-2	line	36
41-3	Identification of Deposit	
41-3-1	Name of depositary institution	American Type Culture Collection
41-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
41-3-3	Date of deposit	20 April 1999 (20.04.1999)
41-3-4	Accession Number	ATCC 203949
41-4	Additional Indications	NONE
41-5	Designated States for Which Indications are Made	all designated States

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41-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
42	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
42-1	page	99
42-2	line	37
42-3	Identification of Deposit	
42-3-1	Name of depositary institution	American Type Culture Collection
42-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
42-3-3	Date of deposit	15 December 1998 (15.12.1998)
42-3-4	Accession Number	ATCC 203539
42-4	Additional Indications	NONE
42-5	Designated States for Which Indications are Made	all designated States
42-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
43	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
43-1	page	99
43-2	line	38
43-3	Identification of Deposit	
43-3-1	Name of depositary institution	American Type Culture Collection
43-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
43-3-3	Date of deposit	23 March 1999 (23.03.1999)
43-3-4	Accession Number	ATCC 203871
43-4	Additional Indications	NONE
43-5	Designated States for Which Indications are Made	all designated States
43-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
44	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
44-1	page	99
44-2	line	39
44-3	Identification of Deposit	
44-3-1	Name of depositary institution	American Type Culture Collection
44-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
44-3-3	Date of deposit	23 March 1999 (23.03.1999)
44-3-4	Accession Number	ATCC 203862

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44-4	Additional Indications	NONE
44-5	Designated States for Which Indications are Made	all designated States
44-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
45	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
45-1	page	99
45-2	line	40
45-3	Identification of Deposit	
45-3-1	Name of depositary institution	American Type Culture Collection
45-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
45-3-3	Date of deposit	10 August 1999 (10.08.1999)
45-3-4	Accession Number	ATCC PTA-510
45-4	Additional Indications	NONE
45-5	Designated States for Which Indications are Made	all designated States
45-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
46	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
46-1	page	99
46-2	line	41
46-3	Identification of Deposit	
46-3-1	Name of depositary institution	American Type Culture Collection
46-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
46-3-3	Date of deposit	20 January 1999 (20.01.1999)
46-3-4	Accession Number	ATCC 203603
46-4	Additional Indications	NONE
46-5	Designated States for Which Indications are Made	all designated States
46-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
47	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
47-1	page	99
47-2	line	42



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47-3	Identification of Deposit	
47-3-1	Name of depositary institution	American Type Culture Collection
47-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
47-3-3	Date of deposit	02 March 1999 (02.03.1999)
47-3-4	Accession Number	ATCC 203813
47-4	Additional Indications	NONE
47-5	Designated States for Which Indications are Made	all designated States
47-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
48	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
48-1	page	99
48-2	line	43
48-3	Identification of Deposit	
48-3-1	Name of depositary institution	American Type Culture Collection
48-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
48-3-3	Date of deposit	02 March 1999 (02.03.1999)
48-3-4	Accession Number	ATCC 203812
48-4	Additional Indications	NONE
48-5	Designated States for Which Indications are Made	all designated States
48-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
49	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
49-1	page	99
49-2	line	44
49-3	Identification of Deposit	
49-3-1	Name of depositary institution	American Type Culture Collection
49-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
49-3-3	Date of deposit	29 October 1998 (29.10.1998)
49-3-4	Accession Number	ATCC 203391
49-4	Additional Indications	NONE
49-5	Designated States for Which Indications are Made	all designated States
49-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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50	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
50-1	page	99
50-2	line	45
50-3	Identification of Deposit	
50-3-1	Name of depositary institution	American Type Culture Collection
50-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
50-3-3	Date of deposit	27 April 1999 (27.04.1999)
50-3-4	Accession Number	ATCC 203965
50-4	Additional Indications	NONE
50-5	Designated States for Which Indications are Made	all designated States
50-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
51	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
51-1	page	99
51-2	line	46
51-3	Identification of Deposit	
51-3-1	Name of depositary institution	American Type Culture Collection
51-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
51-3-3	Date of deposit	02 March 1999 (02.03.1999)
51-3-4	Accession Number	ATCC 203816
51-4	Additional Indications	NONE
51-5	Designated States for Which Indications are Made	all designated States
51-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
52	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
52-1	page	99
52-2	line	47
52-3	Identification of Deposit	
52-3-1	Name of depositary institution	American Type Culture Collection
52-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
52-3-3	Date of deposit	02 March 1999 (02.03.1999)
52-3-4	Accession Number	ATCC 203814
52-4	Additional Indications	NONE
52-5	Designated States for Which Indications are Made	all designated States

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52-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
53	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
53-1	page	99
53-2	line	48
53-3	Identification of Deposit	
53-3-1	Name of depositary institution	American Type Culture Collection
53-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
53-3-3	Date of deposit	02 March 1999 (02.03.1999)
53-3-4	Accession Number	ATCC 203810
53-4	Additional Indications	NONE
53-5	Designated States for Which Indications are Made	all designated States
53-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
54	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
54-1	page	99
54-2	line	49
54-3	Identification of Deposit	
54-3-1	Name of depositary institution	American Type Culture Collection
54-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
54-3-3	Date of deposit	04 May 1999 (04.05.1999)
54-3-4	Accession Number	ATCC PTA-22
54-4	Additional Indications	NONE
54-5	Designated States for Which Indications are Made	all designated States
54-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
55	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
55-1	page	99
55-2	line	50
55-3	Identification of Deposit	
55-3-1	Name of depositary institution	American Type Culture Collection
55-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
55-3-3	Date of deposit	12 January 1999 (12.01.1999)
55-3-4	Accession Number	ATCC 203580

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55-4	Additional Indications	NONE
55-5	Designated States for Which Indications are Made	all designated States
55-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
56	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
56-1	page	99
56-2	line	51
56-3	Identification of Deposit	
56-3-1	Name of depositary institution	American Type Culture Collection
56-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
56-3-3	Date of deposit	30 March 1999 (30.03.1999)
56-3-4	Accession Number	ATCC 203889
56-4	Additional Indications	NONE
56-5	Designated States for Which Indications are Made	all designated States
56-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
57	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
57-1	page	99
57-2	line	52
57-3	Identification of Deposit	
57-3-1	Name of depositary institution	American Type Culture Collection
57-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
57-3-3	Date of deposit	27 April 1999 (27.04.1999)
57-3-4	Accession Number	ATCC 203964
57-4	Additional Indications	NONE
57-5	Designated States for Which Indications are Made	all designated States
57-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
58	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
58-1	page	99
58-2	line	53

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58-3	Identification of Deposit	
58-3-1	Name of depositary institution	American Type Culture Collection
58-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
58-3-3	Date of deposit	22 December 1998 (22.12.1998)
58-3-4	Accession Number	ATCC 203548
58-4	Additional Indications	NONE
58-5	Designated States for Which Indications are Made	all designated States
58-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
59	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
59-1	page	99
59-2	line	54
59-3	Identification of Deposit	
59-3-1	Name of depositary institution	American Type Culture Collection
59-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
59-3-3	Date of deposit	02 March 1999 (02.03.1999)
59-3-4	Accession Number	ATCC 203817
59-4	Additional Indications	NONE
59-5	Designated States for Which Indications are Made	all designated States
59-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
60	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
60-1	page	99
60-2	line	55
60-3	Identification of Deposit	
60-3-1	Name of depositary institution	American Type Culture Collection
60-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
60-3-3	Date of deposit	15 June 1999 (15.06.1999)
60-3-4	Accession Number	ATCC PTA-235
60-4	Additional Indications	NONE
60-5	Designated States for Which Indications are Made	all designated States
60-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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61	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
61-1	page	100
61-2	line	2
61-3	Identification of Deposit	
61-3-1	Name of depositary institution	American Type Culture Collection
61-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
61-3-3	Date of deposit	27 April 1999 (27.04.1999)
61-3-4	Accession Number	ATCC 203968
61-4	Additional Indications	NONE
61-5	Designated States for Which Indications are Made	all designated States
61-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
62	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
62-1	page	100
62-2	line	3
62-3	Identification of Deposit	
62-3-1	Name of depositary institution	American Type Culture Collection
62-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
62-3-3	Date of deposit	30 March 1999 (30.03.1999)
62-3-4	Accession Number	ATCC 203894
62-4	Additional Indications	NONE
62-5	Designated States for Which Indications are Made	all designated States
62-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
63	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
63-1	page	100
63-2	line	4
63-3	Identification of Deposit	
63-3-1	Name of depositary institution	American Type Culture Collection
63-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
63-3-3	Date of deposit	30 March 1999 (30.03.1999)
63-3-4	Accession Number	ATCC 203893
63-4	Additional Indications	NONE
63-5	Designated States for Which Indications are Made	all designated States

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63-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
64	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
64-1	page	100
64-2	line	5
64-3	Identification of Deposit	
64-3-1	Name of depositary institution	American Type Culture Collection
64-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
64-3-3	Date of deposit	02 March 1999 (02.03.1999)
64-3-4	Accession Number	ATCC 203811
64-4	Additional Indications	NONE
64-5	Designated States for Which Indications are Made	all designated States
64-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
65	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
65-1	page	100
65-2	line	6
65-3	Identification of Deposit	
65-3-1	Name of depositary institution	American Type Culture Collection
65-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
65-3-3	Date of deposit	23 March 1999 (23.03.1999)
65-3-4	Accession Number	ATCC 203867
65-4	Additional Indications	NONE
65-5	Designated States for Which Indications are Made	all designated States
65-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
66	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
66-1	page	100
66-2	line	7
66-3	Identification of Deposit	
66-3-1	Name of depositary institution	American Type Culture Collection
66-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
66-3-3	Date of deposit	27 April 1999 (27.04.1999)
66-3-4	Accession Number	ATCC 203963

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66-4	Additional Indications	NONE
66-5	Designated States for Which Indications are Made	all designated States
66-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
67	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
67-1	page	100
67-2	line	8
67-3	Identification of Deposit	
67-3-1	Name of depositary institution	American Type Culture Collection
67-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
67-3-3	Date of deposit	02 March 1999 (02.03.1999)
67-3-4	Accession Number	ATCC 203815
67-4	Additional Indications	NONE
67-5	Designated States for Which Indications are Made	all designated States
67-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
68	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
68-1	page	100
68-2	line	9
68-3	Identification of Deposit	
68-3-1	Name of depositary institution	American Type Culture Collection
68-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
68-3-3	Date of deposit	30 March 1999 (30.03.1999)
68-3-4	Accession Number	ATCC 203890
68-4	Additional Indications	NONE
68-5	Designated States for Which Indications are Made	all designated States
68-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
69	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
69-1	page	100
69-2	line	10



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69-3	Identification of Deposit	
69-3-1	Name of depositary institution	American Type Culture Collection
69-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
69-3-3	Date of deposit	25 May 1999 (25.05.1999)
69-3-4	Accession Number	ATCC PTA-130
69-4	Additional Indications	NONE
69-5	Designated States for Which Indications are Made	all designated States
69-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
70	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
70-1	page	100
70-2	line	11
70-3	Identification of Deposit	
70-3-1	Name of depositary institution	American Type Culture Collection
70-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
70-3-3	Date of deposit	27 April 1999 (27.04.1999)
70-3-4	Accession Number	ATCC 203970
70-4	Additional Indications	NONE
70-5	Designated States for Which Indications are Made	all designated States
70-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
71	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
71-1	page	100
71-2	line	12
71-3	Identification of Deposit	
71-3-1	Name of depositary institution	American Type Culture Collection
71-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
71-3-3	Date of deposit	16 March 1999 (16.03.1999)
71-3-4	Accession Number	ATCC 203845
71-4	Additional Indications	NONE
71-5	Designated States for Which Indications are Made	all designated States
71-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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72	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
72-1	page	100
72-2	line	13
72-3	Identification of Deposit	
72-3-1	Name of depositary institution	American Type Culture Collection
72-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
72-3-3	Date of deposit	23 March 1999 (23.03.1999)
72-3-4	Accession Number	ATCC 203861
72-4	Additional Indications	NONE
72-5	Designated States for Which Indications are Made	all designated States
72-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
73	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
73-1	page	100
73-2	line	14
73-3	Identification of Deposit	
73-3-1	Name of depositary institution	American Type Culture Collection
73-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
73-3-3	Date of deposit	16 March 1999 (16.03.1999)
73-3-4	Accession Number	ATCC 203844
73-4	Additional Indications	NONE
73-5	Designated States for Which Indications are Made	all designated States
73-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
74	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
74-1	page	100
74-2	line	15
74-3	Identification of Deposit	
74-3-1	Name of depositary institution	American Type Culture Collection
74-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
74-3-3	Date of deposit	10 August 1999 (10.08.1999)
74-3-4	Accession Number	ATCC PTA-513
74-4	Additional Indications	NONE
74-5	Designated States for Which Indications are Made	all designated States

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74-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
75	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
75-1	page	100
75-2	line	16
75-3	Identification of Deposit	
75-3-1	Name of depositary institution	American Type Culture Collection
75-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
75-3-3	Date of deposit	09 February 1999 (09.02.1999)
75-3-4	Accession Number	ATCC 203663
75-4	Additional Indications	NONE
75-5	Designated States for Which Indications are Made	all designated States
75-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
76	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
76-1	page	100
76-2	line	17
76-3	Identification of Deposit	
76-3-1	Name of depositary institution	American Type Culture Collection
76-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
76-3-3	Date of deposit	16 March 1999 (16.03.1999)
76-3-4	Accession Number	ATCC 203851
76-4	Additional Indications	NONE
76-5	Designated States for Which Indications are Made	all designated States
76-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
77	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
77-1	page	100
77-2	line	18
77-3	Identification of Deposit	
77-3-1	Name of depositary institution	American Type Culture Collection
77-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
77-3-3	Date of deposit	20 April 1999 (20.04.1999)
77-3-4	Accession Number	ATCC 203950

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77-4	Additional Indications	NONE
77-5	Designated States for Which Indications are Made	all designated States
77-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
78	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
78-1	page	100
78-2	line	19
78-3	Identification of Deposit	
78-3-1	Name of depositary institution	American Type Culture Collection
78-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
78-3-3	Date of deposit	30 March 1999 (30.03.1999)
78-3-4	Accession Number	ATCC 203895
78-4	Additional Indications	NONE
78-5	Designated States for Which Indications are Made	all designated States
78-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
79	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
79-1	page	100
79-2	line	20
79-3	Identification of Deposit	
79-3-1	Name of depositary institution	American Type Culture Collection
79-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
79-3-3	Date of deposit	25 May 1999 (25.05.1999)
79-3-4	Accession Number	ATCC PTA-134
79-4	Additional Indications	NONE
79-5	Designated States for Which Indications are Made	all designated States
79-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
80	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
80-1	page	100
80-2	line	21

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80-3	Identification of Deposit	
80-3-1	Name of depositary institution	American Type Culture Collection
80-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
80-3-3	Date of deposit	16 March 1999 (16.03.1999)
80-3-4	Accession Number	ATCC 203852
80-4	Additional Indications	NONE
80-5	Designated States for Which Indications are Made	all designated States
80-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
81	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
81-1	page	100
81-2	line	22
81-3	Identification of Deposit	
81-3-1	Name of depositary institution	American Type Culture Collection
81-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
81-3-3	Date of deposit	22 June 1999 (22.06.1999)
81-3-4	Accession Number	ATCC PTA-258
81-4	Additional Indications	NONE
81-5	Designated States for Which Indications are Made	all designated States
81-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
82	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
82-1	page	100
82-2	line	23
82-3	Identification of Deposit	
82-3-1	Name of depositary institution	American Type Culture Collection
82-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
82-3-3	Date of deposit	22 June 1999 (22.06.1999)
82-3-4	Accession Number	ATCC PTA-259
82-4	Additional Indications	NONE
82-5	Designated States for Which Indications are Made	all designated States
82-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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83	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
83-1	page	100
83-2	line	24
83-3	Identification of Deposit	
83-3-1	Name of depositary institution	American Type Culture Collection
83-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
83-3-3	Date of deposit	23 March 1999 (23.03.1999)
83-3-4	Accession Number	ATCC 203866
83-4	Additional Indications	NONE
83-5	Designated States for Which Indications are Made	all designated States
83-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
84	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
84-1	page	100
84-2	line	25
84-3	Identification of Deposit	
84-3-1	Name of depositary institution	American Type Culture Collection
84-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
84-3-3	Date of deposit	16 March 1999 (16.03.1999)
84-3-4	Accession Number	ATCC 203853
84-4	Additional Indications	NONE
84-5	Designated States for Which Indications are Made	all designated States
84-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
85	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
85-1	page	100
85-2	line	26
85-3	Identification of Deposit	
85-3-1	Name of depositary institution	American Type Culture Collection
85-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
85-3-3	Date of deposit	30 March 1999 (30.03.1999)
85-3-4	Accession Number	ATCC 203892
85-4	Additional Indications	NONE
85-5	Designated States for Which Indications are Made	all designated States

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85-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
86	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
86-1	page	100
86-2	line	27
86-3	Identification of Deposit	
86-3-1	Name of depositary institution	American Type Culture Collection
86-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
86-3-3	Date of deposit	16 March 1999 (16.03.1999)
86-3-4	Accession Number	ATCC 203847
86-4	Additional Indications	NONE
86-5	Designated States for Which Indications are Made	all designated States
86-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
87	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
87-1	page	100
87-2	line	28
87-3	Identification of Deposit	
87-3-1	Name of depositary institution	American Type Culture Collection
87-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
87-3-3	Date of deposit	04 May 1999 (04.05.1999)
87-3-4	Accession Number	ATCC PTA-21
87-4	Additional Indications	NONE
87-5	Designated States for Which Indications are Made	all designated States
87-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
88	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
88-1	page	100
88-2	line	29
88-3	Identification of Deposit	
88-3-1	Name of depositary institution	American Type Culture Collection
88-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
88-3-3	Date of deposit	25 May 1999 (25.05.1999)
88-3-4	Accession Number	ATCC PTA-121

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88-4	Additional Indications	NONE
88-5	Designated States for Which Indications are Made	all designated States
88-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
89	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
89-1	page	100
89-2	line	30
89-3	Identification of Deposit	
89-3-1	Name of depositary institution	American Type Culture Collection
89-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
89-3-3	Date of deposit	20 April 1999 (20.04.1999)
89-3-4	Accession Number	ATCC 203951
89-4	Additional Indications	NONE
89-5	Designated States for Which Indications are Made	all designated States
89-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
90	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
90-1	page	100
90-2	line	31
90-3	Identification of Deposit	
90-3-1	Name of depositary institution	American Type Culture Collection
90-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
90-3-3	Date of deposit	23 March 1999 (23.03.1999)
90-3-4	Accession Number	ATCC 203869
90-4	Additional Indications	NONE
90-5	Designated States for Which Indications are Made	all designated States
90-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
91	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
91-1	page	100
91-2	line	32



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91-3	Identification of Deposit	
91-3-1	Name of depositary institution	American Type Culture Collection
91-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
91-3-3	Date of deposit	15 June 1999 (15.06.1999)
91-3-4	Accession Number	ATCC PTA-232
91-4	Additional Indications	NONE
91-5	Designated States for Which Indications are Made	all designated States
91-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
92	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
92-1	page	100
92-2	line	33
92-3	Identification of Deposit	
92-3-1	Name of depositary institution	American Type Culture Collection
92-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
92-3-3	Date of deposit	20 July 1999 (20.07.1999)
92-3-4	Accession Number	ATCC PTA-385
92-4	Additional Indications	NONE
92-5	Designated States for Which Indications are Made	all designated States
92-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
93	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
93-1	page	100
93-2	line	34
93-3	Identification of Deposit	
93-3-1	Name of depositary institution	American Type Culture Collection
93-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
93-3-3	Date of deposit	23 March 1999 (23.03.1999)
93-3-4	Accession Number	ATCC 203864
93-4	Additional Indications	NONE
93-5	Designated States for Which Indications are Made	all designated States
93-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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94	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
94-1	page	100
94-2	line	35
94-3	Identification of Deposit	
94-3-1	Name of depositary institution	American Type Culture Collection
94-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
94-3-3	Date of deposit	22 June 1999 (22.06.1999)
94-3-4	Accession Number	ATCC PTA-262
94-4	Additional Indications	NONE
94-5	Designated States for Which Indications are Made	all designated States
94-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
95	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
95-1	page	100
95-2	line	36
95-3	Identification of Deposit	
95-3-1	Name of depositary institution	American Type Culture Collection
95-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
95-3-3	Date of deposit	20 July 1999 (20.07.1999)
95-3-4	Accession Number	ATCC PTA-381
95-4	Additional Indications	NONE
95-5	Designated States for Which Indications are Made	all designated States
95-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
96	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
96-1	page	100
96-2	line	37
96-3	Identification of Deposit	
96-3-1	Name of depositary institution	American Type Culture Collection
96-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
96-3-3	Date of deposit	04 May 1999 (04.05.1999)
96-3-4	Accession Number	ATCC PTA-15
96-4	Additional Indications	NONE
96-5	Designated States for Which Indications are Made	all designated States

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96-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
97	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
97-1	page	100
97-2	line	38
97-3	Identification of Deposit	
97-3-1	Name of depositary institution	American Type Culture Collection
97-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
97-3-3	Date of deposit	15 June 1999 (15.06.1999)
97-3-4	Accession Number	ATCC PTA-239
97-4	Additional Indications	NONE
97-5	Designated States for Which Indications are Made	all designated States
97-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
98	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
98-1	page	100
98-2	line	39
98-3	Identification of Deposit	
98-3-1	Name of depositary institution	American Type Culture Collection
98-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
98-3-3	Date of deposit	20 July 1999 (20.07.1999)
98-3-4	Accession Number	ATCC PTA-384
98-4	Additional Indications	NONE
98-5	Designated States for Which Indications are Made	all designated States
98-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
99	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
99-1	page	100
99-2	line	40
99-3	Identification of Deposit	
99-3-1	Name of depositary institution	American Type Culture Collection
99-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
99-3-3	Date of deposit	03 August 1999 (03.08.1999)
99-3-4	Accession Number	ATCC PTA-475

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99-4	Additional Indications	NONE
99-5	Designated States for Which Indications are Made	all designated States
99-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
100	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
100-1	page	100
100-2	line	41
100-3	Identification of Deposit	
100-3-1	Name of depositary institution	American Type Culture Collection
100-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
100-3-3	Date of deposit	16 March 1999 (16.03.1999)
100-3-4	Accession Number	ATCC 203854
100-4	Additional Indications	NONE
100-5	Designated States for Which Indications are Made	all designated States
100-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
101	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
101-1	page	100
101-2	line	42
101-3	Identification of Deposit	
101-3-1	Name of depositary institution	American Type Culture Collection
101-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
101-3-3	Date of deposit	20 July 1999 (20.07.1999)
101-3-4	Accession Number	ATCC PTA-378
101-4	Additional Indications	NONE
101-5	Designated States for Which Indications are Made	all designated States
101-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
102	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
102-1	page	100
102-2	line	43

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102-3	Identification of Deposit	
102-3-1	Name of depositary institution	American Type Culture Collection
102-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
102-3-3	Date of deposit	22 June 1999 (22.06.1999)
102-3-4	Accession Number	ATCC PTA-257
102-4	Additional Indications	NONE
102-5	Designated States for Which Indications are Made	all designated States
102-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
103	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
103-1	page	100
103-2	line	44
103-3	Identification of Deposit	
103-3-1	Name of depositary institution	American Type Culture Collection
103-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
103-3-3	Date of deposit	15 June 1999 (15.06.1999)
103-3-4	Accession Number	ATCC PTA-231
103-4	Additional Indications	NONE
103-5	Designated States for Which Indications are Made	all designated States
103-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
104	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
104-1	page	100
104-2	line	45
104-3	Identification of Deposit	
104-3-1	Name of depositary institution	American Type Culture Collection
104-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
104-3-3	Date of deposit	20 July 1999 (20.07.1999)
104-3-4	Accession Number	ATCC PTA-388
104-4	Additional Indications	NONE
104-5	Designated States for Which Indications are Made	all designated States
104-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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105	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
105-1	page	100
105-2	line	46
105-3	Identification of Deposit	
105-3-1	Name of depositary institution	American Type Culture Collection
105-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
105-3-3	Date of deposit	31 August 1999 (31.08.1999)
105-3-4	Accession Number	ATCC PTA-620
105-4	Additional Indications	NONE
105-5	Designated States for Which Indications are Made	all designated States
105-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
106	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
106-1	page	100
106-2	line	47
106-3	Identification of Deposit	
106-3-1	Name of depositary institution	American Type Culture Collection
106-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
106-3-3	Date of deposit	25 May 1999 (25.05.1999)
106-3-4	Accession Number	ATCC PTA-118
106-4	Additional Indications	NONE
106-5	Designated States for Which Indications are Made	all designated States
106-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
107	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
107-1	page	100
107-2	line	48
107-3	Identification of Deposit	
107-3-1	Name of depositary institution	American Type Culture Collection
107-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
107-3-3	Date of deposit	03 August 1999 (03.08.1999)
107-3-4	Accession Number	ATCC PTA-477
107-4	Additional Indications	NONE
107-5	Designated States for Which Indications are Made	all designated States

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107-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
108	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
108-1	page	100
108-2	line	49
108-3	Identification of Deposit	
108-3-1	Name of depositary institution	American Type Culture Collection
108-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
108-3-3	Date of deposit	03 August 1999 (03.08.1999)
108-3-4	Accession Number	ATCC PTA-488
108-4	Additional Indications	NONE
108-5	Designated States for Which Indications are Made	all designated States
108-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
109	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
109-1	page	100
109-2	line	50
109-3	Identification of Deposit	
109-3-1	Name of depositary institution	American Type Culture Collection
109-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
109-3-3	Date of deposit	16 March 1999 (16.03.1999)
109-3-4	Accession Number	ATCC 203849
109-4	Additional Indications	NONE
109-5	Designated States for Which Indications are Made	all designated States
109-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
110	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
110-1	page	100
110-2	line	51
110-3	Identification of Deposit	
110-3-1	Name of depositary institution	American Type Culture Collection
110-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
110-3-3	Date of deposit	09 March 1999 (09.03.1999)
110-3-4	Accession Number	ATCC 203837

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110-4	Additional Indications	NONE
110-5	Designated States for Which Indications are Made	all designated States
110-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
111	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
111-1	page	100
111-2	line	52
111-3	Identification of Deposit	
111-3-1	Name of depositary institution	American Type Culture Collection
111-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
111-3-3	Date of deposit	20 July 1999 (20.07.1999)
111-3-4	Accession Number	ATCC PTA-380
111-4	Additional Indications	NONE
111-5	Designated States for Which Indications are Made	all designated States
111-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
112	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
112-1	page	100
112-2	line	53
112-3	Identification of Deposit	
112-3-1	Name of depositary institution	American Type Culture Collection
112-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
112-3-3	Date of deposit	11 May 1999 (11.05.1999)
112-3-4	Accession Number	ATCC PTA-44
112-4	Additional Indications	NONE
112-5	Designated States for Which Indications are Made	all designated States
112-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
113	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
113-1	page	100
113-2	line	54



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113-3	Identification of Deposit	
113-3-1	Name of depositary institution	American Type Culture Collection
113-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
113-3-3	Date of deposit	11 May 1999 (11.05.1999)
113-3-4	Accession Number	ATCC PTA-42
113-4	Additional Indications	NONE
113-5	Designated States for Which Indications are Made	all designated States
113-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
114	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
114-1	page	100
114-2	line	55
114-3	Identification of Deposit	
114-3-1	Name of depositary institution	American Type Culture Collection
114-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
114-3-3	Date of deposit	25 May 1999 (25.05.1999)
114-3-4	Accession Number	ATCC PTA-123
114-4	Additional Indications	NONE
114-5	Designated States for Which Indications are Made	all designated States
114-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
115	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
115-1	page	101
115-2	line	2
115-3	Identification of Deposit	
115-3-1	Name of depositary institution	American Type Culture Collection
115-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
115-3-3	Date of deposit	03 August 1999 (03.08.1999)
115-3-4	Accession Number	ATCC PTA-482
115-4	Additional Indications	NONE
115-5	Designated States for Which Indications are Made	all designated States
115-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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116	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
116-1	page	101
116-2	line	3
116-3	Identification of Deposit	
116-3-1	Name of depositary institution	American Type Culture Collection
116-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
116-3-3	Date of deposit	03 August 1999 (03.08.1999)
116-3-4	Accession Number	ATCC PTA-483
116-4	Additional Indications	NONE
116-5	Designated States for Which Indications are Made	all designated States
116-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
117	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
117-1	page	101
117-2	line	4
117-3	Identification of Deposit	
117-3-1	Name of depositary institution	American Type Culture Collection
117-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
117-3-3	Date of deposit	03 August 1999 (03.08.1999)
117-3-4	Accession Number	ATCC PTA-485
117-4	Additional Indications	NONE
117-5	Designated States for Which Indications are Made	all designated States
117-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
118	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
118-1	page	101
118-2	line	5
118-3	Identification of Deposit	
118-3-1	Name of depositary institution	American Type Culture Collection
118-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
118-3-3	Date of deposit	03 August 1999 (03.08.1999)
118-3-4	Accession Number	ATCC PTA-480
118-4	Additional Indications	NONE
118-5	Designated States for Which Indications are Made	all designated States

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118-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
119	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
119-1	page	101
119-2	line	6
119-3	Identification of Deposit	
119-3-1	Name of depositary institution	American Type Culture Collection
119-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
119-3-3	Date of deposit	03 August 1999 (03.08.1999)
119-3-4	Accession Number	ATCC PTA-476
119-4	Additional Indications	NONE
119-5	Designated States for Which Indications are Made	all designated States
119-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
120	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
120-1	page	101
120-2	line	7
120-3	Identification of Deposit	
120-3-1	Name of depositary institution	American Type Culture Collection
120-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
120-3-3	Date of deposit	03 August 1999 (03.08.1999)
120-3-4	Accession Number	ATCC PTA-472
120-4	Additional Indications	NONE
120-5	Designated States for Which Indications are Made	all designated States
120-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
121	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
121-1	page	101
121-2	line	8
121-3	Identification of Deposit	
121-3-1	Name of depositary institution	American Type Culture Collection
121-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
121-3-3	Date of deposit	03 August 1999 (03.08.1999)
121-3-4	Accession Number	ATCC PTA-487

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121-4	Additional Indications	NONE
121-5	Designated States for Which Indications are Made	all designated States
121-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
122	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
122-1	page	101
122-2	line	9
122-3	Identification of Deposit	
122-3-1	Name of depositary institution	American Type Culture Collection
122-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
122-3-3	Date of deposit	03 August 1999 (03.08.1999)
122-3-4	Accession Number	ATCC PTA-484
122-4	Additional Indications	NONE
122-5	Designated States for Which Indications are Made	all designated States
122-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
123	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
123-1	page	101
123-2	line	10
123-3	Identification of Deposit	
123-3-1	Name of depositary institution	American Type Culture Collection
123-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
123-3-3	Date of deposit	17 August 1999 (17.08.1999)
123-3-4	Accession Number	ATCC PTA-546
123-4	Additional Indications	NONE
123-5	Designated States for Which Indications are Made	all designated States
123-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
124	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
124-1	page	101
124-2	line	11

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124-3	Identification of Deposit	
124-3-1	Name of depositary institution	American Type Culture Collection
124-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
124-3-3	Date of deposit	10 August 1999 (10.08.1999)
124-3-4	Accession Number	ATCC PTA-515
124-4	Additional Indications	NONE
124-5	Designated States for Which Indications are Made	all designated States
124-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
125	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
125-1	page	101
125-2	line	12
125-3	Identification of Deposit	
125-3-1	Name of depositary institution	American Type Culture Collection
125-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
125-3-3	Date of deposit	19 October 1999 (19.10.1999)
125-3-4	Accession Number	ATCC PTA-861
125-4	Additional Indications	NONE
125-5	Designated States for Which Indications are Made	all designated States
125-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
126	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
126-1	page	101
126-2	line	13
126-3	Identification of Deposit	
126-3-1	Name of depositary institution	American Type Culture Collection
126-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
126-3-3	Date of deposit	10 August 1999 (10.08.1999)
126-3-4	Accession Number	ATCC PTA-518
126-4	Additional Indications	NONE
126-5	Designated States for Which Indications are Made	all designated States
126-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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127	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
127-1	page	101
127-2	line	14
127-3	Identification of Deposit	
127-3-1	Name of depositary institution	American Type Culture Collection
127-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
127-3-3	Date of deposit	10 August 1999 (10.08.1999)
127-3-4	Accession Number	ATCC PTA-512
127-4	Additional Indications	NONE
127-5	Designated States for Which Indications are Made	all designated States
127-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
128	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
128-1	page	101
128-2	line	15
128-3	Identification of Deposit	
128-3-1	Name of depositary institution	American Type Culture Collection
128-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
128-3-3	Date of deposit	03 August 1999 (03.08.1999)
128-3-4	Accession Number	ATCC PTA-489
128-4	Additional Indications	NONE
128-5	Designated States for Which Indications are Made	all designated States
128-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
129	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
129-1	page	101
129-2	line	16
129-3	Identification of Deposit	
129-3-1	Name of depositary institution	American Type Culture Collection
129-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
129-3-3	Date of deposit	31 August 1999 (31.08.1999)
129-3-4	Accession Number	ATCC PTA-614
129-4	Additional Indications	NONE
129-5	Designated States for Which Indications are Made	all designated States

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129-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
130	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
130-1	page	101
130-2	line	17
130-3	Identification of Deposit	
130-3-1	Name of depositary institution	American Type Culture Collection
130-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
130-3-3	Date of deposit	16 November 1999 (16.11.1999)
130-3-4	Accession Number	ATCC PTA-957
130-4	Additional Indications	NONE
130-5	Designated States for Which Indications are Made	all designated States
130-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
131	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
131-1	page	101
131-2	line	18
131-3	Identification of Deposit	
131-3-1	Name of depositary institution	American Type Culture Collection
131-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
131-3-3	Date of deposit	05 October 1999 (05.10.1999)
131-3-4	Accession Number	ATCC PTA-819
131-4	Additional Indications	NONE
131-5	Designated States for Which Indications are Made	all designated States
131-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
132	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
132-1	page	101
132-2	line	19
132-3	Identification of Deposit	
132-3-1	Name of depositary institution	American Type Culture Collection
132-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
132-3-3	Date of deposit	18 September 1997 (18.09.1997)
132-3-4	Accession Number	ATCC 209280

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132-4	Additional Indications	NONE
132-5	Designated States for Which Indications are Made	all designated States
132-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
133	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
133-1	page	101
133-2	line	20
133-3	Identification of Deposit	
133-3-1	Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
133-3-2	Address of depositary institution	
133-3-3	Date of deposit	
133-3-4	Accession Number	
133-4	Additional Indications	NONE
133-5	Designated States for Which Indications are Made	all designated States
133-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
134	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
134-1	page	101
134-2	line	21
134-3	Identification of Deposit	
134-3-1	Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
134-3-2	Address of depositary institution	
134-3-3	Date of deposit	
134-3-4	Accession Number	
134-4	Additional Indications	NONE
134-5	Designated States for Which Indications are Made	all designated States
134-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
135	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
135-1	page	101
135-2	line	22



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135-3	Identification of Deposit	
135-3-1	Name of depositary institution	American Type Culture Collection
135-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
135-3-3	Date of deposit	23 September 1997 (23.09.1997)
135-3-4	Accession Number	ATCC 209296
135-4	Additional Indications	NONE
135-5	Designated States for Which Indications are Made	all designated States
135-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
136	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
136-1	page	101
136-2	line	23
136-3	Identification of Deposit	
136-3-1	Name of depositary institution	American Type Culture Collection
136-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
136-3-3	Date of deposit	18 September 1997 (18.09.1997)
136-3-4	Accession Number	ATCC 209279
136-4	Additional Indications	NONE
136-5	Designated States for Which Indications are Made	all designated States
136-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
137	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
137-1	page	101
137-2	line	24
137-3	Identification of Deposit	
137-3-1	Name of depositary institution	American Type Culture Collection
137-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
137-3-3	Date of deposit	05 March 1998 (05.03.1998)
137-3-4	Accession Number	ATCC 209653
137-4	Additional Indications	NONE
137-5	Designated States for Which Indications are Made	all designated States
137-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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138	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
138-1	page	101
138-2	line	25
138-3	Identification of Deposit	
138-3-1	Name of depositary institution	American Type Culture Collection
138-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
138-3-3	Date of deposit	16 October 1997 (16.10.1997)
138-3-4	Accession Number	ATCC 209385
138-4	Additional Indications	NONE
138-5	Designated States for Which Indications are Made	all designated States
138-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
139	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
139-1	page	101
139-2	line	26
139-3	Identification of Deposit	
139-3-1	Name of depositary institution	American Type Culture Collection
139-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
139-3-3	Date of deposit	16 September 1997 (16.09.1997)
139-3-4	Accession Number	ATCC 209261
139-4	Additional Indications	NONE
139-5	Designated States for Which Indications are Made	all designated States
139-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
140	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
140-1	page	101
140-2	line	27
140-3	Identification of Deposit	
140-3-1	Name of depositary institution	American Type Culture Collection
140-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
140-3-3	Date of deposit	16 October 1997 (16.10.1997)
140-3-4	Accession Number	ATCC 209384
140-4	Additional Indications	NONE
140-5	Designated States for Which Indications are Made	all designated States

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140-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
141	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
141-1	page	101
141-2	line	28
141-3	Identification of Deposit	
141-3-1	Name of depositary institution	American Type Culture Collection
141-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
141-3-3	Date of deposit	16 September 1997 (16.09.1997)
141-3-4	Accession Number	ATCC 209258
141-4	Additional Indications	NONE
141-5	Designated States for Which Indications are Made	all designated States
141-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
142	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
142-1	page	101
142-2	line	29
142-3	Identification of Deposit	
142-3-1	Name of depositary institution	American Type Culture Collection
142-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
142-3-3	Date of deposit	16 September 1997 (16.09.1997)
142-3-4	Accession Number	ATCC 209257
142-4	Additional Indications	NONE
142-5	Designated States for Which Indications are Made	all designated States
142-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
143	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
143-1	page	101
143-2	line	30
143-3	Identification of Deposit	
143-3-1	Name of depositary institution	American Type Culture Collection
143-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
143-3-3	Date of deposit	30 May 1997 (30.05.1997)
143-3-4	Accession Number	ATCC 209087

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143-4	Additional Indications	NONE
143-5	Designated States for Which Indications are Made	all designated States
143-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
144	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
144-1	page	101
144-2	line	31
144-3	Identification of Deposit	
144-3-1	Name of depositary institution	American Type Culture Collection
144-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
144-3-3	Date of deposit	16 October 1997 (16.10.1997)
144-3-4	Accession Number	ATCC 209381
144-4	Additional Indications	NONE
144-5	Designated States for Which Indications are Made	all designated States
144-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
145	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
145-1	page	101
145-2	line	32
145-3	Identification of Deposit	
145-3-1	Name of depositary institution	American Type Culture Collection
145-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
145-3-3	Date of deposit	16 September 1997 (16.09.1997)
145-3-4	Accession Number	ATCC 209262
145-4	Additional Indications	NONE
145-5	Designated States for Which Indications are Made	all designated States
145-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
146	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
146-1	page	101
146-2	line	33

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146-3	Identification of Deposit	
146-3-1	Name of depositary institution	American Type Culture Collection
146-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
146-3-3	Date of deposit	28 October 1997 (28.10.1997)
146-3-4	Accession Number	ATCC 209420
146-4	Additional Indications	NONE
146-5	Designated States for Which Indications are Made	all designated States
146-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
147	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
147-1	page	101
147-2	line	34
147-3	Identification of Deposit	
147-3-1	Name of depositary institution	American Type Culture Collection
147-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
147-3-3	Date of deposit	16 September 1997 (16.09.1997)
147-3-4	Accession Number	ATCC 209256
147-4	Additional Indications	NONE
147-5	Designated States for Which Indications are Made	all designated States
147-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
148	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
148-1	page	101
148-2	line	35
148-3	Identification of Deposit	
148-3-1	Name of depositary institution	American Type Culture Collection
148-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
148-3-3	Date of deposit	16 September 1997 (16.09.1997)
148-3-4	Accession Number	ATCC 209251
148-4	Additional Indications	NONE
148-5	Designated States for Which Indications are Made	all designated States
148-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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149	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
149-1	page	101
149-2	line	36
149-3	Identification of Deposit	
149-3-1	Name of depositary institution	American Type Culture Collection
149-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
149-3-3	Date of deposit	16 September 1997 (16.09.1997)
149-3-4	Accession Number	ATCC 209263
149-4	Additional Indications	NONE
149-5	Designated States for Which Indications are Made	all designated States
149-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
150	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
150-1	page	101
150-2	line	37
150-3	Identification of Deposit	
150-3-1	Name of depositary institution	American Type Culture Collection
150-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
150-3-3	Date of deposit	16 September 1997 (16.09.1997)
150-3-4	Accession Number	ATCC 209264
150-4	Additional Indications	NONE
150-5	Designated States for Which Indications are Made	all designated States
150-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
151	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
151-1	page	101
151-2	line	38
151-3	Identification of Deposit	
151-3-1	Name of depositary institution	American Type Culture Collection
151-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
151-3-3	Date of deposit	16 October 1997 (16.10.1997)
151-3-4	Accession Number	ATCC 209376
151-4	Additional Indications	NONE
151-5	Designated States for Which Indications are Made	all designated States

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151-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
152	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
152-1	page	101
152-2	line	39
152-3	Identification of Deposit	
152-3-1	Name of depositary institution	American Type Culture Collection
152-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
152-3-3	Date of deposit	17 October 1997 (17.10.1997)
152-3-4	Accession Number	ATCC 209391
152-4	Additional Indications	NONE
152-5	Designated States for Which Indications are Made	all designated States
152-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
153	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
153-1	page	101
153-2	line	40
153-3	Identification of Deposit	
153-3-1	Name of depositary institution	American Type Culture Collection
153-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
153-3-3	Date of deposit	28 October 1997 (28.10.1997)
153-3-4	Accession Number	ATCC 209417
153-4	Additional Indications	NONE
153-5	Designated States for Which Indications are Made	all designated States
153-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
154	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
154-1	page	101
154-2	line	41
154-3	Identification of Deposit	
154-3-1	Name of depositary institution	American Type Culture Collection
154-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
154-3-3	Date of deposit	16 September 1997 (16.09.1997)
154-3-4	Accession Number	ATCC 209253

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154-4	Additional Indications	NONE
154-5	Designated States for Which Indications are Made	all designated States
154-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
155	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
155-1	page	101
155-2	line	42
155-3	Identification of Deposit	
155-3-1	Name of depositary institution	American Type Culture Collection
155-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
155-3-3	Date of deposit	12 May 1998 (12.05.1998)
155-3-4	Accession Number	ATCC 209855
155-4	Additional Indications	NONE
155-5	Designated States for Which Indications are Made	all designated States
155-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
156	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
156-1	page	101
156-2	line	43
156-3	Identification of Deposit	
156-3-1	Name of depositary institution	American Type Culture Collection
156-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
156-3-3	Date of deposit	10 December 1997 (10.12.1997)
156-3-4	Accession Number	ATCC 209526
156-4	Additional Indications	NONE
156-5	Designated States for Which Indications are Made	all designated States
156-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
157	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
157-1	page	101
157-2	line	44



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<b>157-3</b>	<b>Identification of Deposit</b>	
<b>157-3-1</b>	Name of depositary institution	<b>American Type Culture Collection</b>
<b>157-3-2</b>	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209 United States of America</b>
<b>157-3-3</b>	Date of deposit	<b>16 September 1997 (16.09.1997)</b>
<b>157-3-4</b>	Accession Number	<b>ATCC 209252</b>
<b>157-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>157-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>157-6</b>	<b>Separate Furnishing of Indications</b>	<b>NONE</b>
	These indications will be submitted to the International Bureau later	
<b>158</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
<b>158-1</b>	page	<b>101</b>
<b>158-2</b>	line	<b>45</b>
<b>158-3</b>	<b>Identification of Deposit</b>	
<b>158-3-1</b>	Name of depositary institution	<b>American Type Culture Collection</b>
<b>158-3-2</b>	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209 United States of America</b>
<b>158-3-3</b>	Date of deposit	<b>16 October 1997 (16.10.1997)</b>
<b>158-3-4</b>	Accession Number	<b>ATCC 209374</b>
<b>158-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>158-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>158-6</b>	<b>Separate Furnishing of Indications</b>	<b>NONE</b>
	These indications will be submitted to the International Bureau later	
<b>159</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
<b>159-1</b>	page	<b>101</b>
<b>159-2</b>	line	<b>46</b>
<b>159-3</b>	<b>Identification of Deposit</b>	
<b>159-3-1</b>	Name of depositary institution	<b>American Type Culture Collection</b>
<b>159-3-2</b>	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209 United States of America</b>
<b>159-3-3</b>	Date of deposit	<b>10 December 1997 (10.12.1997)</b>
<b>159-3-4</b>	Accession Number	<b>ATCC 209528</b>
<b>159-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>159-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>159-6</b>	<b>Separate Furnishing of Indications</b>	<b>NONE</b>
	These indications will be submitted to the International Bureau later	

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160	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
160-1	page	101
160-2	line	47
160-3	Identification of Deposit	
160-3-1	Name of depositary institution	American Type Culture Collection
160-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
160-3-3	Date of deposit	16 September 1997 (16.09.1997)
160-3-4	Accession Number	ATCC 209265
160-4	Additional Indications	NONE
160-5	Designated States for Which Indications are Made	all designated States
160-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
161	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
161-1	page	101
161-2	line	48
161-3	Identification of Deposit	
161-3-1	Name of depositary institution	American Type Culture Collection
161-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
161-3-3	Date of deposit	17 October 1997 (17.10.1997)
161-3-4	Accession Number	ATCC 209396 .
161-4	Additional Indications	NONE
161-5	Designated States for Which Indications are Made	all designated States
161-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
162	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
162-1	page	101
162-2	line	49
162-3	Identification of Deposit	
162-3-1	Name of depositary institution	American Type Culture Collection
162-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
162-3-3	Date of deposit	18 August 1997 (18.08.1997)
162-3-4	Accession Number	ATCC 209201
162-4	Additional Indications	NONE
162-5	Designated States for Which Indications are Made	all designated States

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162-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
163	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
163-1	page	101
163-2	line	50
163-3	Identification of Deposit	
163-3-1	Name of depositary institution	American Type Culture Collection
163-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
163-3-3	Date of deposit	28 October 1997 (28.10.1997)
163-3-4	Accession Number	ATCC 209416
163-4	Additional Indications	NONE
163-5	Designated States for Which Indications are Made	all designated States
163-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
164	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
164-1	page	101
164-2	line	51
164-3	Identification of Deposit	
164-3-1	Name of depositary institution	American Type Culture Collection
164-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
164-3-3	Date of deposit	17 October 1997 (17.10.1997)
164-3-4	Accession Number	ATCC 209403
164-4	Additional Indications	NONE
164-5	Designated States for Which Indications are Made	all designated States
164-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
165	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
165-1	page	101
165-2	line	52
165-3	Identification of Deposit	
165-3-1	Name of depositary institution	American Type Culture Collection
165-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
165-3-3	Date of deposit	28 October 1997 (28.10.1997)
165-3-4	Accession Number	ATCC 209419

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165-4	Additional Indications	NONE
165-5	Designated States for Which Indications are Made	all designated States
165-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
166	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
166-1	page	101
166-2	line	53
166-3	Identification of Deposit	
166-3-1	Name of depositary institution	American Type Culture Collection
166-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
166-3-3	Date of deposit	17 October 1997 (17.10.1997)
166-3-4	Accession Number	ATCC 209402
166-4	Additional Indications	NONE
166-5	Designated States for Which Indications are Made	all designated States
166-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
167	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
167-1	page	101
167-2	line	54
167-3	Identification of Deposit	
167-3-1	Name of depositary institution	American Type Culture Collection
167-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
167-3-3	Date of deposit	16 October 1997 (16.10.1997)
167-3-4	Accession Number	ATCC 209378
167-4	Additional Indications	NONE
167-5	Designated States for Which Indications are Made	all designated States
167-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
168	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
168-1	page	101
168-2	line	55

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168-3	Identification of Deposit	
168-3-1	Name of depositary institution	American Type Culture Collection
168-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
168-3-3	Date of deposit	21 November 1997 (21.11.1997)
168-3-4	Accession Number	ATCC 209489
168-4	Additional Indications	NONE
168-5	Designated States for Which Indications are Made	all designated States
168-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
169	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
169-1	page	102
169-2	line	2
169-3	Identification of Deposit	
169-3-1	Name of depositary institution	American Type Culture Collection
169-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
169-3-3	Date of deposit	17 October 1997 (17.10.1997)
169-3-4	Accession Number	ATCC 209401
169-4	Additional Indications	NONE
169-5	Designated States for Which Indications are Made	all designated States
169-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
170	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
170-1	page	102
170-2	line	3
170-3	Identification of Deposit	
170-3-1	Name of depositary institution	American Type Culture Collection
170-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
170-3-3	Date of deposit	17 October 1997 (17.10.1997)
170-3-4	Accession Number	ATCC 209397
170-4	Additional Indications	NONE
170-5	Designated States for Which Indications are Made	all designated States
170-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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171	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
171-1	page	102
171-2	line	4
171-3	Identification of Deposit	
171-3-1	Name of depositary institution	American Type Culture Collection
171-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
171-3-3	Date of deposit	17 October 1997 (17.10.1997)
171-3-4	Accession Number	ATCC 209389
171-4	Additional Indications	NONE
171-5	Designated States for Which Indications are Made	all designated States
171-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
172	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
172-1	page	102
172-2	line	5
172-3	Identification of Deposit	
172-3-1	Name of depositary institution	American Type Culture Collection
172-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
172-3-3	Date of deposit	07 November 1997 (07.11.1997)
172-3-4	Accession Number	ATCC 209438
172-4	Additional Indications	NONE
172-5	Designated States for Which Indications are Made	all designated States
172-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
173	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
173-1	page	102
173-2	line	6
173-3	Identification of Deposit	
173-3-1	Name of depositary institution	American Type Culture Collection
173-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
173-3-3	Date of deposit	21 November 1997 (21.11.1997)
173-3-4	Accession Number	ATCC 209492
173-4	Additional Indications	NONE
173-5	Designated States for Which Indications are Made	all designated States

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173-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
174	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
174-1	page	102
174-2	line	7
174-3	Identification of Deposit	
174-3-1	Name of depositary institution	American Type Culture Collection
174-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
174-3-3	Date of deposit	17 October 1997 (17.10.1997)
174-3-4	Accession Number	ATCC 209388
174-4	Additional Indications	NONE
174-5	Designated States for Which Indications are Made	all designated States
174-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
175	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
175-1	page	102
175-2	line	8
175-3	Identification of Deposit	
175-3-1	Name of depositary institution	American Type Culture Collection
175-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
175-3-3	Date of deposit	07 November 1997 (07.11.1997)
175-3-4	Accession Number	ATCC 209432
175-4	Additional Indications	NONE
175-5	Designated States for Which Indications are Made	all designated States
175-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
176	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
176-1	page	102
176-2	line	9
176-3	Identification of Deposit	
176-3-1	Name of depositary institution	American Type Culture Collection
176-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
176-3-3	Date of deposit	07 November 1997 (07.11.1997)
176-3-4	Accession Number	ATCC 209439

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176-4	Additional Indications	NONE
176-5	Designated States for Which Indications are Made	all designated States
176-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
177	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
177-1	page	102
177-2	line	10
177-3	Identification of Deposit	
177-3-1	Name of depositary institution	American Type Culture Collection
177-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
177-3-3	Date of deposit	07 November 1997 (07.11.1997)
177-3-4	Accession Number	ATCC 209433
177-4	Additional Indications	NONE
177-5	Designated States for Which Indications are Made	all designated States
177-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
178	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
178-1	page	102
178-2	line	11
178-3	Identification of Deposit	
178-3-1	Name of depositary institution	American Type Culture Collection
178-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
178-3-3	Date of deposit	05 February 1998 (05.02.1998)
178-3-4	Accession Number	ATCC 209618
178-4	Additional Indications	NONE
178-5	Designated States for Which Indications are Made	all designated States
178-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
179	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
179-1	page	102
179-2	line	12



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179-3	Identification of Deposit	
179-3-1	Name of depositary institution	American Type Culture Collection
179-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
179-3-3	Date of deposit	21 November 1997 (21.11.1997)
179-3-4	Accession Number	ATCC 209484
179-4	Additional Indications	NONE
179-5	Designated States for Which Indications are Made	all designated States
179-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
180	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
180-1	page	102
180-2	line	13
180-3	Identification of Deposit	
180-3-1	Name of depositary institution	American Type Culture Collection
180-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
180-3-3	Date of deposit	21 November 1997 (21.11.1997)
180-3-4	Accession Number	ATCC 209487
180-4	Additional Indications	NONE
180-5	Designated States for Which Indications are Made	all designated States
180-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
181	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
181-1	page	102
181-2	line	14
181-3	Identification of Deposit	
181-3-1	Name of depositary institution	American Type Culture Collection
181-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
181-3-3	Date of deposit	07 November 1997 (07.11.1997)
181-3-4	Accession Number	ATCC 209434
181-4	Additional Indications	NONE
181-5	Designated States for Which Indications are Made	all designated States
181-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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182	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
182-1	page	102
182-2	line	15
182-3	Identification of Deposit	
182-3-1	Name of depositary institution	American Type Culture Collection
182-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
182-3-3	Date of deposit	26 March 1998 (26.03.1998)
182-3-4	Accession Number	ATCC 209704
182-4	Additional Indications	NONE
182-5	Designated States for Which Indications are Made	all designated States
182-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
183	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
183-1	page	102
183-2	line	16
183-3	Identification of Deposit	
183-3-1	Name of depositary institution	American Type Culture Collection
183-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
183-3-3	Date of deposit	28 April 1998 (28.04.1998)
183-3-4	Accession Number	ATCC 209808
183-4	Additional Indications	NONE
183-5	Designated States for Which Indications are Made	all designated States
183-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
184	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
184-1	page	102
184-2	line	17
184-3	Identification of Deposit	
184-3-1	Name of depositary institution	American Type Culture Collection
184-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
184-3-3	Date of deposit	06 May 1998 (06.05.1998)
184-3-4	Accession Number	ATCC 209847
184-4	Additional Indications	NONE
184-5	Designated States for Which Indications are Made	all designated States

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184-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
185	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
185-1	page	102
185-2	line	18
185-3	Identification of Deposit	
185-3-1	Name of depositary institution	American Type Culture Collection
185-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
185-3-3	Date of deposit	05 February 1998 (05.02.1998)
185-3-4	Accession Number	ATCC 209616
185-4	Additional Indications	NONE
185-5	Designated States for Which Indications are Made	all designated States
185-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
186	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
186-1	page	102
186-2	line	19
186-3	Identification of Deposit	
186-3-1	Name of depositary institution	American Type Culture Collection
186-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
186-3-3	Date of deposit	05 February 1998 (05.02.1998)
186-3-4	Accession Number	ATCC 209619
186-4	Additional Indications	NONE
186-5	Designated States for Which Indications are Made	all designated States
186-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
187	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
187-1	page	102
187-2	line	20
187-3	Identification of Deposit	
187-3-1	Name of depositary institution	American Type Culture Collection
187-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
187-3-3	Date of deposit	11 August 1998 (11.08.1998)
187-3-4	Accession Number	ATCC 203109

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187-4	Additional Indications	NONE
187-5	Designated States for Which Indications are Made	all designated States
187-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
188	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
188-1	page	102
188-2	line	21
188-3	Identification of Deposit	
188-3-1	Name of depositary institution	American Type Culture Collection
188-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
188-3-3	Date of deposit	31 March 1998 (31.03.1998)
188-3-4	Accession Number	ATCC 209715
188-4	Additional Indications	NONE
188-5	Designated States for Which Indications are Made	all designated States
188-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
189	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
189-1	page	102
189-2	line	22
189-3	Identification of Deposit	
189-3-1	Name of depositary institution	American Type Culture Collection
189-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
189-3-3	Date of deposit	11 March 1998 (11.03.1998)
189-3-4	Accession Number	ATCC 209669
189-4	Additional Indications	NONE
189-5	Designated States for Which Indications are Made	all designated States
189-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
190	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
190-1	page	102
190-2	line	23

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190-3	Identification of Deposit	
190-3-1	Name of depositary institution	American Type Culture Collection
190-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
190-3-3	Date of deposit	23 June 1998 (23.06.1998)
190-3-4	Accession Number	ATCC 203002
190-4	Additional Indications	NONE
190-5	Designated States for Which Indications are Made	all designated States
190-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
191	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
191-1	page	102
191-2	line	24
191-3	Identification of Deposit	
191-3-1	Name of depositary institution	American Type Culture Collection
191-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
191-3-3	Date of deposit	26 March 1998 (26.03.1998)
191-3-4	Accession Number	ATCC 209705
191-4	Additional Indications	NONE
191-5	Designated States for Which Indications are Made	all designated States
191-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
192	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
192-1	page	102
192-2	line	25
192-3	Identification of Deposit	
192-3-1	Name of depositary institution	American Type Culture Collection
192-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
192-3-3	Date of deposit	16 June 1998 (16.06.1998)
192-3-4	Accession Number	ATCC 209981
192-4	Additional Indications	NONE
192-5	Designated States for Which Indications are Made	all designated States
192-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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193	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
193-1	page	102
193-2	line	26
193-3	Identification of Deposit	
193-3-1	Name of depositary institution	American Type Culture Collection
193-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
193-3-3	Date of deposit	07 April 1998 (07.04.1998)
193-3-4	Accession Number	ATCC 209749
193-4	Additional Indications	NONE
193-5	Designated States for Which Indications are Made	all designated States
193-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
194	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
194-1	page	102
194-2	line	27
194-3	Identification of Deposit	
194-3-1	Name of depositary institution	American Type Culture Collection
194-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
194-3-3	Date of deposit	12 May 1998 (12.05.1998)
194-3-4	Accession Number	ATCC 209859
194-4	Additional Indications	NONE
194-5	Designated States for Which Indications are Made	all designated States
194-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
195	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
195-1	page	102
195-2	line	28
195-3	Identification of Deposit	
195-3-1	Name of depositary institution	American Type Culture Collection
195-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
195-3-3	Date of deposit	06 May 1998 (06.05.1998)
195-3-4	Accession Number	ATCC 209845
195-4	Additional Indications	NONE
195-5	Designated States for Which Indications are Made	all designated States

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195-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
196	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
196-1	page	102
196-2	line	29
196-3	Identification of Deposit	
196-3-1	Name of depositary institution	American Type Culture Collection
196-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
196-3-3	Date of deposit	07 April 1998 (07.04.1998)
196-3-4	Accession Number	ATCC 209748
196-4	Additional Indications	NONE
196-5	Designated States for Which Indications are Made	all designated States
196-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
197	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
197-1	page	102
197-2	line	30
197-3	Identification of Deposit	
197-3-1	Name of depositary institution	American Type Culture Collection
197-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
197-3-3	Date of deposit	11 August 1998 (11.08.1998)
197-3-4	Accession Number	ATCC 203107
197-4	Additional Indications	NONE
197-5	Designated States for Which Indications are Made	all designated States
197-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
198	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
198-1	page	102
198-2	line	31
198-3	Identification of Deposit	
198-3-1	Name of depositary institution	American Type Culture Collection
198-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
198-3-3	Date of deposit	23 April 1998 (23.04.1998)
198-3-4	Accession Number	ATCC 209801

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198-4	Additional Indications	NONE
198-5	Designated States for Which Indications are Made	all designated States
198-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
199	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
199-1	page	102
199-2	line	32
199-3	Identification of Deposit	
199-3-1	Name of depositary institution	American Type Culture Collection
199-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
199-3-3	Date of deposit	09 June 1998 (09.06.1998)
199-3-4	Accession Number	ATCC 209948
199-4	Additional Indications	NONE
199-5	Designated States for Which Indications are Made	all designated States
199-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
200	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
200-1	page	102
200-2	line	33
200-3	Identification of Deposit	
200-3-1	Name of depositary institution	American Type Culture Collection
200-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
200-3-3	Date of deposit	20 May 1998 (20.05.1998)
200-3-4	Accession Number	ATCC 209883
200-4	Additional Indications	NONE
200-5	Designated States for Which Indications are Made	all designated States
200-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
201	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
201-1	page	102
201-2	line	34



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201-3	Identification of Deposit	
201-3-1	Name of depositary institution	American Type Culture Collection
201-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
201-3-3	Date of deposit	01 July 1998 (01.07.1998)
201-3-4	Accession Number	ATCC 203049
201-4	Additional Indications	NONE
201-5	Designated States for Which Indications are Made	all designated States
201-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
202	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
202-1	page	102
202-2	line	35
202-3	Identification of Deposit	
202-3-1	Name of depositary institution	American Type Culture Collection
202-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
202-3-3	Date of deposit	06 May 1998 (06.05.1998)
202-3-4	Accession Number	ATCC 209846
202-4	Additional Indications	NONE
202-5	Designated States for Which Indications are Made	all designated States
202-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
203	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
203-1	page	102
203-2	line	36
203-3	Identification of Deposit	
203-3-1	Name of depositary institution	American Type Culture Collection
203-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
203-3-3	Date of deposit	12 May 1998 (12.05.1998)
203-3-4	Accession Number	ATCC 209857
203-4	Additional Indications	NONE
203-5	Designated States for Which Indications are Made	all designated States
203-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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204	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
204-1	page	102
204-2	line	37
204-3	Identification of Deposit	
204-3-1	Name of depositary institution	American Type Culture Collection
204-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
204-3-3	Date of deposit	14 May 1998 (14.05.1998)
204-3-4	Accession Number	ATCC 209864
204-4	Additional Indications	NONE
204-5	Designated States for Which Indications are Made	all designated States
204-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
205	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
205-1	page	102
205-2	line	38
205-3	Identification of Deposit	
205-3-1	Name of depositary institution	American Type Culture Collection
205-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
205-3-3	Date of deposit	20 May 1998 (20.05.1998)
205-3-4	Accession Number	ATCC 209880
205-4	Additional Indications	NONE
205-5	Designated States for Which Indications are Made	all designated States
205-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
206	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
206-1	page	102
206-2	line	39
206-3	Identification of Deposit	
206-3-1	Name of depositary institution	American Type Culture Collection
206-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
206-3-3	Date of deposit	14 May 1998 (14.05.1998)
206-3-4	Accession Number	ATCC 209869
206-4	Additional Indications	NONE
206-5	Designated States for Which Indications are Made	all designated States

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206-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
207	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
207-1	page	102
207-2	line	40
207-3	Identification of Deposit	
207-3-1	Name of depositary institution	American Type Culture Collection
207-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
207-3-3	Date of deposit	09 June 1998 (09.06.1998)
207-3-4	Accession Number	ATCC 209950
207-4	Additional Indications	NONE
207-5	Designated States for Which Indications are Made	all designated States
207-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
208	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
208-1	page	102
208-2	line	41
208-3	Identification of Deposit	
208-3-1	Name of depositary institution	American Type Culture Collection
208-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
208-3-3	Date of deposit	23 June 1998 (23.06.1998)
208-3-4	Accession Number	ATCC 203008
208-4	Additional Indications	NONE
208-5	Designated States for Which Indications are Made	all designated States
208-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
209	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
209-1	page	102
209-2	line	42
209-3	Identification of Deposit	
209-3-1	Name of depositary institution	American Type Culture Collection
209-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
209-3-3	Date of deposit	23 June 1998 (23.06.1998)
209-3-4	Accession Number	ATCC 203014

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209-4	Additional Indications	NONE
209-5	Designated States for Which Indications are Made	all designated States
209-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
210	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
210-1	page	102
210-2	line	43
210-3	Identification of Deposit	
210-3-1	Name of depositary institution	American Type Culture Collection
210-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
210-3-3	Date of deposit	11 August 1998 (11.08.1998)
210-3-4	Accession Number	ATCC 203110
210-4	Additional Indications	NONE
210-5	Designated States for Which Indications are Made	all designated States
210-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
211	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
211-1	page	102
211-2	line	44
211-3	Identification of Deposit	
211-3-1	Name of depositary institution	American Type Culture Collection
211-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
211-3-3	Date of deposit	23 June 1998 (23.06.1998)
211-3-4	Accession Number	ATCC 203009
211-4	Additional Indications	NONE
211-5	Designated States for Which Indications are Made	all designated States
211-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
212	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
212-1	page	102
212-2	line	45

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212-3	Identification of Deposit	
212-3-1	Name of depositary institution	American Type Culture Collection
212-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
212-3-3	Date of deposit	09 June 1998 (09.06.1998)
212-3-4	Accession Number	ATCC 209961
212-4	Additional Indications	NONE
212-5	Designated States for Which Indications are Made	all designated States
212-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
213	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
213-1	page	102
213-2	line	46
213-3	Identification of Deposit	
213-3-1	Name of depositary institution	American Type Culture Collection
213-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
213-3-3	Date of deposit	09 June 1998 (09.06.1998)
213-3-4	Accession Number	ATCC 209962
213-4	Additional Indications	NONE
213-5	Designated States for Which Indications are Made	all designated States
213-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
214	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
214-1	page	102
214-2	line	47
214-3	Identification of Deposit	
214-3-1	Name of depositary institution	American Type Culture Collection
214-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
214-3-3	Date of deposit	14 May 1998 (14.05.1998)
214-3-4	Accession Number	ATCC 209866
214-4	Additional Indications	NONE
214-5	Designated States for Which Indications are Made	all designated States
214-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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215	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
215-1	page	102
215-2	line	48
215-3	Identification of Deposit	
215-3-1	Name of depositary institution	American Type Culture Collection
215-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
215-3-3	Date of deposit	25 August 1998 (25.08.1998)
215-3-4	Accession Number	ATCC 203157
215-4	Additional Indications	NONE
215-5	Designated States for Which Indications are Made	all designated States
215-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
216	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
216-1	page	102
216-2	line	49
216-3	Identification of Deposit	
216-3-1	Name of depositary institution	American Type Culture Collection
216-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
216-3-3	Date of deposit	11 August 1998 (11.08.1998)
216-3-4	Accession Number	ATCC 203106
216-4	Additional Indications	NONE
216-5	Designated States for Which Indications are Made	all designated States
216-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
217	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
217-1	page	102
217-2	line	50
217-3	Identification of Deposit	
217-3-1	Name of depositary institution	American Type Culture Collection
217-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
217-3-3	Date of deposit	09 June 1998 (09.06.1998)
217-3-4	Accession Number	ATCC 209945
217-4	Additional Indications	NONE
217-5	Designated States for Which Indications are Made	all designated States

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217-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
218	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
218-1	page	102
218-2	line	51
218-3	Identification of Deposit	
218-3-1	Name of depositary institution	American Type Culture Collection
218-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
218-3-3	Date of deposit	16 June 1998 (16.06.1998)
218-3-4	Accession Number	ATCC 209989
218-4	Additional Indications	NONE
218-5	Designated States for Which Indications are Made	all designated States
218-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
219	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
219-1	page	102
219-2	line	52
219-3	Identification of Deposit	
219-3-1	Name of depositary institution	American Type Culture Collection
219-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
219-3-3	Date of deposit	11 August 1998 (11.08.1998)
219-3-4	Accession Number	ATCC 203108
219-4	Additional Indications	NONE
219-5	Designated States for Which Indications are Made	all designated States
219-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
220	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
220-1	page	102
220-2	line	53
220-3	Identification of Deposit	
220-3-1	Name of depositary institution	American Type Culture Collection
220-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
220-3-3	Date of deposit	11 August 1998 (11.08.1998)
220-3-4	Accession Number	ATCC 203111

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220-4	Additional Indications	NONE
220-5	Designated States for Which Indications are Made	all designated States
220-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
221	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
221-1	page	102
221-2	line	54
221-3	Identification of Deposit	
221-3-1	Name of depositary institution	American Type Culture Collection
221-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
221-3-3	Date of deposit	20 October 1998 (20.10.1998)
221-3-4	Accession Number	ATCC 203359
221-4	Additional Indications	NONE
221-5	Designated States for Which Indications are Made	all designated States
221-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
222	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
222-1	page	102
222-2	line	55
222-3	Identification of Deposit	
222-3-1	Name of depositary institution	American Type Culture Collection
222-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
222-3-3	Date of deposit	16 June 1998 (16.06.1998)
222-3-4	Accession Number	ATCC 209988
222-4	Additional Indications	NONE
222-5	Designated States for Which Indications are Made	all designated States
222-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
223	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
223-1	page	103
223-2	line	2



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223-3	Identification of Deposit	
223-3-1	Name of depositary institution	American Type Culture Collection
223-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
223-3-3	Date of deposit	16 June 1998 (16.06.1998)
223-3-4	Accession Number	ATCC 209978
223-4	Additional Indications	NONE
223-5	Designated States for Which Indications are Made	all designated States
223-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
224	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
224-1	page	103
224-2	line	3
224-3	Identification of Deposit	
224-3-1	Name of depositary institution	American Type Culture Collection
224-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
224-3-3	Date of deposit	04 August 1998 (04.08.1998)
224-3-4	Accession Number	ATCC 203098
224-4	Additional Indications	NONE
224-5	Designated States for Which Indications are Made	all designated States
224-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
225	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
225-1	page	103
225-2	line	4
225-3	Identification of Deposit	
225-3-1	Name of depositary institution	American Type Culture Collection
225-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
225-3-3	Date of deposit	16 June 1998 (16.06.1998)
225-3-4	Accession Number	ATCC 209980
225-4	Additional Indications	NONE
225-5	Designated States for Which Indications are Made	all designated States
225-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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226	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
226-1	page	103
226-2	line	5
226-3	Identification of Deposit	
226-3-1	Name of depositary institution	American Type Culture Collection
226-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
226-3-3	Date of deposit	04 August 1998 (04.08.1998)
226-3-4	Accession Number	ATCC 203091
226-4	Additional Indications	NONE
226-5	Designated States for Which Indications are Made	all designated States
226-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
227	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
227-1	page	103
227-2	line	6
227-3	Identification of Deposit	
227-3-1	Name of depositary institution	American Type Culture Collection
227-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
227-3-3	Date of deposit	04 August 1998 (04.08.1998)
227-3-4	Accession Number	ATCC 203090
227-4	Additional Indications	NONE
227-5	Designated States for Which Indications are Made	all designated States
227-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
228	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
228-1	page	103
228-2	line	7
228-3	Identification of Deposit	
228-3-1	Name of depositary institution	American Type Culture Collection
228-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
228-3-3	Date of deposit	04 August 1998 (04.08.1998)
228-3-4	Accession Number	ATCC 203092
228-4	Additional Indications	NONE
228-5	Designated States for Which Indications are Made	all designated States

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228-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
229	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
229-1	page	103
229-2	line	8
229-3	Identification of Deposit	
229-3-1	Name of depositary institution	American Type Culture Collection
229-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
229-3-3	Date of deposit	10 November 1998 (10.11.1998)
229-3-4	Accession Number	ATCC 203452
229-4	Additional Indications	NONE
229-5	Designated States for Which Indications are Made	all designated States
229-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
230	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
230-1	page	103
230-2	line	9
230-3	Identification of Deposit	
230-3-1	Name of depositary institution	American Type Culture Collection
230-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
230-3-3	Date of deposit	01 September 1998 (01.09.1998)
230-3-4	Accession Number	ATCC 203173
230-4	Additional Indications	NONE
230-5	Designated States for Which Indications are Made	all designated States
230-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
231	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
231-1	page	103
231-2	line	10
231-3	Identification of Deposit	
231-3-1	Name of depositary institution	American Type Culture Collection
231-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
231-3-3	Date of deposit	17 November 1998 (17.11.1998)
231-3-4	Accession Number	ATCC 203464

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231-4	Additional Indications	NONE
231-5	Designated States for Which Indications are Made	all designated States
231-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
232	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
232-1	page	103
232-2	line	11
232-3	Identification of Deposit	
232-3-1	Name of depositary institution	American Type Culture Collection
232-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
232-3-3	Date of deposit	18 August 1998 (18.08.1998)
232-3-4	Accession Number	ATCC 203132
232-4	Additional Indications	NONE
232-5	Designated States for Which Indications are Made	all designated States
232-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
233	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
233-1	page	103
233-2	line	12
233-3	Identification of Deposit	
233-3-1	Name of depositary institution	American Type Culture Collection
233-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
233-3-3	Date of deposit	09 September 1998 (09.09.1998)
233-3-4	Accession Number	ATCC 203254
233-4	Additional Indications	NONE
233-5	Designated States for Which Indications are Made	all designated States
233-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
234	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
234-1	page	103
234-2	line	13

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234-3	Identification of Deposit	
234-3-1	Name of depositary institution	American Type Culture Collection
234-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
234-3-3	Date of deposit	20 October 1998 (20.10.1998)
234-3-4	Accession Number	ATCC 203358
234-4	Additional Indications	NONE
234-5	Designated States for Which Indications are Made	all designated States
234-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
235	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
235-1	page	103
235-2	line	14
235-3	Identification of Deposit	
235-3-1	Name of depositary institution	American Type Culture Collection
235-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
235-3-3	Date of deposit	04 August 1998 (04.08.1998)
235-3-4	Accession Number	ATCC 203093
235-4	Additional Indications	NONE
235-5	Designated States for Which Indications are Made	all designated States
235-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
236	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
236-1	page	103
236-2	line	15
236-3	Identification of Deposit	
236-3-1	Name of depositary institution	American Type Culture Collection
236-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
236-3-3	Date of deposit	03 November 1998 (03.11.1998)
236-3-4	Accession Number	ATCC 203457
236-4	Additional Indications	NONE
236-5	Designated States for Which Indications are Made	all designated States
236-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	

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237	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
237-1	page	103
237-2	line	16
237-3	Identification of Deposit	
237-3-1	Name of depositary institution	American Type Culture Collection
237-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
237-3-3	Date of deposit	09 September 1998 (09.09.1998)
237-3-4	Accession Number	ATCC 203241
237-4	Additional Indications	NONE
237-5	Designated States for Which Indications are Made	all designated States
237-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
238	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
238-1	page	103
238-2	line	17
238-3	Identification of Deposit	
238-3-1	Name of depositary institution	American Type Culture Collection
238-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
238-3-3	Date of deposit	09 September 1998 (09.09.1998)
238-3-4	Accession Number	ATCC 203249
238-4	Additional Indications	NONE
238-5	Designated States for Which Indications are Made	all designated States
238-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
239	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
239-1	page	103
239-2	line	18
239-3	Identification of Deposit	
239-3-1	Name of depositary institution	American Type Culture Collection
239-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
239-3-3	Date of deposit	09 September 1998 (09.09.1998)
239-3-4	Accession Number	ATCC 203250
239-4	Additional Indications	NONE
239-5	Designated States for Which Indications are Made	all designated States

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239-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
240	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
240-1	page	103
240-2	line	19
240-3	Identification of Deposit	
240-3-1	Name of depositary institution	American Type Culture Collection
240-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
240-3-3	Date of deposit	18 August 1998 (18.08.1998)
240-3-4	Accession Number	ATCC 203131
240-4	Additional Indications	NONE
240-5	Designated States for Which Indications are Made	all designated States
240-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
241	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
241-1	page	103
241-2	line	20
241-3	Identification of Deposit	
241-3-1	Name of depositary institution	American Type Culture Collection
241-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
241-3-3	Date of deposit	15 September 1998 (15.09.1998)
241-3-4	Accession Number	ATCC 203223
241-4	Additional Indications	NONE
241-5	Designated States for Which Indications are Made	all designated States
241-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
242	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
242-1	page	103
242-2	line	21
242-3	Identification of Deposit	
242-3-1	Name of depositary institution	American Type Culture Collection
242-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
242-3-3	Date of deposit	15 September 1998 (15.09.1998)
242-3-4	Accession Number	ATCC 203233

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242-4	Additional Indications	NONE
242-5	Designated States for Which Indications are Made	all designated States
242-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
243	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
243-1	page	103
243-2	line	22
243-3	Identification of Deposit	
243-3-1	Name of depositary institution	American Type Culture Collection
243-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
243-3-3	Date of deposit	09 September 1998 (09.09.1998)
243-3-4	Accession Number	ATCC 203252
243-4	Additional Indications	NONE
243-5	Designated States for Which Indications are Made	all designated States
243-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
244	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
244-1	page	103
244-2	line	23
244-3	Identification of Deposit	
244-3-1	Name of depositary institution	American Type Culture Collection
244-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
244-3-3	Date of deposit	17 November 1998 (17.11.1998)
244-3-4	Accession Number	ATCC 203476
244-4	Additional Indications	NONE
244-5	Designated States for Which Indications are Made	all designated States
244-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
245	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
245-1	page	103
245-2	line	24



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245-3	Identification of Deposit	
245-3-1	Name of depositary institution	American Type Culture Collection
245-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
245-3-3	Date of deposit	04 August 1998 (04.08.1998)
245-3-4	Accession Number	ATCC 203094
245-4	Additional Indications	NONE
245-5	Designated States for Which Indications are Made	all designated States
245-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
246	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
246-1	page	103
246-2	line	25
246-3	Identification of Deposit	
246-3-1	Name of depositary institution	American Type Culture Collection
246-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
246-3-3	Date of deposit	15 September 1998 (15.09.1998)
246-3-4	Accession Number	ATCC 203235
246-4	Additional Indications	NONE
246-5	Designated States for Which Indications are Made	all designated States
246-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
247	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
247-1	page	103
247-2	line	26
247-3	Identification of Deposit	
247-3-1	Name of depositary institution	American Type Culture Collection
247-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
247-3-3	Date of deposit	22 September 1998 (22.09.1998)
247-3-4	Accession Number	ATCC 203267
247-4	Additional Indications	NONE
247-5	Designated States for Which Indications are Made	all designated States
247-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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248	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
248-1	page	103
248-2	line	27
248-3	Identification of Deposit	
248-3-1	Name of depositary institution	American Type Culture Collection
248-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
248-3-3	Date of deposit	22 September 1998 (22.09.1998)
248-3-4	Accession Number	ATCC 203282
248-4	Additional Indications	NONE
248-5	Designated States for Which Indications are Made	all designated States
248-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
249	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
249-1	page	103
249-2	line	28
249-3	Identification of Deposit	
249-3-1	Name of depositary institution	American Type Culture Collection
249-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
249-3-3	Date of deposit	09 February 1999 (09.02.1999)
249-3-4	Accession Number	ATCC 203657
249-4	Additional Indications	NONE
249-5	Designated States for Which Indications are Made	all designated States
249-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
250	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
250-1	page	103
250-2	line	29
250-3	Identification of Deposit	
250-3-1	Name of depositary institution	American Type Culture Collection
250-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
250-3-3	Date of deposit	22 September 1998 (22.09.1998)
250-3-4	Accession Number	ATCC 203276
250-4	Additional Indications	NONE
250-5	Designated States for Which Indications are Made	all designated States

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250-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
251	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
251-1	page	103
251-2	line	30
251-3	Identification of Deposit	
251-3-1	Name of depositary institution	American Type Culture Collection
251-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
251-3-3	Date of deposit	25 August 1998 (25.08.1998)
251-3-4	Accession Number	ATCC 203160
251-4	Additional Indications	NONE
251-5	Designated States for Which Indications are Made	all designated States
251-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
252	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
252-1	page	103
252-2	line	31
252-3	Identification of Deposit	
252-3-1	Name of depositary institution	American Type Culture Collection
252-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
252-3-3	Date of deposit	18 August 1998 (18.08.1998)
252-3-4	Accession Number	ATCC 203135
252-4	Additional Indications	NONE
252-5	Designated States for Which Indications are Made	all designated States
252-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
253	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
253-1	page	103
253-2	line	32
253-3	Identification of Deposit	
253-3-1	Name of depositary institution	American Type Culture Collection
253-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
253-3-3	Date of deposit	03 November 1998 (03.11.1998)
253-3-4	Accession Number	ATCC 203459

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253-4	Additional Indications	NONE
253-5	Designated States for Which Indications are Made	all designated States
253-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
254	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
254-1	page	103
254-2	line	33
254-3	Identification of Deposit	
254-3-1	Name of depositary institution	American Type Culture Collection
254-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
254-3-3	Date of deposit	22 September 1998 (22.09.1998)
254-3-4	Accession Number	ATCC 203270
254-4	Additional Indications	NONE
254-5	Designated States for Which Indications are Made	all designated States
254-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
255	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
255-1	page	103
255-2	line	34
255-3	Identification of Deposit	
255-3-1	Name of depositary institution	American Type Culture Collection
255-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
255-3-3	Date of deposit	12 January 1999 (12.01.1999)
255-3-4	Accession Number	ATCC 203573
255-4	Additional Indications	NONE
255-5	Designated States for Which Indications are Made	all designated States
255-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
256	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
256-1	page	103
256-2	line	35

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256-3	Identification of Deposit	
256-3-1	Name of depositary institution	American Type Culture Collection
256-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
256-3-3	Date of deposit	17 November 1998 (17.11.1998)
256-3-4	Accession Number	ATCC 203477
256-4	Additional Indications	NONE
256-5	Designated States for Which Indications are Made	all designated States
256-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
257	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
257-1	page	103
257-2	line	36
257-3	Identification of Deposit	
257-3-1	Name of depositary institution	American Type Culture Collection
257-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
257-3-3	Date of deposit	06 October 1998 (06.10.1998)
257-3-4	Accession Number	ATCC 203315
257-4	Additional Indications	NONE
257-5	Designated States for Which Indications are Made	all designated States
257-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
258	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
258-1	page	103
258-2	line	37
258-3	Identification of Deposit	
258-3-1	Name of depositary institution	American Type Culture Collection
258-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
258-3-3	Date of deposit	06 October 1998 (06.10.1998)
258-3-4	Accession Number	ATCC 203313
258-4	Additional Indications	NONE
258-5	Designated States for Which Indications are Made	all designated States
258-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

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259	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
259-1	page	103
259-2	line	38
259-3	Identification of Deposit	
259-3-1	Name of depositary institution	American Type Culture Collection
259-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
259-3-3	Date of deposit	27 October 1998 (27.10.1998)
259-3-4	Accession Number	ATCC 203407
259-4	Additional Indications	NONE
259-5	Designated States for Which Indications are Made	all designated States
259-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
260	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
260-1	page	103
260-2	line	39
260-3	Identification of Deposit	
260-3-1	Name of depositary institution	American Type Culture Collection
260-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
260-3-3	Date of deposit	22 December 1998 (22.12.1998)
260-3-4	Accession Number	ATCC 203553
260-4	Additional Indications	NONE
260-5	Designated States for Which Indications are Made	all designated States
260-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
261	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
261-1	page	103
261-2	line	40
261-3	Identification of Deposit	
261-3-1	Name of depositary institution	American Type Culture Collection
261-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
261-3-3	Date of deposit	22 December 1998 (22.12.1998)
261-3-4	Accession Number	ATCC 203549
261-4	Additional Indications	NONE
261-5	Designated States for Which Indications are Made	all designated States

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261-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
262	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
262-1	page	103
262-2	line	41
262-3	Identification of Deposit	
262-3-1	Name of depositary institution	American Type Culture Collection
262-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
262-3-3	Date of deposit	22 December 1998 (22.12.1998)
262-3-4	Accession Number	ATCC 203550
262-4	Additional Indications	NONE
262-5	Designated States for Which Indications are Made	all designated States
262-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
263	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
263-1	page	103
263-2	line	42
263-3	Identification of Deposit	
263-3-1	Name of depositary institution	American Type Culture Collection
263-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
263-3-3	Date of deposit	08 June 1999 (08.06.1999)
263-3-4	Accession Number	ATCC PTA-204
263-4	Additional Indications	NONE
263-5	Designated States for Which Indications are Made	all designated States
263-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
264	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
264-1	page	103
264-2	line	43
264-3	Identification of Deposit	
264-3-1	Name of depositary institution	American Type Culture Collection
264-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
264-3-3	Date of deposit	29 October 1998 (29.10.1998)
264-3-4	Accession Number	ATCC 203391

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264-4	Additional Indications	NONE
264-5	Designated States for Which Indications are Made	all designated States
264-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
265	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
265-1	page	103
265-2	line	44
265-3	Identification of Deposit	
265-3-1	Name of depositary institution	American Type Culture Collection
265-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
265-3-3	Date of deposit	23 March 1999 (23.03.1999)
265-3-4	Accession Number	ATCC 203863
265-4	Additional Indications	NONE
265-5	Designated States for Which Indications are Made	all designated States
265-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
266	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
266-1	page	103
266-2	line	45
266-3	Identification of Deposit	
266-3-1	Name of depositary institution	American Type Culture Collection
266-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
266-3-3	Date of deposit	09 March 1999 (09.03.1999)
266-3-4	Accession Number	ATCC 203834
266-4	Additional Indications	NONE
266-5	Designated States for Which Indications are Made	all designated States
266-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
267	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
267-1	page	103
267-2	line	46



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267-3	Identification of Deposit	
267-3-1	Name of depositary institution	American Type Culture Collection
267-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
267-3-3	Date of deposit	20 July 1999 (20.07.1999)
267-3-4	Accession Number	ATCC PTA-382
267-4	Additional Indications	NONE
267-5	Designated States for Which Indications are Made	all designated States
267-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

## FOR RECEIVING OFFICE USE ONLY

0-4	This form was received with the international application: (yes or no)	
0-4-1	Authorized officer	

## FOR INTERNATIONAL BUREAU USE ONLY

0-5	This form was received by the International Bureau on:	
0-5-1	Authorized officer	

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID

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NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) and Figure 550 (SEQ ID NO:550).

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2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID

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NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figure 525 (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547) and Figure 549 (SEQ ID NO:549).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:1390), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ

ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225),  
5 Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ  
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15 Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figure 311 (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ  
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25 Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ  
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ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figure 525 (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547) and Figure 549 (SEQ ID NO:549).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.

6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

7. A host cell comprising the vector of Claim 5.

8. The host cell of Claim 7, wherein said cell is a CHO cell.

9. The host cell of Claim 7, wherein said cell is an *E. coli*.

10. The host cell of Claim 7, wherein said cell is a yeast cell.

11. A process for producing a PRO polypeptides comprising culturing the host cell of Claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10),



Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48),  
5 Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86),  
10 Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure

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Figure 550 (SEQ ID NO:550).

13. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

14. A chimeric molecule comprising a polypeptide according to Claim 12 fused to a heterologous amino acid sequence.

15. The chimeric molecule of Claim 14, wherein said heterologous amino acid sequence is an epitope tag sequence.

16. The chimeric molecule of Claim 14, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

17. An antibody which specifically binds to a polypeptide according to Claim 12.

18. The antibody of Claim 17, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

19. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ

ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158),  
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 20 Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2  
 25 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100),

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Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID

NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114),  
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30 20. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20  
 35 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID

NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312),

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(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ

5 ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26  
(SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure  
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Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID  
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NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure

270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure

536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550), lacking its associated signal peptide.

21. A method of detecting a PRO1801 polypeptide in a sample suspected of containing a PRO1801 polypeptide, said method comprising contacting said sample with a PRO1114 or PRO4978 polypeptide and determining the formation of a PRO1801/PRO1114 or PRO1801/PRO4978 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1801 polypeptide in said sample.

22. The method according to Claim 21, wherein said sample comprises cells suspected of expressing said PRO1801 polypeptide.

23. The method according to Claim 21, wherein said PRO1114 or PRO4978 polypeptide is labeled with a detectable label.

24. The method according to Claim 21, wherein said PRO1114 or PRO4978 polypeptide is attached to a solid support.

25. A method of detecting a PRO1114 or PRO4978 polypeptide in a sample suspected of containing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said sample with a PRO1801 polypeptide and determining the formation of a PRO1801/PRO1114 or PRO1801/PRO4978 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1114 or PRO4978 polypeptide in said sample.

26. The method according to Claim 25, wherein said sample comprises cells suspected of expressing said PRO1114 or PRO4978 polypeptide.

27. The method according to Claim 25, wherein said PRO1801 polypeptide is labeled with a detectable label.

28. The method according to Claim 25, wherein said PRO1801 polypeptide is attached to a solid support.

29. A method of linking a bioactive molecule to a cell expressing a PRO1801 polypeptide, said method comprising contacting said cell with a PRO1114 or PRO4978 polypeptide that is bound to said bioactive molecule and allowing said PRO1801 and said PRO1114 or PRO4978 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.



30. The method according to Claim 29, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

31. The method according to Claim 29, wherein said bioactive molecule causes the death of said cell.

5 32. A method of linking a bioactive molecule to a cell expressing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said cell with a PRO1801 polypeptide that is bound to said bioactive molecule and allowing said PRO1801 and said PRO1114 or PRO4978 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

10 33. The method according to Claim 32, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

15 34. The method according to Claim 32, wherein said bioactive molecule causes the death of said cell.

20 35. A method of modulating at least one biological activity of a cell expressing a PRO1801 polypeptide, said method comprising contacting said cell with a PRO1114 or PRO4978 polypeptide or an anti-PRO1801 polypeptide antibody, whereby said PRO1114 or PRO4978 polypeptide or anti-PRO1801 polypeptide antibody binds to said PRO1801 polypeptide, thereby modulating at least one biological activity of said cell.

36. The method according to Claim 35, wherein said cell is killed.

25 37. A method of modulating at least one biological activity of a cell expressing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said cell with a PRO1801 polypeptide or an anti-PRO1114 or anti-PRO4978 polypeptide antibody, whereby said PRO1801 polypeptide or anti-PRO1114 or anti-PRO4978 polypeptide antibody binds to said PRO1114 or PRO4978 polypeptide, thereby modulating at least one biological activity of said cell.

30 38. The method according to Claim 37, wherein said cell is killed.

35 39. A method of detecting a PRO1114 polypeptide in a sample suspected of containing a PRO1114 polypeptide, said method comprising contacting said sample with a PRO100 polypeptide and determining the formation of a PRO100/PRO1114 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1114 polypeptide in said sample.

40. The method according to Claim 39, wherein said sample comprises cells suspected of expressing said PRO1114 polypeptide.

41. The method according to Claim 39, wherein said PRO100 polypeptide is labeled with a detectable label.

42. The method according to Claim 39, wherein said PRO100 polypeptide is attached to a solid support.

43. A method of detecting a PRO100 polypeptide in a sample suspected of containing a PRO100 polypeptide, said method comprising contacting said sample with a PRO1114 polypeptide and determining the formation of a PRO100/PRO1114 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO100 polypeptide in said sample.

44. The method according to Claim 43, wherein said sample comprises cells suspected of expressing said PRO100 polypeptide.

45. The method according to Claim 43, wherein said PRO1114 polypeptide is labeled with a detectable label.

46. The method according to Claim 43, wherein said PRO1114 polypeptide is attached to a solid support.

47. A method of linking a bioactive molecule to a cell expressing a PRO100 polypeptide, said method comprising contacting said cell with a PRO1114 polypeptide that is bound to said bioactive molecule and allowing said PRO100 and said PRO1114 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

48. The method according to Claim 47, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

49. The method according to Claim 47, wherein said bioactive molecule causes the death of said cell.

50. A method of linking a bioactive molecule to a cell expressing a PRO1114 polypeptide, said method comprising contacting said cell with a PRO100 polypeptide that is bound to said bioactive molecule and allowing said PRO100 and said PRO1114 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

51. The method according to Claim 50, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

52. The method according to Claim 50, wherein said bioactive molecule causes the death of said cell.

53. A method of modulating at least one biological activity of a cell expressing a PRO100 polypeptide, said method comprising contacting said cell with a PRO1114 polypeptide or an anti-PRO100 polypeptide antibody, whereby said PRO1114 polypeptide or anti-PRO100 polypeptide antibody binds to said PRO100 polypeptide, thereby modulating at least one biological activity of said cell.

54. The method according to Claim 53, wherein said cell is killed.

55. A method of modulating at least one biological activity of a cell expressing a PRO1114 polypeptide, said method comprising contacting said cell with a PRO100 polypeptide or an anti-PRO1114 polypeptide antibody, whereby said PRO100 polypeptide or anti-PRO1114 polypeptide antibody binds to said PRO1114 polypeptide, thereby modulating at least one biological activity of said cell.

56. The method according to Claim 55, wherein said cell is killed.

57. A method for stimulating the release of TNF- $\alpha$  from human blood, said method comprising contacting said blood with a PRO195, PRO202, PRO215, PRO221, PRO217, PRO222, PRO198, PRO245, PRO172, PRO265, PRO266, PRO344, PRO337, PRO322, PRO1286, PRO1279, PRO1338 or PRO1343 polypeptide, wherein the release of TNF- $\alpha$  from said blood is stimulated.

58. A method for modulating the uptake of glucose or FFA by skeletal muscle cells, said method comprising contacting said cells with a PRO182, PRO366, PRO198, PRO172 or PRO719 polypeptide, wherein the uptake of glucose or FFA by said cells is modulated.

59. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO182, PRO366, PRO198, PRO1868, PRO202, PRO224, PRO172, PRO301 or PRO1312 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

60. A method for modulating the uptake of glucose or FFA by adipocyte cells, said method comprising contacting said cells with a PRO202, PRO211, PRO344 or PRO1338 polypeptide, wherein the uptake of glucose or FFA by said cells is modulated.

61. A method for stimulating the proliferation of or gene expression in pericyte cells, said method comprising contacting said cells with a PRO366 polypeptide, wherein the proliferation of or gene expression in said cells is stimulated.

5 62. A method for stimulating the release of proteoglycans from cartilage, said method comprising contacting said cartilage with a PRO216 polypeptide, wherein the release of proteoglycans from said cartilage is stimulated.

10 63. A method for stimulating the proliferation of inner ear utricular supporting cells, said method comprising contacting said cells with a PRO172 polypeptide, wherein the proliferation of said cells is stimulated.

64. A method for stimulating the proliferation of T-lymphocyte cells, said method comprising contacting said cells with a PRO344 polypeptide, wherein the proliferation of said cells is stimulated.

15 65. A method for stimulating the release of a cytokine from PBMC cells, said method comprising contacting said cells with a PRO526 or PRO1343 polypeptide, wherein the release of a cytokine from said cells is stimulated.

20 66. A method for inhibiting the binding of A-peptide to factor VIIA, said method comprising contacting a composition comprising said A-peptide and said factor VIIA with a PRO182 polypeptide, wherein the binding of said A-peptide to said factor VIIA is inhibited.

67. A method for inhibiting the differentiation of adipocyte cells, said method comprising contacting said cells with a PRO185 or PRO198 polypeptide, wherein the differentiation of said cells is inhibited.

25 68. A method for stimulating the proliferation of endothelial cells, said method comprising contacting said cells with a PRO222 polypeptide, wherein the proliferation of said cells is inhibited.

30 69. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

35 70. The method of Claim 69, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

71. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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**FIGURE 1**

GTTACTCGGTGGTGGCGGAGTCTACGGAAGCCGTTTTTCGCTTCACTTTTCCTGGCTGTAGAGC  
GCTTTCCCCCTGGCGGGTGAGAGTGCAGAGACGAAGGTGCGAGATGAGCACTATGTTGCGCGGA  
CACTCTCCTCATCGTTTTTATCTCTGTGTGCACGGCTCTGCTCGCAGAGGGCATAACCTGGGT  
CCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGGAACAGAGTAAAAA  
ATTGGAAGAAGAAGGAACAATAACAGAGTCAGCTGGTCGACAACAGAAAAAGAAATAGA  
GAGACAAGAAGAGAACTGAAGAATAACAACAGAGATCTATCAATGGTTCGAATGAAATCCAT  
GTTTGCTATTGGCTTTTGTCTTACTGCCCTAATGGGAATGTTCAATTCCATATTTGATGGTAG  
AGTGGTGGCAAAGCTTCCTTTTACCCCTCTTCTTACATCCAAGGACTGTCTCATCGAAATCT  
GCTGGGAGATGACACCACAGACTGTTCCCTCATTTTCCTGTATATTCTCTGTACTATGTGAT  
TCGACAGAACATTCAGAAGATTCTCGGCCTTGCCCCTTACGAGCCGCCACCAAGCAGGCAGG  
TGGATTTCTTGGCCCACCACCTCCTTCTGGGAAGTTCTCTTGAACTCAAGAACTCTTTATTTT  
CTATCATTCTTTCTAGACACACACATCAGACTGGCAACTGTTTTGTAGCAAGAGCCATAGG  
TAGCCTTACTACTTGGGCCTCTTCTAGTTTTGAATTATTTCTAAGCCTTTTGGGTATGATTA  
GAGTGAATGGCAGCCAGCAAACCTTGATAGTGCTTTTGGTCCTAGATGATTTTATCAAATA  
AGTGGATTGATTAGTTAAGTTCAGGTAATGTTTATGTAATGAAAAACAAATAGCATCCTTCTT  
GTTTCATTTACATAAGTATTTTCTGTGGGACCGACTCTCAAGGCACTGTGTATGCCCTGCAAG  
TTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTTAGTTTGTTTAACCCTTGTAAC  
GTTTGTTTTGTTGTTGTTTTTTTTTCAAGCCAAATACATGACATAAGATCAATAAAGAGGCCA  
AATTTTGTAGCTGTTTTATGTACAAGGAGAGATCTGTTTCATTTGTTTTGCCGTATTTCTAGA  
TATAAGTTTGTAGCATGGGCCAGGAAGGACTAAAATAAAAGTTTTTAAGGTACAAAAAAAAA  
AAAA

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## **FIGURE 2**

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR  
QKKKKIERQEEKLKNNNRDLSMVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQ  
GLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites..**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

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**FIGURE 3**

AGCCGGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTGGAGGCCGTGAAACAGCCGTTTGAGT  
TTGGCTGCGGGTGGAGAACGTTTGTGAGGGGGCCCGGCCAAGAAGGAGGCCCGCCTGTTACGAT  
GGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGGTTCTACAGCACCCGGTGCTGCGGCTG  
TTGCCATGTCCGCACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTATTGAT  
GGCAATTTTGCTGACTGTGGAAGTGACTCATCCAACTCCATGCCAGCTGTCAACATTCAGTA  
TGAAGTCATCGGTAATTACTATTCGTCTGAGAGAATGGCTGATAATGCCTGTGTTCTTTTGC  
CGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTATGGAGCAATTTCTTATCAAGT  
GGGTTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCCTCAGTTGCCTGGTTGC  
TATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACCTGATTTTCC  
CTACAAAGATGACCTCCTGGCCTTGACTCCAGCTGCCTCCTGTTTCATTGTTCTTGTGTTCTT  
TGCCTTATTCATCATTTTTTAAGGCTTATCTAATTAAGTGTGTTTGGAACTGCTATAAATACAT  
CAACAACCGAAACGTGCCGGAGATTGCTGTGTACCCTGCCTTTGAAAGCACCTCCTCAGTACG  
TTTTGCCAACCTATGAAATGGCCGTGAAAATGCCTGAAAAAGAACCACCACCTCCTTACTTAC  
CTGCCTGAAGAAATTCTGCCTTTGACAATAAATCCTATACCAGCTTTTTGTTTGTTTATGTTA  
CAGAATGCTGCAATTCAGGGCTCTTCAAACCTTGTTTGATATAAAATATGTTGTCTTTGTTTA  
AGCATTTATTTCAAACACTAAGGAGCTTTTTGACATCTGTTAAACGTCTTTTTGTTTTTTTG  
TTAAGTCTTTTACATTTTAATAGTTTTTGAAGACAATCTAGGTAAAGCAAGAGCAAAGTGCCA  
TTGTTTGCCTTTAATTGGGGGGTGGGAAGGGAAGAGGGTACTTGCCACATAGTTTCCTTTTT  
AACTGCACCTTCTTTATATAATCGTTTGCATTTTGTACTTGCTACCCTGAGTACTTTCAGGA  
AGACTGACTTAAATATTCGGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACTTTTCATCTGC  
AGAGGCAAGAAAAATATTTGACATTGTGACTTGACTGTGGAAGATGATGGTTGCATGTTTCTA  
GTTTGTATATGTTTCCATCTTGTGATAAGATGATTTAATAAATCTCTTAAATACTAAAAA  
AAAAA



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## **FIGURE 4**

MVSMSEFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQ  
YEVIGNYYSSERMADNACVLFAVSVLMFIISMLVYGAIQVGVWLIPFFCYRLFDVLSCLV  
AISSLTYLPRIKEYLDQLPDFPYKDDLLALDSSCLLFIVLVFFALFIIFKAYLINCWNCYKY  
INNRRNVPEIAVYPAFESTSSVRFANL

**Important features of the protein:**

**Transmembrane domain (Possible type II transmembrane protein):**

amino acids 30-49, 81-100, 111-131, 158-175

**N-glycosylation site.**

amino acids 9-13

**Tyrosine kinase phosphorylation sites.**

amino acids 8-16, 193-202

**N-myristoylation site.**

amino acids 68-74

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**FIGURE 5**

CCCGCTGGCCCGTCAGTGCTCTCCCCGTCGTTTGCCCTCTCCAGTTCCCCCAGTGCCTGCCCT  
ACGCACCCCGATGGCGGAGCTGCGGCCTAGCGGCGCCCCCGGCCCCACCGCGCCCCCGGCCCT  
TGGCCCGACTGCCCCCGGCCCTTCGCTTCGCTCTTTCCCCCGGGACTGCACGCCATCTACGG  
AGAGTGCCGCGCCCTTTACCCTGACCAGCCGAACCCGCTCCAGGTTACCGCTATCGTCAAGTA  
CTGGTTGGGTGGCCAGACCCCTTGACTATGTTAGCATGTACAGGAATGTGGGGAGCCCTTC  
TGCTAACATCCCCGAGCACTGGCACTACATCAGCTTCGGCCTGAGTGATCTCTATGGTGACAA  
CAGAGTCCATGAGTTTACAGGAACAGATGGACCTAGTGTTTGGCTTTGAGTTGACCTTTTCG  
TCTGAAGAGAGAACTGGGGAGTCTGCCCCACCAACATGGCCCGCAGAGTTAATGCAGGGCTT  
GGCAGGATACGTGTTCCAGTCAGAGAACACCTTCTGCAGTGGGGACCATGTGTCTTGGCACAG  
CCCTTTGGATAACAGTGAGTCAAGAATTCAGCACATGCTGCTGACAGAGGACCCACAGATGCA  
GCCCGTGACAGACCCCTTTGGGGTAGTTACCTTCCTCCAGATCGTTGGTGTCTGCACTGAAGA  
GCTACACTCAGCCCAGCAGTGGAACGGGCAGGGCATCCTGGAGCTGCTGCGGACAGTGCCTAT  
TGCTGGCGGCCCCCTGGCTGATAACTGACATGCGGAGGGGAGAGACCATATTTGAGATCGATCC  
ACACCTGCAAGAGAGAGTTGACAAAGGCATCGAGACAGATGGCTCCAACCTGAGTGGTGTCAG  
TGCCAAGTGTGCCTGGGATGACCTGAGCCGGCCCCCGAGGATGACGAGGACAGCCGGAGCAT  
CTGCATCGGCACACAGCCCCGGCGACTCTCTGGCAAAGACACAGAGCAGATCCGGGAGACCCT  
GAGGAGAGGACTCGAGATCAACAGCAAACCTGTCTTCCACCAATCAACCCTCAGCGGCAGAA  
TGGCCTCGCCACGACCGGGCCCCGAGCCGCAAAGACAGCCTGGAAAGTGACAGCTCCACGGC  
CATCATTCCTCATGAGCTGATTGCGACGCGGCAGCTTGAGAGCGTACATCTGAAATTCAACCA  
GGAGTCCGGAGCCCTCATTCCTCTCTGCCTAAGGGGCAGGCTCCTGCATGGACGGCACTTTAC  
ATATAAAAGTATCACAGGTGACATGGCCATCACGTTTGTCTCCACGGGAGTGGAAGGCGCCTT  
TGCCACTGAGGAGCATCCTTACGCGGCTCATGGACCCTGGTTACAACCTTGAACCTATCCTCG  
GAGCTCTGCCCTCCCGTCCTGGAACGTCTTTCTGCCCTGAGGAGAGGGTAGTCAGCATCTCCA  
ATTTTCAGCAGCTCAAGAACCTTGGCCCCACAGGACTTCGCAGATGTCACATTGCCCCCTCAG  
TCCCCTGAATGCCCTTCGGACCCAACCCCAATTCCCCAAGCCCCTGACCCCCTAGCTGCCGGG  
GTTCCCACTCCCAGTGCCACAACCCCTCACCTCCCCTGGCAGCCCCTCAGCGAGCCTGAGGC  
CCAGCACCCGCTGGCTCCCCAGCACATGGTCCCCTCCCATGGGCTGTTGCCAGGGAACCGGG  
GCGCGGTGGGAACGAGCTGCTGGCCTCGGCATGTTTCAATAAAGTTGCTGTGCTGGGAG

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**FIGURE 6**

MAELRPSGAPGPTAPPAPGPTAPPAFASLFPPGLHAIYGECRRLYPDQPNPLQVTAIVKYWLG  
GPDPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPGSGFGFELTFRLKR  
ETGESAPPTWPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIQHMLLTEDPQMOPVQ  
TPFGVVTFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRRGETIFEIDPHLQ  
ERVDKGIETDGSNLSGVSAKCAWDDLSRPPEDDEDSRSICIGTQPRRLSGKDTEQIRETLRG  
LEINSKPVLPPINPQRQNGLAHDRAPSRKDSLESSTAIIPHELIRTRQLESVHLKFNQESG  
ALIPLCLRGRLLHGRHFTYKSITGDMAITFVSTGVEGAFATEEHPYAAHGPWLQL

**Important features:****N-glycosylation site.**

amino acids 265-268

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**FIGURE 7**

CGCGAATGAAGTTTGCATTTTCCTCTGTTCTTGAGCCCAGCTTCTTCTCGTCTCCCACCCCAG  
CTTCCCGGCATTGGAAGAAGGGACCGTCCTCTTCTTGTTCTTGGCCACCCAAATCCTGGTATC  
GAAAGGGTTGAACGGACCGGAAGTGTGCAGCAGCGACGGGTCCCCAGCTAATCGACGCCGGAA  
GTAGCAATTACTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATTCCCCCAGATTCT  
CTGGCAGCCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTG  
GAAGCATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTACAATGG  
CACAAAATTCCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCCAACAGGGACAGG  
TCGAGGTGGTGCATCTATCTATGGCAAACAATTTGAAGATGAACTTCATCCAGACTTGAAATT  
CACGGGGGGCTGGAATTCTCGCAATGGCCAATGCGGGGGCCAGATACCAATGGCAGCCAGTTCTT  
TGTGACCCTCGCCCCACCCAGTGGCTTGACGGCAAACACACCATTTTTGGCCGAGTGTGTCA  
GGGCATAGGAATGGTGAATCGCGTGGGAATGGTAGAAACAACTCCCAGGACCGCCCTGTGGA  
CGACGTGAAGATCATTAAGGCATACCCTTCTGGGTAGACTTGCTACCCTCTTGAGCAGCTCTT  
CTGAGATGGCCCCAGTGAACCAGCTTCTAGATGACATAGAATGACATGTAATGCTAAATTTCA  
TTTTGGCTTTGCAAGTCATGAAGCTTAGGAGGCCTGGCATCTTGGGTGAGTTAGAGATGGAAG  
TACATTTTAAATAGGATGCTTCTTTTCTCTTCCCCAGTGCCTAGGTTGCCAGAGCATTTCAC  
AAATGCCCCGTGTTATCAATAGGTGACTACTTACTACACATGAACCATAATGCTGCTTCTTGT  
GCATGTCTGCTCTGATATACGTGCAACAATGTAGCAGCCACTGTCATTTCTCAGTGGTTTTGC  
CTAACCAAATCTTCTCCTAAGGAGATTTATATTCTGGCCTACACAGCAGTCCTTGATGGCTGA  
CAGCCACAGAATTCCAAACCAAGTAGTGTCTGTCAGCCCTCTTAATCTGTGCACGCCCTATT  
TCAGTCTTTTACATTTGTTCTTCTAGGGAATGTATGCATCTCTATATATATTTTCCCTCTCAA  
AACCAGAACATCAACAGTGCTGTTTCTGACACTTCAGACATCCCACGCAAAGCCACATTGAAT  
TTTTGCCAAATGAAAAACACATCCAACAATCAAGTTTCTAAGAAGGTGTCAAGTGGGGAATAA  
TAATAATGTATAATAATCAAGAAATTAGTTTATTAAGGAAGCAGAAGCATTGACCATTTTT  
TCCCAGAGAAGAGGAGAAATCTGTAGTGAGCAAAGGACAGACCATGAATCCTCCTTGAGAAGT  
AGTACTCTCAGAAAGGAGAAGCGCCACTCAAGTTCTTTTAACCAAGACTTTAGAGAAATTAG  
GTCCAAGATTTTTATATGTTCAAGTTGTTTATGTATAAAAAATACTTTCTGGATTTTGTGGGGA  
GGAGCAGGAGAGGAAGGAAGTTAATACCTATGTAATACATAGAACTTCCACAATAAAATGCC  
ATTGATGGTTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 8**

MAAIPDSWQPPNVYLETSMGIIVLELYWKHAPKTCKNFAELARRGYNGTKFHRIIKDEMIQ  
GGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLPATQWLDGKH  
TIFGRVCQGIGMVNRVGMVETNSQDRPVDDVKI IKAYPSG

**Important features:**

**N-glycosylation sites:**

amino acids 49-52, 108-111

**N-myristoylation sites:**

amino acids 64-69, 69-74, 143-148

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature:**

amino acids 48-65

FIGURE 9

[illegible]

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**FIGURE 10**

MWHEARKHERKLRGMMVDYKKRAERRREYYEKIKKDPAQFLQVHGRACKVHLD SAVALAAESP  
VNMPWQGD TN NMIDRF DVRAHL DHI PDYTPPLTTISPEQESDERKCN YERYRGLVQND FAG  
ISEEQCLYQIYIDELYGGLQRPSEDEKKKLA EKKASIGYTYEDSTVAEVEKAAEKPEEEESAA  
EEESNSDEDEVIPDIDVEVDVDELNQE QVADLNKQATTYGMADGDFVRMLRKDKEEA EAIKHA  
KALEEEKAMYSGRRSRRQRREFREKRLRGRKISPPSYARRDSPTYDPYKRSPSESSSESRSRS  
RSPTPGREEKITFITSFGGSDEEAAAAAAAAAASGVTTGKPPAPPQPGGPAPGRNASARRRSS  
SSSSSSSASRTSSSRSSSRSSSRSSRRGGGYRSGRHARSRSRSWSRSRSRSRRYSRSRSRGRR  
HSGGGSRDGHRYSRSPARRGGYGPRRRSRSRSHSGDRYRRGGRGLRHHSSSRSSWSLSPSR  
SRSLTRSRSHSPSPSQSRSRSRSSQSPSPSPAREKLTRPAASPAVGEK LKKT EPAAGKETGA  
AKVTQADASGEAETEDAEGAEQAVQGG

**Important features:****N-glycosylation site:**

amino acids 370-373

**Glycosaminoglycan attachment site:**

amino acids 443-446

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**amino acids 159-162, 282-285, 291-294, 374-377, 375-378, 430-433,  
440-443, 466-469**Casein kinase II phosphorylation site:**amino acids 149-152, 166-169, 171-174, 187-190, 193-196, 195-198,  
303-306, 307-310, 335-338, 571-574**N-myristoylation sites:**

amino acids 118-123, 229-234, 350-355, 446-451, 586-591

**Amidation sites:**

amino acids 263-266, 280-283, 438-441

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**FIGURE 11**

GGTAGGCGCGCCCAGACCTGAGACGGGTGGGACTGGGCTGCGTCACGCGCGGGCTCTAAGCG  
CCCCGGGGCCCCGCCCAGTGGCCGGCACAGCCAATCGCAGCGCGGGAAGGCGGTGGGGGCGGGG  
AAGGCCGCCTGGAACTTAAATCCCGAGGCGGGCGAACCTGCACCAGACCGCGGACGTCTGTA  
ATCTCAGAGGCTTGTTTGCTGAGGGTGCCTGCGCAGCTGCGACGGCTGCTGGTTTTGAAACAT  
GAATCTTTCGCTCGTCTGGCTGCCTTTTGCTTGGAATAGCCTCCGCTGTTCCAAAATTTGA  
CCAAAATTTGGATACAAAGTGGTACCAGTGGAAGGCAACACACAGAAGATTATATGGCGCGAA  
TGAAGAAGGATGGAGGAGAGCAGTGTGGGAAAAGAATATGAAAATGATTGAACTGCACAATGG  
GGAATACAGCCAAGGGAAACATGGCTTCACAATGGCCATGAATGCTTTTGGTGACATGACCAA  
TGAAGAATTCAGGCAGATGATGGGTGCTTTCGAAACCAGAAATTCAGGAAGGGGAAAGTGTT  
CCGTGAGCCTCTGTTTCTTGATCTTCCCAAATCTGTGGATTGGAGAAAGAAAGGCTACGTGAC  
GCCAGTGAAGAATCAGAAACAGTGTGGTTCTTGTTGGGCTTTTAGTGCGACTGGTGCTCTTGA  
AGGACAGATGTTCCGGAAAACCTGGGAAACTTGTCTCACTGAGCGAGCAGAATCTGGTGGACTG  
TTCGCGTCCTCAAGGCAATCAGGGCTGCAATGGTGGCTTCATGGCTAGGGCCTTCCAGTATGT  
CAAGGAGAACGGAGGCCTGGACTCTGAGGAATCCTATCCATATGTAGCAGTGGATGAAATCTG  
TAAGTACAGACCTGAGAATTCTGTTGCTAATGACACTGGCTTCACAGTGGTCGCACCTGGAAA  
GGAGAAGGCCCTGATGAAAGCAGTCGCAACTGTGGGGCCCATCTCCGTTGCTATGGATGCAGG  
CCATTTCGTCCTTCCAGTTCTACAAATCAGGCATTTATTTTGAACCAGACTGCAGCAGCAAAAA  
CCTGGATCATGGTGTTCTGGTGGTTGGCTACGGCTTTGAAGGAGCAAATTCGAATAACAGCAA  
GTATTGGCTCGTCAAAAACAGCTGGGGTCCAGAATGGGGCTCGAATGGCTATGTAAAAATAGC  
CAAAGACAAGAACAACCACTGTGGAATCGCCACAGCAGCCAGCTACCCCAATGTGTGAGCTGA  
TGGATGGTGAGGAGGAAGGACTTAAGGACAGCATGTCTGGGGAAATTTTATCTTGAACTGAC  
CAAACGCTTATTGTGTAAGATAAACCACTTGAATCATGGAGGATCCAAGTTGAGATTTTAATT  
CTGTGACATTTTTACAAGGGTAAAATGTTACCACTACTTTAATTATTGTTATACACAGCTTTA  
TGATATCAAAGACTCATTGCTTAATTCTAAGACTTTTGAATTTTCATTTTTTAAAAAGATGTA  
CAAAACAGTTTGAAATAAATTTTAATTCGTATATA



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**FIGURE 12**

MNLSLVLA AFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRRAVWEKNMKMIELHN  
GEYSQGHGFTMAMNAFGDMTNEEFRQMMGCFRNQKFRKGKVFREPLFLDLPKSVDWRKKGYV  
TPVKNQKQCGSCWAFSATGALEGQMERKTGKLVSLSEQNLVDCSRPQGNQGCNGGFMARAFQY  
VKENGGLDSEESYPYVAVDEICKYRPENSVANDTGFTVVAPGKEKALMKAVATVGPISVAMDA  
GHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEGANSNNSKYWLVKNSWGPWGSNGYVKI  
AKDKNNHCGIATAASYPNV

**Important features:****Signal sequence**

amino acids 1-17

**N-glycosylation sites.**

amino acids 2-6, 221-225, 292-296

**N-myristoylation sites.**amino acids 13-19, 93-99, 136-142, 145-151, 174-180, 177-183,  
180-186, 194-200, 288-294, 324-330**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 132-144

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 275-286

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**FIGURE 13**

GGCGGCGTCATGTGATCCGCTTCCCTGCTCCTTTAAGCGTCCACAGGCGGCGGAGCGGCCACA  
ATCACAGCTCCGGGCATTGGGGGAACCCGAGCCGGCTGCGCCGGGGGAATCCGTGCGGGCGCC  
TTCCGTCCCGGTCCCATCCTCGCCGCGCTCCAGCACCTCTGAAGTTTGCAGCGCCCAGAAAG  
GAGGCGAGGAAGGAGGGAGTGTGTGAGAGGAGGGAGCAAAAAGCTCACCTAAAACATTTATT  
TCAAGGAGAAAAGAAAAAGGGGGGCGCAAAAATGGCTGGGGCAATTATAGAAAACATGAGCA  
CCAAGAAGCTGTGCATTGTTGGTGGGATTCTGCTCGTGTTCCAAATCATCGCCTTTCTGGTGG  
GAGGCTTGATTGCTCCAGGGCCACAACGGCAGTGTCTACATGTCGGTGAAATGTGTGGATG  
CCCGTAAGAACCATCACAAAGACAAAATGGTTCGTGCCTTGGGGACCCAATCATTGTGACAAGA  
TCCGAGACATTGAAGAGGCAATTCCAAGGGAAATTGAAGCCAATGACATCGTGTTCCTGTTT  
ACATTCCCCTCCCCACATGGAGATGAGTCCTTGGTTCCAATTCATGCTGTTTATCCTGCAGC  
TGGACATTGCCTTCAAGCTAAACAACCAATCAGAGAAAATGCAGAAGTCTCCATGGACGTTT  
CCCTGGCTTACCGTGATGACGCATTTGCTGAGTGGACTGAAATGGCCCATGAAAGAGTACCAC  
GGAAACTCAAATGCACCTTCACATCTCCAAGACTCCAGAGCATGAGGGCCGTTACTATGAAT  
GTGATGTCCTTCCTTTTCATGGAATTGGGTCTGTGGCCCATAGTTTACCTTTTAAACATCC  
GGCTGCCTGTGAATGAGAAGAAGAAAATCAATGTGGGAATTGGGGAGATAAAGGATATCCGGT  
TGGTGGGGATCCACCAAAATGGAGGCTTCACCAAGGTGTGGTTTGCCATGAAGACCTTCCTTA  
CGCCAGCATCTTCATCATTATGGTGTGGTATTGGAGGAGGATCACCATGATGTCCCGACCCC  
CAGTGCTTCTGGAAAAAGTCATCTTTGCCCTTGGGATTTCCATGACCTTTATCAATATCCCAG  
TGGAATGGTTTTCCATCGGGTTTGGTGGACCTGGATGCTGCTGTTTGGTGACATCCGACAGG  
GCATCTTCTATGCGATGCTTCTGTCTTCTGGATCATCTTCTGTGGCGAGCACATGATGGATC  
AGCACGAGCGGAACCACATCGCAGGGTATTGGAAGCAAGTCGGACCCATTGCCGTTGGCTCCT  
TCTGCCTCTTCATATTTGACATGTGTGAGAGAGGGGTACAACCTACGAATCCCTTCTACAGTA  
TCTGGACTACAGACATTGGAACAGAGCTGGCCATGGCCTTCATCATCGTGGCTGGAATCTGCC  
TCTGCCTCTACTTCTGTTTCTATGCTTCATGGTATTTACAGGTGTTTCGGAACATCAGTGGGA  
AGCAGTCCAGCCTGCCAGCTATGAGCAAGTCCGGCGGCTACACTATGAGGGGCTAATTTTTTA  
GGTTCAAGTTCCTCATGCTTATCACCTTGGCCTGCGCTGCCATGACTGTCTCTTCTCATCG  
TTAGTCAGGTAACGGAAGGCCATTGGAATGGGGCGGCGTCACAGTCCAAGTGAACAGTGCCT  
TTTTACAGGCATCTATGGGATGTGGAATCTGTATGTCTTTGCTCTGATGTTCTGTATGCAC  
CATCCCATAAAACTATGGAGAAGACCAGTCCAATGGCGATCTGGGTGTCCATAGTGGGGAAG  
AACTCCAGCTCACCACCACTATCACCCATGTGGACGGACCCACTGAGATCTACAAGTTGACCC  
GCAAGGAGGCCCAGGAGTAGGAGGCTGCAGCGCCCGGCTGGGACGGTCTCTCCATACCCAGC  
CCCTCTAACTAGAGTGGGGAGCATGCCAGAGAGAGCTCAATGTACAAATGAATGCCTCATGGC  
TCTTAGCTGTGGTTTCTTGGACCAGCGGCATGGACATTTGTCAGTTTGCCTTCTGACGGTAGC  
TTTTGGAGGAAGATTCTTGCAGCCACTAATGCATTGTGTATGATAACAAAACTCTGGTATGA  
CACATTTTCTGTGATCATTGTTAATTAGTGACATAGTAACATCTGTAGCAGCTGGTTAGTAAA  
CCTCATGTGGGGGTGGGGTGGGGGTGTATTCTTGGGGGATGGTTTGGGCCGAATGGGGAGTG  
GAATATTTGACATTTTCTGTTTAAATTCTAGGATAGATTTTAAACATCCTTTGCGGTCCCA  
GTCCAAGGTAGGCTGGTGTATAGTCTTCTCACTCCTAATCCATGACCACTGTTTTTTTCTTA  
TTTATATCACCAGGTAGCCTACTGAGTTAATATTTAAGTTGTCAATAGATAAGTGTCCCTGTT  
TTGTGGCATAATATAACTGAATTTTCATGAGAAGATTTATTCCACCAGGGGTATTTTCACTTTG  
AAACCAATCTGTGTATCTAATACTAACCAATCTGTTGGATGTGGATTTTAAAAAATGTTTGC  
TAACTACCCAAGTAAGATTTACTGTATTAAATGGCCTTCGGGTCTGAAAAGCTTTTTTAAACC  
TCTTGCTTAAATGCGTTTTATTTTGATAAGATACTTCAAATAGCCTCCAAAAGGTAGATCC  
AATCACTTAAATAAACCTGTATGTATATGCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 14**

MAGAI IENMSTKKLCIVGGILLVFQIIAFLVGGLIAPGPTTAVSYMSVKCVDARKNHHKTKWF  
VPWGPNHCDKIRDIEEAIPREIEANDIVFSVHIPLPHMEMSPWFQFMLFILQLDIAFKLNNQI  
RENAEVSMDVSLAYRDDAFAEWTEMAHERVPRKLKCTFTSPKTPEHEGRYYECDVLPFMEIGS  
VAHKFYLLNIRLPVNEKKKINVGIGEIKDIRLVGIHQNGGFTKVWFAMKTFLTSPSIFIIMVWY  
WRRITMMSRPPVLEKVI FALGISMTFINIPVEWFSIGFDWTWMLLFGDIRQGI FYAMLLSFW  
IIFCGEHMMDQHERNHIAGYWKQVGPIAVGSFCLFIFDMCERGVQLTNPFI SIWTTDIGTELA  
MAFIIVAGICLCLYFLFLCFMVFQVFRNISGKQSSLPAMSKVRRRLHYEGLIFRFKFLMLITLA  
CAAMTVIFFIVSQVTEGHWKWGGVTQVNSAFFGTGIYGMWNLYVFALMFLYAPSHKNYGEDQS  
NGDLGVHSGEELQLTTTITHVDGPTEIYKLTRKEAQE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**amino acids 239-253, 269-284, 302-318, 338-352, 377-399, 434-452,  
471-488**N-glycosylation sites.**

amino acids 8-12, 406-410

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 254-258

**N-myristoylation sites.**amino acids 223-229, 274-280, 305-311, 358-364, 374-380, 386-392,  
509-515

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**FIGURE 15**

GTGAGGGGAACAGCTGATCCGTCTGTTGGGAGGACAGATATCTCAAGGCCAGGATGGGAAGAAT  
CACCCTAAGCCGGGCACCATCCCGTGGTGGAGTCAACTTTCTCAATGTAGCCCGGACCTACA  
TCCCCAACACCAAGGTGGAATGTCACCTACACCCCTCCCCCAGGCACCATGCCAGTGCCAGTG  
ACTGGATTGGCATCTTCAAGGTGGAGGCTGCCTGTGTTCTGGGATTACCACACATTTGTGTGGT  
CTTCCGTGCCCTGAAAGTACAACCTGATGGTTCCCCCATTACACACAGTGTCCAGTCCAAGCCA  
GCTACCTGCCCAAACCAGGAGCTCAGCTCTACCAGTTCCGATATGTGAACCGCCAGGGCCAGG  
TGTGTGGGCAGAGCCCCCTTTCCAGTTCGAGAGCCAAGGCCCATGGATGAACTGGTGACCC  
TGGAGGAGGCTGATGGGGGCTCTGACATCCTGCTGGTTGTCCCAAGGCAACTGTGTTACAGA  
ACCAGCTCGATGAGAGCCAGCAAGAACGGAATGACCTGATGCAGCTGAAGCTACAGCTGGAGG  
GACAGGTGACAGAGCTGAGGAGCCGAGTGCAGGAGCTCGAGAGGGCTCTGGCAACTGCCAGGC  
AGGAGCACACGGAGCTGATGGAACAGTACAAGGGGATTTCCCGGTCCCATGGGGAGATCACAG  
AAGAGAGGGACATCCTGAGCCGGCAACAGGGAGACCATGTGGCACGCATCCTGGAGCTAGAGG  
ATGACATCCAGACCATCAGTGAGAAAGTGCTGACGAAGGAAGTGGAGCTGGACAGGCTTAGAG  
ACACAGTGAAGGCCCTGACTCGGGAACAAGAGAAGCTCCTTGGGCAACTGAAAGAAGTACAAG  
CAGACAAGGAGCAAAGTGAGGCTGAGCTCCAAGTGGCACAACAGGAGAACCATCACTTAAATT  
TGGACCTGAAGGAGGCGAAGAGCTGGCAAGAGGAGCAGAGTGCTCAGGCTCAGCGACTGAAAG  
ACAAGGTGGCCCAGATGAAGGACACCCTAGGCCAGGCCAGCAGCGGTGGCCGAGCTGGAGC  
CCTTGAAGGAGCAGCTTCGAGGGGCCAGGAGCTTGCAGCCTCAAGCCAGCAGAAAGCCACCC  
TTCTTGGGGAGGAGTTGGCCAGTGCAGCAGCAGCCAGGGACCGCACCATAGCCGAACTACACC  
GCAGCCGCCTGGAAGTGGCTGAAGTTAACGGCAGGCTGGCTGAGCTCGGTTTGCAGTTGAAGG  
AAGAAAAATGCCAATGGAGCAAGGAGCGGGCAGGGCTGCTGCAGAGTGTGGAGGCAGAGAAGG  
ACAAGATCCTGAAGCTGAGTGCAGAGATACTTCGATTGGAGAAGGCAGTTTCAAGGAGGAGGGA  
CCCAAACCAAGTGTTCAAGACTGAGCTGGCCCGGGAGAAGGATTCTAGCCTGGTACAGTTGT  
CAGAAAGTAAGCGGGAGCTGACAGAGCTGCGGTGAGCCCTGCGTGTGCTCCAGAAGGAAAAGG  
AGCAGTTACAGGAGGAGAAACAGGAATTGCTAGAGTACATGAGAAAGCTAGAGGCCCGCTGG  
AGAAGGTGGCAGATGAGAAGTGAATGAGGATGCCACCACAGAGGATGAGGAGGCCGCTGTGG  
GGCTGAGCTGCCCCGCAGCTCTGACAGACTCAGAGGACGAGTCCCCAGAAGACATGAGGCTCC  
CACCCTATGGCCTTTGTGAGCGTGGAGACCCAGGCTCCTCTCCTGCTGGGCCTCGAGAGGCTT  
CTCCCCTTGTTGTCATCAGCCAGCCGGCTCCCATTTCTCCTCACCTCTCTGGGCCAGCTGAGG  
ACAGTAGCTCTGACTCGGAGGCTGAAGATGAGAAGTCAGTCCTGATGGCAGCTGTGCAGAGTG  
GGGTGAGGAGGCCAACTTACTGCTTCCCTGAAGTGGGCAGTGCCTTCTATGACATGGCCAGTG  
GCTTTACAGTGGGTACCCTGTCAGAAACCAGCACTGGGGGCCCTGCCACCCCCACATGGAAGG  
AGTGTCTATCTGTAAGGAGCGCTTTCCTGCTGAGAGTGACAAGGATGCCCTGGAGGACCACA  
TGGATGGACACTTCTTTTTTCAGCACCCAGGACCCCTTCACCTTTGAGTGATCTTACTCCCTCG  
TACATGCACAAATACACACTCATGCACACACACACTCACACACATGCATACACTTAGGTTTCA  
TGCCCATTTTCTATCACACTGGGCTCCATGATATTCTGTTCCCTAAGAACTGCTTCTGTGTGC  
CCTGTTTTCTATCCCAAGATTTCTCACTTCATCCTCTCCTACCTGGCTCTTTTGTCCCAGGGAG  
GGGTCTGTTCTGGAAGCAGTGGCTGAATTTATCCCTGAAAGTGGTTTTGGAGGAACCGGGAT  
GGAGGAGGCCTTCCCCTGTGGGAATAGAATCGTCCACTCCTAGCCCTGGTTGCTTCTGATACA  
CAGCCACTGCACACACACACTCACACTCACACTCCCTTGTCTGATGCCCCAAAGCCAATTCTT  
GGGGCACCCCTACCCCTCTTATTTGGAGTTTCCGTTGGTTTACCTGAGTTTTCTCTGGGGTCT  
GCACAGAGGCAGCAGCATGGACATCATGGCCTCTCAGGTCCCTTTTGGTTCTCAGTTTTCATTG  
GTTCTCTTTCTGTTCCCCCATTTGACTTCTGTGCCCCACCCTAGCCTTTTCCATAACCTTAGG  
TATTCAAGTTTGGAGGGGTTTTTTGTATTTTTGAGGATTCCTGTATTCTGTATCCTCTCCTCGC  
ATCTCCTCACATGGAAAGAAATAATGTATTTGTGCTTCTGTGAGGAATGGGGGGAACAAGTG  
GTCCCAGGTATCCCCATTTCCAAGGCCCCCTCCCTCTCCAGGTCCCCCACAGCAATAAAAG  
CTTCCCCCTGATATCCATCCCTTTGTAGTTTGAACAAATATATTTATATGATATGTAA

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**FIGURE 16**

MEESPLSRAPSRGGVNFNLNVARTYIPNTKVECHYTLPPGTMPASDWWIGIFKVEAACVRDYHT  
FWSSVPESTTDGSPIHSTSVQFQASYLPKPGAQLYQFRYVNRQGVCGQSPPFQFREPRPMDE  
LVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLMQLKLQLEGQVTELRSRVQELERALA  
TARQEHTELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKVELD  
RLRDTVKALTREQEKLKGQLKEVQADKEQSEAEQVAQQENHHLNLDLKEAKSWQEEQSAQAQ  
RLKDKVAQMKDTLGQAQQRVAELEPLKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIA  
ELHRSRLEVAEVNGRLAELGLHLKEEKQWSKERAGLLQSVEAEKDKILKLSAEILRLEKAVQ  
EERTQNQVFKTELAREKDSSLVQLSESKRELTELRSALRVLQKEKEQLQEEKQELLEMYMRKLE  
ARLEKVADEKWNEDETEDEEAAVGLSCPAALTDSEDESPEDMRLPPYGLCERGDGSSPAGP  
REASPLVVISQPAPISPHLSGPAEDSSSDSEAEDEKSVLMAAVQSGGEEANLLLPELGSAFYD  
MASGFTVGTLSSETSTGGPATPTWKECPICKERFFAESDKDALEDHMDGHHFFSTQDPFTFE

**Important features:****Casein kinase II phosphorylation sites:**

amino acids 28-31, 43-46, 68-71, 72-75, 129-132, 156-159, 208-  
211, 239-242, 282-285, 305-308, 376-379, 383-383, 468-471, 520-  
523, 521-524, 537-540, 539-542, 543-546, 593-596, 595-598, 597-  
600, 612-615, 639-642, 652-655, 667-670, 683-686

**N-myristoylation sites:**

amino acids 39-44, 107-112, 204-209, 414-419, 561-566, 613-618

**Cell attachment sequence:**

amino acids 557-559

**Leucine zipper pattern sequence:**

amino acids 163-184, 475-496, 482-503

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**FIGURE 17**

GCAAGTTGGGAATTTTAGACTGTCACTGCACATGGACCTCTGGGAAGACGTCTGGCGAGAGCT  
AGGCCCACTGGCCCTACAGACGGATCTTGCTGGCTCACCTGTCCCTGTGGAGGTTCCCTGGG  
AAGGCAAGATGCCCAACAACAGCACTGCTCTGTCAATTGGCCAATGTTACCTACATCACCATGG  
AAATTTTCATTGGACTCTGCGCCATAGTGGGCAACGTGCTGGTCATCTGCGTGGTCAAGCTGA  
ACCCAGCCTGCAGACCACCACCTTCTATTTCAATTGTCTCTCTAGCCCTGGCTGACATTGCTG  
TTGGGGTGCTGGTCATGCCTTTGGCCATTGTTGTCAGCCTGGGCATCACAATCCACTTCTACA  
GCTGCCTTTTTATGACTTGCCTACTGCTTATCTTTACCCACGCCTCCATCATGTCCTTGCTGG  
CCATCGCTGTGGACCGATACTTGCGGGTCAAGCTTACCGTCAGATTTCAGAATTCCTGGGCTCC  
CTGGGTGCATTCTATCATTTCCAGTTGAAAGTTTGCTTCCCTTCCAGTCATGTGGCTCTTCATT  
TACTCTCCTTGCTCTCATTTTCAGATGCCATGGTCATGGATGAAAAGGTCAAGAGAAGCTTTG  
TGCTGGACACGGCTTCTGCCATCTGCAACTACAATGCCCACTACAAGAATCACCCCAAATACT  
GGTGCCGAGGCTATTTCCGTGACTACTGCAACATCATCGCCTTCTCCCCTAACAGCACCAATC  
ATGTGGCCCTGAGGGACACAGGGAACCAGCTCATTGTCACTATGTCCTGCCTGACCAAAGAGG  
ACACGGGCTGGTACTGGTGTGGCATCCAGCGGGACTTTGCCAGGGATGACATGGATTTTACAG  
AGCTGATTGTAAGTACGACAAAGGAACCCTGGCCAATGACTTTTGGTCTGGGAAAGACCTAT  
CAGGCAACAAAACCAGAAGCTGCAAGGCTCCCAAAGTTGTCCGCAAGGCTGACCGCTCCAGGA  
CGTCCATTCTCATCATTTGCATACTGATCACGGGTTTGGGAATCATCTCTGTAATCAGTCATT  
TGACCAAAGGAGGAGAAGTCAAAGGAATAGAAGGGTAGGCAACACTTTGAAGCCCTTCTCGC  
GTGTCCTGACTCCAAAGGAAATGGCTCCTACTGAACAGATGTGACTGAAGATTTTTTTAATTT  
AGTTCATAAAGTGATGCTACAACAGAATAATCACCATGACAACCTGGCCACACCTCAGAGACT  
GATTCTGATCTCCCAGGAATTCTGAAGGACCCTCTATCCTTGACAACAATCATTTGCAGCCAG  
GTAGCAACGGCGGTAGTCAGAGGAGCTATGATAGACCACCCCAAGCAAGGCTGCCCTCAAAT  
AACATCTCAAGATCTTAGTTCTTATGCATTCCATCAGTCAGAAGTGAAGAAGAGGTGGAGAAT  
CTGGATTGGGGACCAGGAAATCACTTGTATTTTGTTAGCCAATAAATTCCTAGCCAGTGTTGA  
ATGAAAAAAAAAAAAA

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**FIGURE 18**

MPNNSTALSLANVTYITMEIFIGLCAIVGNVLVICVVKLNPSLQTTTFYFIVSLALADIAVG  
LVMP LAIVVSLGITIHFYSCLEMTCLLLIFTHASIMSL LAIVDRYL RVKLTVRFRIPGLPGC  
ILSFQLKVCFLPVMWLFILLSLALISDAMVMDEKVKRSFVLDTASAICNNAHYKNHPKYWCR  
GYFRDYCNIIAFSPNSTNHVALRDTGNQLIVTMSCLTKEDTGWYWCGIQRDFARDDMDFTLI  
VTDDKGTLANDFWSGKDLSGNKTRSCAPKVVRKADRSRTSILIICILITGLGIISVISHLTK  
RRRSQRNRRVGNTLKPFSRVLTPKEMAPTEQM

**Important features of the protein:****Transmembrane domains:**

amino acids 16-35, 62-80, 89-101, 134-152, 292-311

**N-glycosylation sites.**

amino acids 3-7, 4-8, 12-16, 204-208, 273-277

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 316-320

**N-myristoylation sites.**

amino acids 122-128, 125-131, 258-264

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 214-225

**G-protein coupled receptors proteins.**

amino acids 29-59, 76-116

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**FIGURE 19**

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTTCGCGGCCGGCGCGGCTCTCCAATG  
GCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTCGGCAAAGGCAGTCGAGTGTTCGAGACCGGGGCGAGTC  
CTGTGAAAGCAGATAAAAAGAAAACATTTATTAACGTGTCATTACGAGGGGAGCGCCCGCGGGGCTGTGCGACT  
CCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTCACGTCTG  
TTTCCAGCCAAAGTGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTATTAGCGATGCCCCCTG  
GTTTGTGTGTTACGCACACACAGCTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCCTGGGCG  
AATCCACATCTGTTTCAACTCTCCGCGGAGGGCGAGCAGGAGCGAGAGTGTGTCGAATCTGCGAGTGAAGAGGG  
ACGAGGGAAAAGAAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAACACCAGATCAGCAAAA  
AAAGAAGATGGGCCCCCGAGCCTCGTGCTGTGCTTGTCTGCTCCGCAACTGTGTTCTCCCTGCTGGGTGGAAGCTC  
GGCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCAACATCATCTCT  
GGTGCTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCGGCGCATCATGGAGCA  
GGGCGGGGCGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCACGCTCCTCCATCCTCACTGG  
CAAGTACGTCCACAACCAACACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGCAGGCACAGCACGA  
GAGCCGACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTCGGGAAGTATCTTAATGAATA  
CAACGGCTCCTACGTGCCACCGGCTGGAAGGAGTGGGTCCGACTCCTTAAAAACTCCGCTTTTATAACTACAC  
GCTGTGTGGAACGGGGTGAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCACAGACCTCATCACCAA  
TGACAGCGTGAGCTTCTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCTCATGGTCATCAGCCATGC  
AGCCCCCACGGCCCTGAGGATTCAGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCAGCACATCAGCC  
GAGCTACAACCTACGCGCCCAACCGGACAAACACTGGATCATGCGCTACACGGGGCCCATGAAGCCCATCCACAT  
GGAATTCACCAACATGCTCCAGCGGAAGCGCTTGACAGCCCTCATGTGCGGTGGACGACTCCATGGAGACGATTGA  
CAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGCCGACCAGGTTACCACATCGG  
CCAGTTTGGCCTGTGAAAGGGAAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCC  
CAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTGGCCCCCACCATCCTGGACATTGC  
AGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCTCAAGCTGCTGGACACGGAGCGGCGGTGAATCG  
GTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGACTCCTTCTTGGTGAGAGAGGCAAGCTGCTACACAAGAG  
AGACAATGACAAGGTGGACGCGCCAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTAGCG  
TGCTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGGAGCTGAA  
GCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCCTCTCAACCTCGTGCCCAAGTACTACGG  
GCAGGGCAGCGAGGCTGCACCTGTGACAGCGGGGACTACAAGCTCAGCCTGGCCGACGCGGAAAAAACTCTT  
CAAGAAGAAGTACAAGGCCAGCTATGTCCGCACTGCTCCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGGGT  
GTACCACGTAGGCCTGGGTGATGCCGCCAGCCCCGAAACCTACCAAGCGGCACTGGCCAGGGGCCCCCTGAGGA  
CCAAGATGACAAGGATGGTGGGACTTTCAGTGGCACTGGAGGCTTCCCGACTACTCAGCCGCCAACCCATTAA  
AGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCAGTGTGACCTGGACCTGTACAAGTCCCTGCAGGC  
CTGGAAGACCAAGCTGCACATCGACCAGGATTGAAACCTGCAGAACAAAATTAAGAACCTGAGGGAAGT  
CCGAGGTACCTGAAGAAAAAGCGGCCAGAAGAATGTGACTGTCAAAAATCAGCTACCACACCCAGCACAAAGG  
CCGCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGGCCTGCAGAGAAGGACAAGGTGTGGCTGTT  
GCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGTCAAGCGCCTGCAGAACACGACAGTGCAGCATGCC  
AGGCCTCACGTGCTTACCCACGACAACCAGCACTGGCAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGC  
CTGCACCAGCGCCAACAATAACACGTAAGTGTGATGAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGA  
ATTTGCAACTGGCTTCTAGAGTACTTTGATCTCAACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACT  
GGACAGGGATGTCCTCAACAGCTACAGCTACAGCTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAA  
CCCCGGACTCGAAACATGGACCTGGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGGCC  
AGAAATGAAGAGACCTTCTTCAAATCACTGGGACAATGTGGGAAGGCTGGGAAGGTTAAGAAACAACAGAGGT  
GGACCTCCAAAAACATAGAGGCATCACTGACTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACC  
TGTGCTATTGGCCAGGAGGCTGAGAAAGCAAGCAGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCA  
GCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTGGCCCTGCTTTTGGATTATACCTCACCAGCTGCAC  
AAAATGCATTTTTCGTATCAAAAAGTCAACCTAACCTCCCCAGAGCTCACAAAGGAAAACGGAGAGAGCG  
AGCGAGAGAGATTTCTTGGAAATTTCTCCCAAGGGCGAAAGTCAATGGAAATTTTAAATCATAGGGGAAAAGCA  
GTCCTGTTCTAAATCCTCTTATCTTTTGGTTTGTCAAAAGAAGGAATAAGAAGCAGGACAGAGGCAAGTGG  
AGAGGCTGAAAACAGTGCAGAGACGTTTGACAATGAGTCAGTAGACAAAAGAGATGACATTTACCTAGCACTAT  
AAACCTGGTTGCCTCTGAAGAACTGCCTTCAATGTATATATGTGACTATTTACATGTAATCAACATGGGAAT  
TTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTGGTCAATAAACGCTCTGTGGCCAGTGTAAAA  
GAAAA



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**FIGURE 20**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQV  
MNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHESTR  
FAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSK  
DYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITPSYNY  
APNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQTLMSVDDSMETIYNMLVETGELDNTYIYVT  
ADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNEAGCLNPHIVLNIDLAPTILDIAGLDIP  
ADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQR  
VKDLCQRAEYQTACEQLGQKWQCVEDATGKLKHLKCKGPMRLGGSRALSNLVPKYYGQGSEAC  
TCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHW  
PGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLH  
IDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKD  
KVWLLREQRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNT  
YWCMRTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGY  
KQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**Important features:****Signal peptide:**

amino acids 1-17

**Sulfatases signature 1.**

amino acids 86-99

**Homologous region to sulfatase:**

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

**N-glycosylation sites.**amino acids 65-69, 112-116, 132-136, 149-153, 171-175, 198-202,  
241-245, 561-565, 608-612, 717-721, 754-758, 764-768

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**FIGURE 21**

GGGCGCGGAGAGCTGCTAGGGCGGTTTCTCTGCCTCGGGCCTGTTGGGCAGGGCCGGCT  
AAGGTGCGCGTGCTCGCTGGTTCTAACCCCTTCTGTTGGGCGTTTCTGCTGAGAGGCGGGA  
GGCGCTGAGAGTCTGTGCGGAGGTCCGTGGACAGACTGCTTTGCTCGTTGTTGCTCTTCG  
GAGGCGGCGATCCCCGAAGGCGAGCTGAAATACGGCTGCAGGCTACAATTTGCAGCCGAC  
GATTATGGAAGACGGAAGCGGGAGAGGTGGCCCACCCTCATGGAGCGCTTGTGCTCGGAT  
GGCTTCGCATTTCCCCAATACCCCATTAACCGTATCATCTGAAGAGGATCCACAGAGCT  
GTCTTACATGGTAATCTAGAGAACTGAAGTACCTTCTGCTCACGTATTATGACGCCAAT  
AAGAGAGACAGGAAGGAAAGGACCGCCCTACATTTGGCCTGTGCCACTGGCCAACCGGAA  
ATGGTACATCTCCTGGTGTCCAGAAGATGTGAGCTTAACCTCTGCGACCGTGAAGACAGG  
ACACCTCTGATCAAGGCTGTACAACCTGAGGCAGGAGGCTTGTGCAACTCTTCTGCTGCAA  
AATGGCGCCAATCCAAATATTACGGATTTCTTTGGAAGGACTGCTCTGCACTACGCTGTG  
TATAATGAAGATACATCCATGATAGAAAACTTCTTTCACATGGTACAAATATTGAAGAA  
TGCAGCAAGGTATAGGTCAACCAATGTTATTTTCAAACCTATCTGAAATGAATTTATTTTA  
ACATTGACACATGTAAGGGTCAATTTTTCATATTTGGAAGCTCAAACATTCCCTTGAATGA  
AAATATTTTGAATGCCTTAACTGTCTAAGATTTTACTTTAAATATTGGAACCTTTAAAG  
AAGCATTATAGGGAACAGCCTTTTTTTCATGCACTTATGGTAAATAACTATAAAAACAAT  
GAATTACAATAAATTTATAATTCATGACAACCTGAATTTGGGAAAGGTAATAGTTAAGTGT  
TTTTCCACTAAATTACTTTTT

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## **FIGURE 22**

MERLCSDGFAFPQYPIKPYHLKRIHRAVLHGNLEKLKYLLLTYYDANKRDRKERTALHLACAT  
GQPEMVHLLVSRRCELNLCREDRTPLIKAVQLRQEACATLLLQNGANPNITDFFGRTALHYA  
VYNEDTSMIEKLLSHGTNIEECSKV

**Important features of the protein:**

**N-glycosylation site.**

amino acids 113-117

**N-myristoylation site.**

amino acids 109-115

**Microbodies C-terminal targeting signal.**

amino acids 149-153

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**FIGURE 23**

GAGGCAGAAAGGCAGAAAGGAGAAAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTG  
CCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGT  
CACTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAG  
GGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGT  
TTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGC  
TGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTCTACCAGGTGGC  
CGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCT  
GCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACT  
GAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG  
TGCCGTTTCAAGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAGTGA  
AACACCAACTATACAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGG  
AAGTGCCCTAGAAGAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATA  
TGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGT  
CCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGA  
AACACTACCCAATAATTCCTGCTATTACAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACT  
CCAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTTGG  
TGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCTCCCTTTCTCTGT  
ACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAA

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**FIGURE 24**

MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCCLTV  
VSFYQVAALQGD LASLRAELQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS  
QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL EEEKENKILVKE  
TGYFFIYGQVLYTDKTYAMGH LIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAK  
LEEGDELQLAIPRENAQISLDGDVTFFGALKLL

**Transmembrane domain:**

amino acids 47-72

**N-glycosylation site.**

amino acids 124-127, 242-245

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36, 173-176

**N-myristoylation site.**

amino acids 96-101

**TNF family proteins.**

amino acids 172-206

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**FIGURE 25**

CTGCTTGGATACCTCCAGTCCCCAACTGTGTTCCAGGAGTTTCTTGGCCGAAGCTGCCCGA  
TGTTTGAGCCTTTTCTTCCCAGAGAAGAAGATGGACTGAAAGCTGCCAGTTGGGGACTTTTTG  
TGATCACGGCGTTGCAGCGTTTTAAAGGAGGTGATGGGGCTTGCGCTGGCTTGCTTCCCACC  
CAAGTGAAGAGTTGATGTTCACTGGTTATGCTTAGACAATGTGCAGTTTGTGTTAATTTAAAA  
TTTTGGGTGGGATAGGGGCATAGGCTTGTAAGGGCAGTCCGGATCCGGAGGAACCTCGTCTTT  
GTCCCTGGTAGGAGAGACACCCCGAGTCTATCCTCGATGCCGTGAGCCTTGGCCATCTTCACT  
TGCCGCCCCGAACCTCGCACCCGTTTCAGGAGCGTCATGTCTACCTGGACGAGCCCATCAAAATC  
GGCCGCTCAGTGGCCCGCTGTGACCAGCGCAGAATAATGCCACTTTTGATTGCAAAGTGCTA  
TCAAGGAACACGCTCTCGTCTGGTTGATCACAAGACGGGCAAGTTTTATCTTCAAGACACT  
AAAAGTAGTAATGGTACTTTTATAAATAGCCAGAGATTGAGTCGAGGCTCTGAAGAAAGTCCA  
CCATGTGAAATTCTTCCGGTGACATTATCCAGTTTGGAGTAGACGTGACAGAGAATACACGG  
AAAGTTACCCATGGGTGTATTGTTCCACAATAAACTTTTTCTACCAGATGGTATGGAAGCC  
CGGCTCCGCTCAGATGTCATCCATGCACCATTACCAAGTCCTGTTGACAAAGTTGCTGCTAAC  
ACTCCAAGTATGTACTCTCAGGAACATATCCAGCTTTCTCAGTATCTACAGGAGGCCTTACAT  
CGGGAACAAATGTTGGAACAGAAGTTAGCCACGCTTCAGCGGCTACTAGCCATCACCCAAGAG  
GCTTCAGATACCAGTTGGCAGGCTTTAATAGATGAAGATAGACTCTTATCACGGTTAGAAGTT  
ATGGGAAACCAATTACAGGCATGCTCCAAAAATCAAACAGAAGATAGTTTACGAAAGGAAGTT  
ATAGCATTACAAGAGGATAAACATACTATGAGACAACAGCCAAAGAGTCCCTGAGGCGGGTT  
CTTCAGGAGAAAATTGAAGTGGTTAGAAAACCTTTCAGAAGTTGAGCGAAGTCTGAGTAATACT  
GAAGATGAATGTACCCATCTGAAAGAAATGAATGAAAGGACTCAGGAAGAATTAAGAGAATTA  
GCCAACAAATATAATGGAGCAGTTAATGAGATTAAAGATTTATCTGATAAATTAAGGTAGCA  
GAGGGAAAACAAGAGGAAATCCAACAGAAGGGACAGGCTGAGAAAAAAGAATTACAACATAAA  
ATAGATGAAATGGAAGAAAAAGAACAGGAGCTCCAGGCAAAAAATAGAAGCTTTGCAAGTGAT  
AATGATTTACCAATGAAAGGCTAACAGCTTTACAAGTACGGTTAGAACATCTTTCAGGAGAAA  
ACTCTTAAAGAATGCAGCAGCTTGGCTGATCGTCAAGGGCATCTAACCAAAGCGGTAGAAGA  
AACAAAGCTTTCAAAGGTTTGTCTTCTGTTTTCTATGTTTTTTGACAGTTCTTTTGGATAA  
TGAAGGTTAGTGTATATTTTCAAGGTTATAGTATTTTAAACCATCAGTTTACTTCTTATAGCTC  
ACAAAATAGCAAGCCAGTAACAGTATCAGATAATATATAAAATAATCAGACTTCTGTTTTAAG  
AAGGGTATCGTAACTGGAATGTGTCTTTTTAAGTGGATGTATATTTATGGTTTTTTGAATGTT  
AGTACTTGATATAGGTTTCTTTAGGTATTAAAGATTTGTTGCAATCTCTGTCATTCCCAGCAT  
TAATTTTCAGCTTTGATCTCAAATTTTAAATCAAACACAATGTAAGTCGTTTGTGATACAACCTA  
AGTGAACATGCTTGCACTTCTATTTTGGGGGTACAGTACCTTTAAATCTCTTATGATGTT  
TAATATTTCCCTAATTTTGGCATCTCAGTTTGATTTAAACAAAATTAATGACTTTTGTGAAT  
GTAGAATCTTCTTATATTTTATGAGTAGTCCAGTAATTGCCCAAAGTAGTTTATTGTGTTAAT  
TCTGTTACAGTTGTCAGAGAAGAAAAGTGAGTTTTAAAGCACCATATTGTCAAGTCACTTTTA  
TACATAGGGAAATTAGGCAAATAAATTTGGTGGCATGTGTTTATCATAGTAGAACTTTCATTA  
GACTATACCAGTATAAAATTTAAACTAGATTACAGTCCTTTTGGCCAATTAACCATTTGAG  
TTACAAAAGTTTGAGATACTTAATTTTAGTACATTCTATTTTATTAAAGTAAGTGGATTCAAT  
TGACTTTTTTAACCATGTAAGAGGATGGTGTATTTCAAATATCTCGTGGTTTCCATTCTGAA  
TTTTGTGCACGGCAGATGCCATATTTGGGGAAAAAATGCATAGAATATGCATCATTAAATATTG  
TTTTGGCAAACAGGCATTGAGTTTCAGAACAGTGAAGTATTTTATGATACATATGGCAATTTTT  
TTCACCTTATTAAAGTGAAGTGAAGAACAGACCTTAAATAGCTTTTACCTCACCATCCAAATA  
CCTATTCAGATTAGTTGGTTGAATAGCCAGCACTTTGAAGTAGAGCCTTAGG

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**FIGURE 26**

MEARLRSDVIHAPLPSPVDKVAANTPSMYSQELFQLSQYLQEALHREQMLEQKLATLQRLAI  
TQEASDTSWQALIDEDRLLSRLEVMGNQLQACSKNQTEDSLRKELIALQEDKHNYETTAKESL  
RRVLQEKIEVVRKLSEVERSLSNTEDECTHLKEMNERTQEELRELANKYNGAVNEIKDLSDKL  
KVAEGKQEEIQQKGQAEKKELQHKIDEMEEKEQELQAKIEALQADNDFTNERLTALQVRLEHL  
QEKTLKECSSLADRRRRASNQSGRRNKAFKRFFCFMFFDSSFG

**Important features of the protein:****N-glycosylation sites.**

amino acids 98-102, 271-275

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 138-142, 267-271

**Amidation site.**

amino acids 273-277

**Tropomyosins proteins.**

amino acids 169-217

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**FIGURE 27**

GAACCTGGCGCCGCCGGAAGCTGATCGCGGCCTAGTCCCGACGCGTGTGTGCTAGTGAGCCGGA  
GCCGGCGACGGCGGCAGTGGCGGCCCGGCCTGCAGGAGCCCGACGGGGTCTCTGCCATGGGGG  
AGTGACGCGCCTGCACCCGCTGTTCCGCGGCAGCGGCAGACATGAGGAGACCCCGCGACAGG  
GGCAGCGCGCGCGGCTCGTGAGCCCCGGGATCGAGGAGAAAATACGGCGGGGACGTGCTGGCCG  
GCCCCGGCGCGCGCGGCCTTGGGCCGTGGACGTACCCAGCGCTCGATTAAACAAAATATA  
TTGTGTTACTATGTTTCACTAAATTTTTGAAGGCTGTGGGACTTTTTCGAATCATATGATCTCC  
TAAAAGCTGTTACATTGTTTCAGTTCATTTTTATATTAATACTTGGGACTGCATTTTTTATGG  
TTTTGTTTCAAAGCCATTTTCTTCTGGGAAAACATATTACCAAACACCAGTGGATCAAAATAT  
TTAAACATGCAGTTGCTGGGTGTATTATTTCACTCTTGTGGTTTTTTGGCCTCACTCTTTGTG  
GACCACTAAGGACTTTGCTGCTATTTGAGCACAGTGATATTGTTGTCATTTCACTACTCAGTG  
TTTTGTTTACCAGTTCTGGAGGAGGACCAGCAAAGACAAGGGGAGCTGCTTTTTTTCATTATTG  
CTGTGATCTGTTTATTGCTTTTTGACAATGATGATCTCATGGCTAAAATGGCTGAACACCCCTG  
AAGGACATCATGACAGTGCTCTAAGCTCATATGCTTTACACAGCCATTGCCTTCTTAGGTGTGG  
CAGATCACAAGGGTGGAGTATTATTGCTAGTACTGGCTTTGTGTTGTAAAGTTGGTTTTTCATA  
CAGCTTCCAGAAAGCTCTCTGTGCGACGTTGGTGGAGCTAAACGCTCTTCAAGCTTTATCTCATC  
TTGTTTTCTGTGCTTCTCTTGTGCCCATGGGTCAATTGTTCTTTCTGTGACAACTGAGAGTAAAG  
TGGAGTCTTGGTTTTCTCTCATTATGCCTTTTGCAACGGTTATCTTTTTTGTGTCATGATCCTGG  
ATTTCTACGTGGATTCCATTTGTTTCAGTCAAAATGGAAGTTTCCAAATGTGCTCGTTATGGAT  
CCTTTCCCATTTTTATTAGTGCTCTCCTTTTTTGAAATTTTTGGACACATCCAATAACAGACC  
AGCTTCGGGCTATGAACAAAGCAGCACACCAGGAGAGCACTGAACACGTCCTGTCTGGAGGAG  
TGGTAGTGAGTGCTATATTCTTCATTTTGTCTGCCAATATCTTATCATCTCCCTCTAAGAGAG  
GACAAAAAGGTACCCTTATTGGATATTCTCCTGAGGAACACCTCTTTATAACTTCATGGGTG  
ATGCTTTTTCAGCATAGCTCTCAATCGATCCCTAGGTTTATTAAGGAATCACTAAAACAAATTC  
TTGAGGAGAGTGACTCTAGGCAGATCTTTTACTTCTTGTGCTTGAATCTGCTTTTACCTTTG  
TGGAATTATTCTATGGCGTGCTGACCAATAGTCTGGGCCTGATCTCGGATGGATTCCACATGC  
TTTTTGACTGCTCTGCTTTAGTCATGGGACTTTTTGCTGCCCTGATGAGTAGGTGGAAAGCCA  
CTCGGATTTTCTCCTATGGGTACGGCCGAATAGAAATTCTGTCTGGATTTATTAATGGACTTT  
TTCTAATAGTAATAGCGTTTTTTGTGTTTATGGAGTCAGTGGCTAGATTGATTGATCCTCCAG  
AATTAGACACTCACATGTTAACACCAGTCTCAGTTGGAGGGCTGATAGTAAACCTTATTGGTA  
TCTGTGCCTTTAGCCATGCCCATAGCCATGCCCATGGAGCTTCTCAAGGAAGCTGTCACTCAT  
CTGATCACAGCCATTACACCATATGCATGGACACAGTGACCATGGGCATGGTCACAGCCACG  
GATCTGCGGGTGGAGGCATGAATGCTAACATGAGGGGTGATTTTCTACATGTTTTGGCAGATA  
CACTTGGCAGCATTGGTGTGATCGTATCCACAGTTCTTATAGAGCAGTTTGGATGGTTCATCG  
CTGACCCACTCTGTTCTCTTTCTACTGCTATATTAATATTTCTCAGTGTTGTTCCACTGATTA  
AAGATGCCTGCCAGGTTCTACTCCTGAGATTGCCACCAGAATATGAAAAAGAACTACATATTG  
CTTTAGAAAAGATACAGAAAATTGAAGGATTAATATCATACCGAGACCCCTCATTTTTTGGCGTC  
ATTCTGCTAGTATTGTGGCAGGAACAATTATATACAGGTGACATCTGATGTGCTAGAACAAA  
GAATAGTACAGCAGGTACAGGAATACTTAAAGATGCTGGAGTAAACAATTTAACAATTCAG  
TGGAAGAGGAGGCATACCTTTCAACATATGTCTGGCCTAAGTACTGGATTTTCATGATGTTCTGG  
CTATGACAAAACAAATGGAATCCATGAAATACTGCAAGATGGTACTTACATCATGTGAGATA  
ACTCAAGAAATTACCCCTGGAGAATAAACAATGAAGATTAAATGACTCAGTATTTGTAATATTG  
CCAGAAGGATAAAAAATTACACATTAAGTGTACAGAAACAGAGTTCCCTACTACTGGATCAAGG  
AATCTTTCTTGAAGGAAATTTAAATACAGAATGAAACATTAATGGTAAAAAAA



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**FIGURE 28**

MEEKYGGDVLAGPGGGGGLGPVDVPSARLTKYIVLLCFTKFLKAVGLFESYDLLKAVHIVQFI  
FILKLGTAFFMVLFQKPFSSGKTITKHQWIKIFKHAVAGCIISLLWFFGLTLCGPLRTLLLFE  
HSDIVVISLLSVLFTSSGGGPAKTRGAFFIIAIVICLLLFNDNDLMAKMAEHPEGHDSALTH  
MLYTAIAFLGVADHKGGVLLLVLALCCKVGFHTASRKLSVDVGGAKRLQALSHLVSVLLCPW  
VIVLSVTTESKVESWFSLIMPFATVIEFFVMILDFYVDSICSVKMEVSKCARYGSFPIFISALL  
FGNFWTHPITDQLRAMNKAHQESTEHLVSGGVVSAIFFILSANILSSPSKRGQKGTIGYS  
PEGTPLYNFMGDAFQHSQSIPRFIKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTN  
SLGLISDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGFINGLFLIVIAFFVF  
MESVARLIDPPELDTHMLTPVSVGGLIVNLIGICAFSHAHAHSHAHGASQGSCHSSDHS SHHMH  
GHS DHGHGSHSGSAGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIADPLCSLSTA  
ILIFLSVPLIKDACQVLLRLPPEYEKELHIALEKIQKIEGLISYRDPHFWRHSASIVAGTI  
HIQVTS DVLEQRIVQQVTGILKDAGVNNLTIQVEKEAYFQHMSGSLSTGFHDVLAMTKQMESMK  
YCKDGTIIM.

**Important features of the protein:****Signal peptide:**

amino acids 1-46

**Transmembrane domains:**amino acids 59-77, 101-119, 150-167, 205-223, 239-258, 267-284,  
305-324, 343-360, 421-440, 452-469, 486-505, 522-539, 592-612,  
621-641**N-glycosylation site.**

amino acids 721-725

**Glycosaminoglycan attachment site.**

amino acids 143-147

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 225-229

**Tyrosine kinase phosphorylation sites.**

amino acids 750-758, 756-764

**N-myristoylation sites.**amino acids 14-20, 46-52, 102-108, 112-118, 144-150, 317-323,  
347-353, 369-375, 372-378, 437-443, 462-468, 529-535, 549-555,  
553-559, 579-585, 582-588, 583-589, 584-590, 605-611, 737-743**Multicopper oxidases protein:**

amino acids 561-569

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**FIGURE 29**

GGCACGAGGGCAGGATATTAGAAATGGCTACTCCCCAGTCAATTTTCATCTTTGCAATCTGCA  
TTTAAATGATAACAGAATTAATTCTGGCCTCAAAAAGCTACTATGATATCTTAGGTGTGCCAA  
AATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTTCACAAGTTGGCCATGAAGTACCACCCTG  
ACAAAAATAAGAGCCCGGATGCTGAAGCAAAATTCAGAGAGATTGCAGAAGCATATGAAACAC  
TCTCAGATGCTAATAGACGAAAAGAGTATGATACACTTGGACACAGTGCTTTTACTAGTGGTA  
AAGGACAAAGAGGTAGTGAAGTTCTTTTGAGCAGTCATTTAACTTCAATTTTGATGACTTAT  
TTAAAGACTTTGGCTTTTTTGGTCAAAACCAAAACACTGGATCCAAGAAGCGTTTTGAAATC  
ATTTCCAGACACGCCAGGATGGTGGTTCAGTAGACAAAGGCATCATTTCCAAGAATTTCTT  
TTGGAGGTGGATTATTTGATGACATGTTTGAAGATATGGAGAAAATGTTTTCTTTTAGTGGTT  
TTGACTCTACCAATCAGCATAAGTACAGACTGAAAATAGATTTTCATGGATCTAGCAAGCACT  
GCAGGACTGTCCTCAACGAAGAGGAAATATGGTTACTACATACACTGACTGTTCAAGGACAGT  
AGTTCTTATTCTATTCTCACTAAATCCAACCTGGTTGACTCTTCCTCATTATCTTTGATGCTAA  
ACAATTTTCTGTGAACATTTTTGACAAGTGCATGATTTCACTTTAAACAATTTGATATAGCTA  
TTAAATATATTTAAGGGTTTTTTTTTTTTTGACAAATTCAACATTCAACGAGTAGACAAAATGCT  
AATTATTTCCCTGATTAGGAAAGTTTCTTTAAAAACACGTAATTTTGCCTAGTGCTTTTTCT  
CTACCTGCCCTTGGGCTCACTAATATCACCAGTATTATTACCAAGAAAATATTGAGTTTACCT  
GATTAACTTTAAAAGTTAATTGTAGATTTAAATTGTGTGAACCTAATGATTTTTGCAGTGAA  
ACCTTTACTAATTCAAAGTTGCATGTTCTATGACATCTGTGACTTGCCTTGCAGAGTGACAT  
GAACTGTATAATTGAGTCATTCAGTAAAGGAGAACAGTATCTTGGTTAATTGCTACTGAAAG  
GTTGAGAAAGGAATGGTTTGATATTTACCACAGCGCTGTGCCTTTCTACAGTAGAACTGGGGT  
AAAGGAAATGGTTTTATTGCCCATAGTCATTTAGGCTGGAAAAAGTTGAAAACCTAACGAAA  
TATTGCCAAGAGATTGTTATGTGTTGGTTCCAGCCTAAAAATGATTTTGTAGTGTGAAATC  
ATAGCTACTTACATAGCTTTTTTCATATTTCTTTCTTAGTTGTTGGCACTCTTAGGTCTTAGTA  
TGGATTTATGTGTTGTGTGTGTGTAGTTTATCCTCTCTCATCTTTATCTAGAGATTGACT  
GATACCTCATTCTGTTTGTAACCAGCCAGTAATTTCTGTGCAACCTTACTATGTGCAATAT  
TTTTAAATCCTGAGAAATGTGTGCTTTTGTTTTCGGATAGACTTATTTCTTTAGTTCTGCACT  
TTTCCACATTATACTCCATATGAGTATTAATCCTATGGATACATATTAAACAAGTGTCTCAT

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## **FIGURE 30**

MATPQSIFIFAICILMITELILASKSYDILGVPKSASERQIKKAFHKLAMKYHPDKNKSPDA  
EAKFREIAEAYETLS DANRRKEYDTLGHS AFTSGKGQRGSGSSFEQSFNFNFDDLKDFGFFG  
QNQNTGSKKR FENHFQTRQDGGSSRQRHHFQEFSFGGGLFDDMFEDMEKMFSFSGFDSTNQHT  
VQTENRFHGSSKHCRTVTQRRGNMVTITYTDCSGQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Nt-dnaJ domain signature.**

amino acids 27-59, 66-90

**Glycosaminoglycan attachment site.**

amino acids 96-100

**N-myristoylation sites.**

amino acids 32-38, 99-105, 102-108, 126-132, 211-217

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**FIGURE 31**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTGG  
GCAGAAAGGAGGGTGTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACAAT  
TCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCTGAG  
ATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCAAATG  
CAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCTACGCA  
TTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTCTCTGTA  
CTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGAAACAGTG  
TACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCTGGATCCCC  
AGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATCACGGCCACT  
GTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTGGAGCATCCTG  
AAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGATCACCAAAGAT  
GGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTAC  
TGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGGGGGTATTCCAGTG  
CACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGACATTCGTGAAGGCC  
ATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCC  
CTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTTCGTGCCACTGTTC  
GTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCTCCAGACACC  
TTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGT  
GCCACGGCTGTGATGTCTCCTGAGGAACCTCAGGGCCTGGATCTCATAAGTTTTGCGGAAGG  
GCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT  
TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTCTAG  
AAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACTGACTGAGGCTTAGGGGATGTG  
ACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACCCTGGGAAAAGTGACTTCATCCCT  
TCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCTGCTAAACACACACAC  
ACAGAGTCTCTCTCTATATATACACACGTACACATAAATACACCCAGCACTTGCAAGGCTAGA  
GGGAAACTGGTGACACTCTACAGTCTGACTGATTCAAGTGTCTGGAGAGCAGGACATAAATG  
TATGATGAGAATGATCAAGGACTCTACACACTGGGTGGCTTGGAGAGCCCACTTTCCCAGAAT  
AATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGTGTGAGTTCACCTCAAGCCCAATGCCG  
GTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGTAGGTGACCTGGAGGAAGGTCACAGCCACA  
CTGAAAATGGGATGTGCATGAACACGGAGGATCCATGAACTACTGTAAAGTGTGACAGTGTG  
TGCACACTGCAGACAGCAGGTGAAATGTATGTGTGCAATGCGACGAGAATGCAGAAGTCAGTA  
ACATGTGCATGTTTGTGTGCTCCTTTTTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAA  
AGGGCCACCCTGGCCAAAAGCGGTAAAAA

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## **FIGURE 32**

MQTFTMVLEEIWTSLFMWWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHELLMWSPVIAPGET  
VYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVDITATVPYNLRVRATLGSQTSAWSI  
LKHFPNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIP  
VHLETMEPGAAYCVKAQTFVKAIGRYSQTECEVQGEAIPVLALFAFVGFMILILVVVPL  
FVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-44, 134-138

**Tissue factor proteins.**

amino acids 92-120

**Integrins alpha chain proteins.**

amino acids 232-263

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**FIGURE 33**

GAGACACGCGAGCGGGGAGACCTCCAAGGCAGCGAGGCATCGGACATGTGTGTCAGCACATCTGG  
GGCGCACATCCGTCGAGCCCGAGGGGAGATTTGCCGGAACAATTCAAACCTGCGATATTGATCT  
TGGGGGTGACTGTCCCTGGCCGGCTGTCCGGTGGGAGTGCGAGTGTGCACTCGCTCGGAAGTG  
TGTGCGAGTGTGTATGTGTGTGTGCCGTGTCCGGCTCCCCCTTCCCCCGTTTTCCCGTCGA  
GTGATGCACTTGAATGAGAATCAGAGGATGGAAATAGTCTGGGAGGTGCTTTTTCTTCTTCA  
AGCCAATTTTCATCGTCTGCATATCAGCTCAACAGAATTCACCAAAAATCCATGAAGGCTGGTG  
GGCATAACAAGGAGGTGGTCCAGGGAAGCTTTGTTCCAGTTCCTTCTTCTGGGGATTGGTGAA  
CTCAGCTTGAATCTTTGCTCTGTGGGGAAACGGCAGTCCGAGTCAACATAGAGACCAGTCA  
CATGATCTTCGACCCCTTTCTGACACCTCTTCGCATCAACACGGGGGGCAGGAAGGTCAGTGG  
GACCATGTACAACACTGGAAGACACGTATCCCTTCGCCTGGACAAGGAGCACTTGGTCAACAT  
ATCTGGAGGGCCCATGACATACAGCCACCGGCTGGAGGAGATCCGACTACACTTTGGGAGTGA  
GGACAGCCAAGGGTCGGAGCACCTCCTCAATGGACAGGCCTTCTCTGGGGAGGTGCAGCTCAT  
CCACTATAACCATGAGCTATATACGAATGTCACAGAAGCTGCAAAGAGTCCAAATGGATTGGT  
GGTAGTTTCTATATTTATAAAAGTTTCTGATTCATCAAACCCATTTCTTAATCGAATGCTCAA  
CAGAGATACTATCACAAGAATAACATATAAAAAATGATGCATATTTACTACAGGGGCTTAATAT  
AGAGGAACTATATCCAGAGACCTCTAGTTTCATCACTTACGATGGGTGCGATGACTATCCCACC  
CTGCTATGAGACAGCAAGTTGGATCATAATGAACAAACCTGTCTATATAACCAGGATGCAGAT  
GCATTCTTTCGCGCTGCTCAGCCAGAACCAGCCATCTCAGATCTTCTGAGCATGAGTGACAA  
CTTCAGGCCTGTCCAGCCACTCAACAACCGCTGCATCCGACCAATATCAACTTCAGTTTACA  
GGGGAAGGACTGTCCAAACAACCGAGCCCAGAAGCTTCAGTATAGAGTAAATGAATGGCTCCT  
CAAGTAGGGAACAAAGCCAAGAAGAATCCACCTCAGTGAAATGCTACAACGTGAATTGACG  
TAACCTAGAATGTCCCCCTTCTTGCTTCTCTCTCTCTTCTTCCCCCAAGCCTCATTCTTCTT  
GGGATTGGCCCTTTCTTCATGAAAAGTGTCTGCGAAACCATGGCAGAGGAATACATCTCTCAC  
ACATACTCACAACACACACACAAGCACTTGCACATACATACAAACACATGCAAACATACCTA  
CACACACACACTCTCTTACAACCTCCATCATGGGAAGTCAAGTTTCAGAAACAAAAGTCTCAT  
TCATAAGAGGTCTTAGAAGAAAATAACCAGTTAACCTGATTCAATTTTGATACCGTTTTCTCT  
GAACTAATAAATCTACCCAATGAGACTTTTCAGCCTTTGTACATACAAAATTTCTTCCAAAAGA  
GAGAGGAGAAAATACAGCTCTGATGGCATCAAACGGACTTTGCATCAAGTAATTTTCAGATAGT  
GTCCTAGGATCCTTTGAGGGTGCTGGTAGCAGGTGAGCAGGACAAAGTTGACCAAGGACACTT  
ATTTCTAGATTATGATTCTTCTGTTTACTCAACAATTTACAAAGAAAAAAGGACAGACATTG  
AAGAGCTACACATTGTATATATATCACCACAGACTATAAGGAAATGGAATTATTTCCCTCTTT  
GTCACATATCTGTAGTAGGATTTGCCAAGATCAGAAATGATCCATTTGCTGTTTCTTGTTTTTC  
CAAAGGTCATACATTGTGTTTGGTTATTGTTACCAGCTCAATAAATGTGTTTAAACGAGTTAAT  
TTCATTTTTCTGGCTTTGGTCTGTTCTCCTTACAGGCTAAGCCCTGGCTCCATGCAACT  
GCATTCTTTGATTTCACTTGTTCTTCTCATCTACATGTTTTGTTCAATTTGCAGCCAGTTTTTAC  
TGAGTTTGTGGCAATCAGGAATGCATTTGCTAAGCAAGTATGACTTTAATTCCTCCATGGC  
TCAATCATTACATGAGGTGAGCTTCAGCCTGAGATAGCAGGCGACAGACTTCTTGCGTTTCA  
AACTGCCATGCCCCCTGTGATGCTCCCGTGAAGGAATGCACTTTGCCCTGTAAGTTCCCTGG  
GAAAGGGGTATGTTTTCTCTCCAGGTGCAGCCAGATCTCACAAGTACAAAACGAATGCCTTT  
CTTTCTTGTTTATAATGGTCACTCACTGTGTTTGGTTACTGTCAAGAAATCAATAAATGTGT  
TTAACAAGTTA

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## **FIGURE 34**

MEIVWEVLFLQLQANFIVCISAQQNSPKIHEGWWAYKEVVQGSFVPVPSFWGLVNSAWNLCSVG  
KRQSPVNIETSHMIFDPFLTPLRINTGGRKVS GMTYNTGRHVSLRLDKEHLVNISGGPMTYSH  
RLEEIRLHFGSEDSQGSEHLLNGQAFSGEVQLIHYNHELYTNVTEAAKSPNGLVVVSIFIKVS  
DSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFITYDGSM TIPPCYETASWII  
MNKPVIYITRMQMHSRLRLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTNINFSLOGKDCPNRA  
QKLQYRVNEWLLK

**Important features:**

**Signal peptide:**

amino acids 1-20

**Eukaryotic-type carbonic anhydrases proteins.**

amino acids 126-162, 220-269, 43-91

**N-glycosylation sites.**

amino acids 116-119, 168-171, 302-305

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**FIGURE 35**

GTCCGAACCCCTCAGGCCACCCTCGGGAGTCCTGGGGTCCAGAGGGGTGTCCCTGTACCCCTTGACAC  
ACAGGACCCCTCACTCTGCAGGGATAAGCCAGCTGCGCCTGCAGCCTAGGGTGCCAAGGAGGCTGCTGA  
TTGTGGCCACAGCCTCATCTGAACGCCAGGAGACCAGGATAACGAGGCACCGGATCCCTCTCTGTG  
CCCTGGGGAGCCCCAGTGTGCCCAGTCACCCAGGGCTGAGGTCTGCGTCCCTAGTGGTGCAAGGCC  
TGGTAGGACCACGGGGCAGGGAATGTGAGCGCCATCCGAGCTCACGGTGTCTGAGTCGCGGCTTCGT  
GACTTTGGCAGGGGCTCCGGACCAGTGACCCAGTCAAACCCAGAGGGTCTTGGGCGGCAGCGACGA  
AGGAGGTATTAGGCTCCAGGCCAGGTGGGGCCGACGCCCCAGCCATCCACCATGGTGGTGACACA  
CCCCACCGCCACTGCCACCACCACGCCCCTGCACTGTACGGCCACCGTTGTGATGACCACGGCCA  
CCATGGACCTGCGGGACTGGCTGTTCTCTGCTACGGGCTCATCGCCTTCTGACGGAGGTTCATCGAC  
AGCACCACCTGCCCCTCGGTGTGCCGCTGCGACAACGGCTTCTACTGCAACGACCGGGGACTCAC  
ATCCATCCCCGAGATATCCCTGATGACGCCACCACCCTCTACCTGCAGAACAACAGATCAACAACG  
CCGGCATCCCCAGGACCTCAAGACCAAGGTCAACGTGCAGGTCTACTATACGAGAATGACCTG  
GATGAGTTCCCATCAACCTGCCCCGCTCCCTCCGGGAGCTGCACCTGCAGGACAACAATGTGCGCAC  
CATTGCCAGGGACTCGCTGGCCCGCATCCCGCTGCTGGAGAAGCTGCACCTGGATGACAACCTCGTGT  
CCACCGTCAGCATTGAGGAGGACGCTTCCGGACAGCAAACAGCTCAAGCTGCTCTTCTGAGCCGG  
AACCACCTGAGCAGCATCCCTCGGGGCTGCCGACACGCTGGAGGAGCTGCGGCTGGATGACAACCG  
CATCTCCACCATCCCGCTGCATGCCCTCAAGGGCTCAACAGCCTGCGGCGCTGGTGTGACCGGTA  
ACCTGCTGGCAACCAGCGCATCGCCGACGACACCTTCAGCCGCTACAGAACCTCACAGAGCTCTCG  
CTGGTGCGCAATTGCTGGCCGCGCCACCCCTCAACCTGCCAGCGCCACCTGCAGAAGCTCTACCT  
CGAGGACAATGCCATCAGCCACATCCCTTACAACAGCTGGCCAAGATGCGTGAGCTGGAGCGGTGG  
ACCTGTCCAACAACAACCTGACCACGCTGCCCCGCGGCTGTTGACGACCTGGGGAACCTGGCCAG  
CTGCTGCTCAGGAACAACCTTGGTTTTGTGGCTGCAACCTCATGTGGCTGCGGGACTGGGTGAAGGC  
ACGGGCGGCGCTGGTCAACGTGCGGGGCTCATGTGCCAGGGCCCTGAGAAGGTCCGGGGCATGGCCA  
TCAAGGACATTACCAGCGAGATGGACGAGTGTGAGACGGGGCCGAGGGCGGCTGGCCAATGCG  
GCTGCCAAGACCACGGCCAGCAACCACGCTCTGCCACCACGCCCCAGGGTCCCTGTTTACCCTCAA  
GGCCAAAAGGCCAGGGCTGCGCCTCCCCGACTCCAACATTGACTACCCCATGGCCACGGGTGATGGCG  
CCAAGACCCTGGCCATCCACGTGAAGGCCCTGACGGCAGACTCCATCCGCATCACGTGGAAGGCCACG  
CTCCCCGCTCCTCTTTCCGGCTCAGTTGGCTGCGCCTGGGCCACAGCCAGCCGTGGGCTCCATCAC  
GGAGACCTTGGTGACGGGGGACAAGACAGAGTACCTGCTGACAGCCCTGGAGCCCAAGTCCACCTACA  
TCATCTGCATGGTCACCATGGAGACCAGCAATGCCTATGTAGCTGATGAGACACCCGTGTGTGCAAG  
GCAGAGACAGCCGACAGCTATGGCCCTACCACCACACTCAACCAGGAGCAGAACGCTGGCCCCATGGC  
GAGCCTGCCCCCTGGCGGGCATCATCGGCGGGGAGTGGCTCTGGTCTTCTCTTCTGGTCTGGGGG  
CCATCTGCTGGTACGTGCACAGGCTGGCGAGTGTGACCCGGGAGAGGGCCTACAACCGGGGCGAGC  
AGGAAAAGGATGACTATATGGAGTCAGGGACCAAGAAGGATAACTCCATCCTGGAAATCCGCGGCC  
TGGGCTGCAGATGCTGCCATCAACCCGTACCGCGCCAAAGAGGAGTACGTGGTCCACACTATCTCC  
CCTCCAACGGCAGCAGCTCTGCAAGGCCACACACCATTGGCTACGGCACCACGCGGGGTACCGG  
GACGGCGCATCCCCGACATAGACTACTCCTACACATGATGCCCCGCCACCGGGGTGCCCGCCTCA  
GCCCCAGCTGCCCTGGCGTGGCCATGTGGCTTGGCCAGCCTGCTGCAATCCAAGAGAGCAAGGAAGA  
GAAATTCCATGGGTGACTTCTCCGAGAAAGCAAAGTTTGGGGAGGGCTGACGATTTGTAGAACA  
CAACAGTGACAATTTTTTTTAAAGAATAGAAGGCAGGAGGGGAATTGACATTTGTTGAAGACATAA  
TTTATACCAAGTTATGCCAGTTGGGGAGGGAAGGACTAAAAATAATATTGCAGGCAGGGCTGGGTGG  
GTTTTTTTTTTTCCCCCTGAAGTGAAGGATACTACCTGTACAACATCTGTGGACACCTCATGCTCT  
GTTCAAGGCCATCACAAGGAACCGCCAGGGAGAAGCAGCCGGCTCTCAAAGCTCCACGCAGCTCTC  
CCGCACTGGCCACTCGCTGGCGACCCGATGGAAGGTTTTAGGCTCCTCACAAGGAGAGAGGGAAG  
AAAAGATCTTTTGGCCTGGAGATATGGTCTGAAATCTCTCCCTGGCTTATTCATACCATTTCCCT  
TGCAGATTTGCAGAAACATGGCATCTTTCACTGCATTCTTTGAACAATCATGTAGTCGATTAAAAAA  
AAAACAACTTTTTTCTAGGCTGAAGCCCTCTTCAAGTTCCATGCACCACGCTCCGTAGAAGCCCC  
GGCGGAAGCCGTAGCTTTCCCTGCCACCTGGAGGTGCATCTGTCTGCCTGTCTATCCCTGTGCGGGT  
TCTCTAAGTACAGATGGGTAGATAGAGCCACATGCACGGTCTTACCGTTCTTCTGGGTGAGTTCTT  
ACCATTTCTGAACAATAGAATTGTGAAAGTTTAAAAA



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**FIGURE 36**

MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRCDNG  
FIYCNDRLGTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDEFPINLP  
RSLRELHLQDNNVRTIARDSLARIPPLEKLHLDNSVSTVSIEEDAFAFSKQLKLLFLSRNHL  
SSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIADDTFSRLQNLTE  
LSLVRNSLAAPPLNLPSAHLQKLYLQDNAISHIPYNTLAKMRELERLDLSNNNLTTLPRLFD  
DLGNAQLLLRNNPWFCGCNLMWLRLDWVKARAAVNVVRGLMCQGPEKVRGMAIKDITSEMDEC  
FETGPQGGVANAAAKTTASNHASATTPQGSLETLKAKRPGRLPDSNIDYPMATGDGAKTLAI  
HVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSITETLVQGDKTEYLLTALEPKSTYI  
ICMVTMETSNAAYVADETPVCAKAETADSYGPTTTLNQEONAGPMASLPLAGIIGGAVALVFLF  
LVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESGTTKDNSILEIRGPGLQMLPINPYRAK  
EEYVVHTIFPSNGSSLCKATHHTIGYGTTRGYRDGGIPDIDYSYT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 552-573

**N-glycosylation sites.**

amino acids 249-252, 305-308, 642-645

**Leucine zipper pattern.**

amino acids 182-203, 299-320

**Phospholipase A2 aspartic acid active site.**

amino acids 57-67

**FIGURE 37**

[illegible]

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**FIGURE 38**

MAEPGSHHLSARVRRRTERRIPRLWRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTACDS  
TGSRRRVAVPHTPGLCTSLSDPVKGTECSFSCNAGEFLDMKDQCKPCAEGRYSLGTGIRFDE  
WDELPHGFAASLANMELDDSAESTGNCTSSKWVPRGDYIASNTDECTATLMYAVNLKQSGTV  
NFEYYYPDSSIIFFEFFQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNNVLYWRTTAFSVW  
TKVPKPVLVNRNIAITGVAYTSECFCKPGTYADKQGSFCKLCPANSYSNKGETSCHQCDPK  
YSEKSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKICSEDLEGAVKLPAAGVKT  
CPPCNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVGFEYKWWNTLPTNMETTTLVSGI  
NFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLLVVPGRPPQSVMAADTENKEVARITFVFETL  
CSVNCELYFMVGVNSRTNTPVETWKGSKGQSYTYIIIEENTTTSTWAFQRTTFHEASRKYTN  
DVAKIYSINVTNVMNGVASYCRPCALEASDVSSCTSCPAGYYIDRDSGTCHSCPPNTILKAH  
QPYGVQACVPCGPGTKNNKIHSCLYNDCTFSRNTPTRTFNYNFSALANTVTLAGGPSFTSKGL  
KYFHHFTLSLCGNQGRKMSVCTDNVTDLRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVS  
SQPVSLADRLIGVTTDMTLDGITSFAELFHLES LGIPDVIFFYRSNDVTQSCSSGRSTTIRVR  
CSPQKTVPGSLLLPGTCSGTGDCGNFHLWESAAACPLCSVADYHAIVSSCVAGIQXTTYVX  
REPKLCSGGISLPEQRTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKL  
VNATLKDCLPAADSCAIMEGEDVEDDLIFTSKKSIFGKIKSFTSKRTPDGFDSVPLKTSSGG  
PMDL

**Important features of the protein:****N-glycosylation sites:**

amino acids 153-156, 390-393, 391-394, 404-407, 544-547, 576-579,  
672-675, 717-720, 947-950

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 15-18, 563-566, 709-712

**Casein kinase II phosphorylation sites:**

amino acids 42-45, 59-62, 81-84, 146-149, 168-171, 282-285, 331-  
334, 340-343, 431-434, 449-452, 465-468, 523-526, 557-560, 761-  
764, 780-783, 835-838, 860-863, 893-896, 949-952

**Tyrosine kinase phosphorylation sites:**

amino acids 50-56, 109-116

**N-myristoylation sites:**

amino acids 77-82, 88-93, 152-157, 268-273, 288-293, 320-325,  
400-405, 405-410, 414-419, 463-468, 599-604, 616-621, 634-639,  
644-649, 839-844, 874-879, 912-917, 916-921

**Amidation site:**

amino acids 707-710

**Cell attachment sequence:**

amino acids 162-164

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**FIGURE 39**

GGGAAGGGGTTCTGGGCTGCCGCAGGCACACAGGCCAGAGCTTCGTGGATACCTGCAGGGCCC  
AAAGGTCCCTCCCTGTTTTGAAGAGTGAGTGATGGCTATGAGGTAGCGGCCAGGCTGATCACC  
CCTGCGTTGGCTGGAGGCAGAATTCTGTAAATCCTCGCCAAGTCTTTCTCCAGGCCACTGGTT  
AGCTCATCTCAGCCTCCTCTGGGAGCATCAACACCAACATGGCACAGGGGACTGCAGTGGTGT  
GCTTTGGACCTGTGTACCCACCCAAGGCTAAAGGCAGAGCCAGGTGACTTTGCGGGGGTCTCT  
TCTCTAGGATTATCTGTACTTCCCCCTCTGTCTCTTTTACTACGGGAGATCGAGCTAGCTATA  
ACCCACCTTCTTTCATGAGAACCACACTAAATTGCAAAAATTATCCCAGTGCTGGAGGAGGGC  
AGCAGGTTGAGATTATGTTGGCAGGAAGAATGTTGGCATTGATTGGCACGCAGGGGACGAGAG  
CTGCTTTGTGCTTTAAAGGAGCCAAGTTACACCCTGTTTAACCCTGCCTTCAAAGGGACGACT  
CTGTAAGATTCTCTGCTACTTATTCAAGTTGACACGATGCCCTTCACACTCCACCTGAGGTCC  
CGCCTTCCCTCTGCCATAAGGAGTTTGATTCTACAAAAGAAACCAACATCAGAAATACATCC  
AGCATGGCTGGAGAGCTCCGACCAGCCAGCCTGGTGGTCTCTGCCAGGTCCCTTGCTCCAGCT  
TTTGAAAGATTCTGCCAGGTCAACACTGGTCTCTACCCCTGCTGGGCCAGAGTGAGCCAGAA  
AAGTGGATGCTGCCCCCTCAAGGTGCTATCTCAGAGACCAGGATGGGCCATCCCCAGTTCTGG  
AAATACGAGTTCGGTGCCTGCACCGGTAGCCTGGCTTCGCTGGAGCAGTACTCGGAGCAGCTG  
AAGGACATGGTGGCCTTCTTCTGGGCTGCAGCTTCTCCCTGGAGGAGGCCTTGGAGAAAGCG  
GGGCTCCCCAGAAGAGACCCAGCAGGTACAGCCAGGCGGGTGCATACAAGACAACAGTGCCT  
TGTGTTACCCATGCTGGCTTCTGCTGCCCTCTGGTGGTACGATGAGGCCATTCCCAAGGAC  
AAGCTGGAAGGGCTGGTGCGGGCTGCTGCTCCCTCGGAGGTGAGCAGGGGCAACCTGTTTAC  
ATGGGCGACCCAGAAGTGTGGGAATCAAAGAGCTTTCCAAACCTGCCTACGGGGATGCCATG  
GTGTGTCCCCCAGGGGAGGTTCCAGTGTCTGGCCTTCTCCGCTGACCAGTCTCGGAGCTGTC  
AGCAGCTGTGAGACCCCACTGGCTTTTGCCAGCATCCAGGCTGCACAGTTATGACTGACCTG  
AAGGATGCAAAGGCTCCACCTGGTTGTCTCACCCAGAGAGAATTCCAGAGGTCCATCACATT  
TCCCAAGATCCTCTGCACACAGCATCGCGTACGTCTCTGCTTCTCAGAAGATCAGAGAATA  
GAGTCTATGATCGGCATAGACCCAGGGAACCGGGGATTGGGCACCTGCTCTGTAAAGATGAG  
CTGCTGAAGGCCTCTCTCTCGCTGTCCCATGCCCGCTCAGTGCTCATCACCCTGGGTCCCC  
ACACATTTCAATCATGAGCCTCCAGAAGAGACAGATGGCCACCAGGAGCTGTTGCTCTGGTT  
GCCTTCTGTCAGGCCTTGGAGAAGGAGGTGCGCCATAATCGTTGACCAGAGAGCCTGGAACCTG  
CACCAGAAGATTGTTGAAGATGCTGTTGAGCAAGGTGTTCTGAAGACGCAGATCCCGATATTA  
ACTTACCAAGGTGGATCAGTGGAAGCTGCTCAGGCATTCCTGTGCAAAAATGGGGACCCGCAG  
ACACCTAGATTTGACCACCTGGTGGCCATAGAGCGTGCCGGAAGAGCTGCTGATGGCAATTAC  
TACAATGCAAGGAAGATGAACATCAAGCACTTGGTTGACCCCATTGACGATCTTTTTCTTGCT  
GCGAAGAAGATTCTTGAATCTCATCAACTGGAGTCGGTGATGGAGGCAACGAGCTTGGGATG  
GGTAAAGTCAAGGAGGCTGTGAGGAGGCACATACGGCACGGGGATGTCATCGCCTGCGACGTG  
GAGGCTGACTTTGCCGTCAATTGCTGGTGTCTTAAGTGGGGAGGCTATGCCCTGGCCTGCGCA  
CTCTACATCCTGTACTCATGTGCTGTCCACAGTCAGTACCTGAGGAAAGCAGTCGGACCCCTCC  
AGGGCACCTGGAGATCAGGCCTGGACTCAGGCCCTCCCGTCGGTCATTAAAGGAAGAAAAAATG  
CTGGGCATCTTGGTGCAGCACAAAGTCCGGAGTGGCGTCTCGGGCATCGTGGGCATGGAGGTG  
GATGGGCTGCCCTTCCACAACACCCACGCCGAGATGATCCAGAAGCTGGTGGACGTCACCACG  
GCACAGGTGTAAACCGTCCATGTTCCGTGTGAGCAGAGTCCCTACCAACGGGCAGGTCTGCATC  
CGGGGAGAATGCAGCTGCTTCTGGCGACAATCCTGCTAGTAAACACTGGTCTTCGGTGAGCAA  
CGAACACTCGCCTGGCCTGGGAAACTGCATGCCCACTTTCTGGGAGGGGTTAGTGCAGGTGCC  
GTGGACAAAGGACAACATTTCTCTGGGGCTTTTTAACTTTTATTCCTAAGACTCTAAAGGCGT  
TGATTTCAACCCTCCTTCACTCTGGCTTCTTCAGGCAACCCACGTGGTCTCCTATGAGAATCT  
TCTCGACAGTTACTTATGGGGACACTTGTGAACAATTAAGTGCCAGGGCAGAGCATGAGAACAA  
AACATTTCCAGGCCATGTAGGATAGGATACTCCAGACTCCAGTCATCCTCCCCCATCCATGGT  
TTCTGTTACTCATGGTTTCAGTTACTCATAGCCAAGTGCAGACCGAAAAATACTAAATGAAAAA  
TTTCAGAAATAAACAACCTCTTAAGTTTTAAAAA

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**FIGURE 40**

MPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAGELRPASLVVLPRSLAPAFERFCQVNTGPL  
PLLGQSEPEKWMLPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGCSF  
SLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVVTRPIPKDKLEGLVRACCSL  
GGEQQQPVHMGDPELLGIKELSKPAYGDAMVCPGGEVPVFWPSPLTSLGAVSSCETPLAFASI  
PGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQKIRELESMIGIDPGNRG  
IGHLLCKDELLKASLSLHARSVLITTFPTFHNHEPPEETDGPPGAVALVAFLQALEKEVAI  
IVDQRAWNLHQKIVEDAVEQGVLTQIPILTYQGGSVAAQAFLECKNGDPQTFRFDHLVAIER  
AGRAADGNYYNARKMNIHLVDPIDDLFLAAKKIPGISSTGVGDGGNELGMGKVKEAVRRHIR  
HGDVIACDVEADFAVIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQAWTQAL  
PSVIKEEKMLGILVQHKVRSVSGIVGMEVDGLPFHNTHAEMIQKLVDVTTAQV

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 358-378, 517-539

**N-glycosylation site.**

amino acids 28-32

**Tyrosine kinase phosphorylation site.**

amino acids 444-452

**N-myristoylation site.**

amino acids 98-104, 102-108, 123-129, 149-155, 181-187, 190-196,  
238-244, 308-314, 399-405, 413-419, 448-454, 477-483, 482-488,  
487-493

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 233-244, 531-542

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**FIGURE 41**

CTTTCCTGTTTTATCCGCAGCCCTTTTCTTCTTTGAGTTAGTAAAGATTTATTCTGTAACCTG  
ACACTCATCTGGCCCTTTGCAGTTTGCCAGCCATATCCCATGTGATTTCCCACTGGATCCAG  
GCCCCATCCGGCTGGCAGGAGGGGGCTCTGACGTACAGGTTGGAAATCAGAAGTCTGTGAGA  
GCGCGGGAGTGATGGCAGCTCTGGGTCCCAGACCTGGCCCGACCCCTCTGCTTCACCTECAG  
CTCTGCTGCTCCTCTACTCTTGGGTGAGATCCCTTTGGAGCCACAGCGAGGAACCCTGTGGT  
CCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGCCCTCTTTTCTGTGTCAAAGCCTGCCCTC  
GGGCTCTGCTCACCTCTGGTGACCCTCCAAGATGCCCTGCCCTCAGTTTCCCCTCATGATCT  
GGCCTCTGCCCCCTTCTCTAGCCACAGCCTCTAGTACACTTTAGCAATACCACCAGACTAGTT  
AGAGTTCCCCACTCACCAAGCAAGACATGCAGTTTCATGCCTCTGTGCCTTCGCTCATGCTGT  
TTCTTCCGACTGGAATGCCTTCCCCTGCTCCTCCTGCCTTGTCTGCCTGGCAAGTTCATCTCT  
CACGATCCCCTCAAAGGCCCCCTCCTCCAGGAAGGCAACCCCTGTGCCCCCTCCCCTCCAGGCT  
ACCTCTGCACCTTGTCAATGCTTCTTGTGGCACTTATCACACTGTATTTTACTTGTTTACA  
TGTTTGTCTCCCCTTCTAGACTGTGAATCCTTAAGGGCATGGACTGTATCTTATGCATCTCTG  
TATTTCTGCGCCTAGCACGGTGCCTAGCACACAGTAGGCGCTCAATAAATGTTGAATGAATGA  
ATGATTT

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## **FIGURE 42**

MQFHASVPSLMLFLPTGMPSAPPALSAWQVHLSRSPQRPPPPGRQPLCPSPPGYLCTLSMLL  
LWHLSHCILLVYMFVSPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Microbodies C-terminal targeting signal.**

amino acids 81-83

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**FIGURE 43**

GTTTCCAACAAGGATGATATGAAGACTTCCCTGAAGAAAGTTGTGAAGGGACCTCCTACGAGA  
TGATGATGCAGTGTGTGTCCCGCATGTTGGCCACCCCCTGCATGTCATCTCAATGCGCTGCA  
TGGTCCAGTTTGTGGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGGAAGATTT  
TCAAAGAGGAAGGGCTGCTGGGATTCTTCGTTGGATTAATCCCTCACCTCCTGGGCGATGTGG  
TTTTCTTGTGGGGCTGTAACCTGCTGGCCCACTTCATCAATGCCTACCTGGTGGATGACAGCT  
TCAGCCAGGCCCTGGCCATCCGGAGCTATACCAAGTTCGTGATGGGGATTGCAGTGAGCATGC  
TGACCTACCCCTTCTGCTAGTTGGCGACCTCATGGCTGTGAACAACCTGCGGGCTGCAAGCTG  
GGCTCCCCCTTACTCCCCAGTGTTCAAATCCTGGATTCACCTGCTGGAAGTACCTGAGTGTGC  
AGGGCCAGCTCTTCCGAGGCTCCAGCCTGCTTTTCCGCCGGGTGTCATCAGGATCATGCTTTG  
CCCTGGAGTAACCTGAATCATCTAAAAAACCGGTCTCAACCTGGCCACTGTGGGTGAGGCCT  
GACCACCTTGGGACACCTGCAAGACGACTCCAACCCAACAACAACCAGATGTGCTCCAGCCCA  
GCCGGGCTTCAGTTCCATATTTGCCATGTGTCTGTCCAGATGTGGGGTTGAGCGGGGGTGGGG  
CTGCACCCAGTGGATTGGGTCACCCGGCAGACCTAGGGAAGGTGAGGCGAGGTGGGGAGTTGG  
CAGAATCCCCATACCTCGCAGATTTGCTGAGTCTGTCTTGTGCAGAGGGCCAGAGAATGGCTT  
ATGGGGGCCCAGGTTGGATGGGGAAAGGCTAATGGGGTCAGACCCACCCCGTCTACCCCTCC  
AGTCAGCCCAGCGCCCATCCTGCAGCTCAGCTGGGAGCATATTCTCCTGCTTTGTACATAGG  
GTGTGGTCCCCTGGCACGTGGCCACCATCATGTCTAGGCCTATGCTAGGAGGCAAATGGCCAG  
GCTCTGCCTGTGTTTTTCTCAACACTACTTTTCTGATATGAGGGCAGCACCTGCCTCTGAATG  
GGAAATCATGCAACTACTCAGAATGTGTCCTCCTCATCTAATGCTCATCTGTTTAATGGTGAT  
GCCTCGCGTACAGGATCTGGTTACCTGTGCAGTTGTGAATACCCAGAGGTTGGGCAGATCAGT  
GTCTCTAGTCCTACCCAGTTTTAAAGTTCATGGTAAGATTTGACCTCATCTCCCGCAAATAAA  
TGTATTGGTGATTTGGAAAAAAAAAAAAAAAAA



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## **FIGURE 44**

MMMQCVSRMLAHPLHVISMRCMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGDV  
VFLWGCNLLAHFINAYLVDDSFSQLAIRSYTKFVMGIAVSMLTYPFLLVGDLMAVNNCGLQA  
GLPPYSPVFKSWIHCWKYLSVQGQLFRGSSLLFRRVSSGSCFALE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 51-72, 97-114

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 160-163

**N-myristoylation sites.**

amino acids 34-39, 100-105, 123-128, 165-170

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**FIGURE 45**

GCTCACTCTTTGGGTCCACACTGCCTTTATGAGCTGTAACACTCACTGGGAATGTCTGCAGCT  
TCACTCCTGAAGCCAGCGAGACCACGAACCCACCAGGAGGAACAAACAACCTCCAGACGCGCAG  
CCTTAAGAGCTGTAACACTCACCGCGAAGGTCTGCAGCTTCACTCCTGAGCCAGCCAGACCAC  
GAACCCACCAGAAGGAAGAACTCCAAACACATCCGAACATCAGAAGGAGCAAACCTCGTGACA  
CGCCACCTTTAAGAACCGTGACACTCAACGCTAGGGTCCGCGGCTTCATTCTTGAAGTCAGTG  
AGACCAAGAACCCACCAATTCCGGACACGGCAAAGTAACATCCTAGACATGGCTTTAGAGATC  
CACATGTCAGACCCCATGTGCCTCATCGAGAACCTTAAATGAGCAGCTGAAGGTTAATCAGGAA  
GCTTTGGAGATCCTGTCTGCCATTACGCAACCTGTAGTTGTGGTAGCGATTGTGGCCCTCTAT  
CGCACTGGCAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAACAAGGGCTTCTCTGTTGCA  
TCTACGGTGCAGTCTCACACCAAGGGAATTTGGATATGGTGTGTGCCTCATCCCAACTGGCCA  
AATCACACATTAGTTCTGCTTGACACCGAGGGCCTGGGAGATGTAGAGAAGGCTGACAACAAG  
AATGATATCCAGATCTTTGCACTGGCACTCTTACTGAGCAGCACCTTTGTGTACAATACTGTG  
AACAAAATTGATCAGGGTGTATCGACCTACTGCACAATGTGACAGAAGTGCAGATCTGCTC  
AAGGCAAGAACTCACCTGACCTTGACAGGGTTGAAGATCCTGCTGACTCTGCGAGCTTCTTC  
CCAGACTTAGTGTGGACTCTGAGAGATTTCTGCTTAGGCCTGGAAATAGATGGGCAACTTGTC  
ACACCAGATGAATACCTGGAGAATTCCCTAAGGCCAAAGCAAGGTAGTGATCAAAGAGTTCAA  
AATTTCAATTTGCCCCGTCTGTGTATACAGAAGTTCTTTCCAAAAAAGAAATGCTTTATCTTT  
GACTTACCTGCTCACCAAAAAAGCTTGCCCAACTTGAAACACTGCCTGATGATGAGCTAGAG  
CCTGAATTTGTGCAACAAGTGACAGAATTCTGTTCTTACATCTTTAGCCATTCTATGACCAAG  
ACTCTCCAGGTGGCATCATGGTCAATGGATCTCGTCTAAAGAACCTGGTGCTGACCTATGTC  
AATGCCATCAGCAGTGGGGATCTGCCTTGATAGAGAATGCAGTCTGGCCTTGGCTCAGAGA  
GAGAACTCAGCTGCAGTGCAAAAGGCCATTGCCCCTATGACCAGCAAATGGGCCAGAAAGTG  
CAGCTGCCCATGGAAACCCCTCCAGGAGCTGTGGACCTGCACAGGACCAGTGAGAGGGAGGCC  
ATTGAAGTCTTCATGAAAACTCTTTCAAGGATGTAGACCAAAGTTTCCAGAAAGAATTGGAG  
ACTCTACTAGATGCAAAACAGAATGACATTTGTAAACGGAACCTGGAAGCATCCTCGGATTAT  
TGCTCGGCTTTACTTAAGGATATTTTTGGTCCCTCTAGAAGAAGCAGTGAAGCAGGGAATTTAT  
TCTAAGCCAGGAGGCCATAATCTCTTCATTCAGAAAACAGAAGAACTGAAGGCAAAGTACTAT  
CGGGAGCCTCGGAAAGGAATACAGGCTGAAGAAGTTCTGCAGAAATATTTAAAGTCCAAGGAG  
TCTGTGAGTCATGCAATATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAAGAAGAAA  
GAGGCACAAGTGAAAGCAGAAGCTGAAAAGGCTGAAGCGCAAAGGTTGGCGGCGATTCAAAGG  
CAGAACGAGCAAATGATGCAGGAGAGGGAGAGACTCCATCAGGAACAAGTGAGACAAATGGAG  
ATAGCCAAACAAAATTGGCTGGCAGAGCAACAGAAAATGCAGGAACAACAGATGCAGGAACAG  
GCTGCACAGCTCAGCACAACATTCCAAGCTCAAAATAGAAGCCTTCTCAGTGAGCTCCAGCAC  
GCCCAGAGGGCTGTTAATAACGATGATCCATGTGTTTTACTCTAAAGTGCTAAATATGGGAGT  
TTCCTTTTTTTACTCTTTGTCACTGATGACACAACAGAAAAGAACTGTAGACCTTGGGACAA  
TCAACATTTAAATAAACTTTATAATTATTAAA

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**FIGURE 46**

MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAKGNK  
GFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTF  
VYNTVKNIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTLRDFCLGLEI  
DGQLVTPDEYLENSLRPKQGSQVRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLETLP  
DDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYNVNAISSGDLPCIENAVL  
ALAQRENSAAVQKAIHYDQQMGQKVQLPMETLQELLDLHRTSERAIEVFMKNSFKDQVDSF  
QKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKPGGHNLFIQKTEEL  
KAKYYREPRKGIQAEVLQKYLKSKESVSHAILQTDQALTETEKKKKEAQVKAEEKAEQAQRL  
AAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQQKMQEQQMQEQQAQLSTTFQAQNRSL  
SELQHAQRAVNNDPCVLL

**Important features of the protein:****Transmembrane domains:**

amino acids 31-49, 114-131

**N-glycosylation sites.**

amino acids 90-94, 144-148, 287-291, 563-567

**N-myristoylation sites.**

amino acids 45-51, 283-289

**Prenyl group binding site.**

amino acids 583-588

**ATP/GTP-binding site motif A (P-loop).**

amino acids 45-53

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**FIGURE 47**

CACTCATTTCATTCCAAAGGGTCTCTCAAGGCAATGGTAATGTGCAAGGAGGTGATACCTAAAT  
GAATGACCAAAAGAACATGCTTCTGCTTTTGTGTGTCTCCTACATTTTAGACATTTGTTTGT  
TCTCTTGGTAGCCTTTAAATTCCTTGAAGCCCAGGACCATGTCTCACTTACCTTTGTGTTTCC  
ACTAACTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAAGCCTGTGAAATAAGTGATGT  
CTATTTCTAGCATATTATTCTGAGATTTAATGATAGATTTAGTGATTGAATGAGATTTCCATT  
TTCAAATACAGCAAAAGCATAACTATTTTCATTTCATTTCATTTCACTTTCATTCTCAAA  
ATTAGGTCCTGAGTTAACTAATAATTACCTTTGAAATGTGTGGGTATTGAGGCAATCAGGT  
GGTGACATTGAGCTCTCAGCCAGAGTTTGTCTGGAATTGATTTCAGTTCCATTGCATTGATT  
TTTGTCTCAGAAGCCAAGGTTTCCCATGAAAAATCATTCCCACTTGAATTGGGCTGTGATTC  
TTGCTGCGTTTAAAGTAAAGGAAGCCTCTTGGTTCTAGTTCTGCAAACCTACACACTGAACTGG  
GACAAGTTTTTGTTTAGAGTAATGGCTGGGAAAAGAGGAACCTTTCATTTTATTTCAGAAGTCA  
AAAACAAAGGCCTCCCAGCCACCTGGAGATGTTTTGTTGCAGACACCAGCCTGGCTCTGTCTT  
TATGCCTAACAAATTGAGCATCCAGTCTTCTTTGTGCTGGGACCATTGCTCAGCTCTGCAAGGG  
GAAAAGAGGGAGAAAGCCAGAGCTGCCAGGCTTCTTGCCTGGGGCCGGGGGAGGGTTCTGG  
GAAGCAGGTGCTCTCTGGCTTCTTGGTACGTGAGGCTCTCGGAGCTGCCTCTCCTCTGACCCT  
CAGGTCCTCACCGAGTTTGTCTCCAGGAGTATATTGAAAACATAACCCAGTGCTCTCTCAAGCAC  
CCACTGCTTAGAGGGCCCAGATTTCTTTTCTTCTTTCCCTTGCAGAGCTGGAGACTGCATCG  
GGCATCTGGTGTTTAACTAAACAGGAAACTGACTAAAGGTCCACAGTGCTCATTGTGTAGA  
CTAGCTGCCCTCCGATGGGTGCTCTGATTATCAGTGGTTCCAGTGCAGGGCCTGTCACTAAAC  
AGGCCTCACTTCCTCCTTGGGGGCTTTCCCATGGGAGGTGTGGCTTTTTACTCTACATGGAAA  
TGACTCTCTGCAGCCACAGAACACAGTCATTTTCTGAATTATCCAGTCTCTCATGCGCCCTG  
GATTCCCTCCAGATGCCTTATATCTCTTGTGCAAAGTTGTCTAAAATTTGGTTCCAGCTTCCA  
AGCCTTGCCTTTTGGCCTTCCCTGGAAGTATTTTGTGATGAGTCGTCTGTCATTATTCTCTA  
AAATGATTTGCTTTTTTGTCTTTTCATTCCCTATTTCCACCCACATATACACACATGCTTCTT  
AACTTAGGGGATTACATGCCAATAAATCTATTGTTGAAAATGCACTAATACTATCGCAAAGAC  
GAAAATTCACAGGCTGAACCGTTGTAAGTCCATATGCTCCTCACTTACATGTGTGATGGAGT  
TATGCCCAAATAAGTCCATCGTCAAGTTGAAAAATCAAAATCAAGCCATCTTAGGTTGAGGAC  
CATTTGTTTGTACCTCCAAAGATGTCATATCTTTAAACATACTCCCTAGCTTTTCTTTTACT  
TTTTATTTTGAAGTAATTATAGAATCACAGAAAGTTGCAAAAAA

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## **FIGURE 48**

MGALIISGSSAGPVTQASLPPWGLSHGRCGFLLYMEMTLCSHRTQSFSELSQSLMRPGFLQM  
PYISCAKLSKIWFPAKPCLLAFLEVFLLMSRLSLFSKMICFLFLSEFLFPPHIYTHAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 88-107

**Casein kinase II phosphorylation site.**

amino acids 47-50

**N-myristoylation site.**

amino acids 24-29

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**FIGURE 49**

GGCTTCTACAGTCCACAACACCCACCAGCCCCAGGCCAGCAGAATGAGCCCAGTGAGTGCCGGGGCTCCAGTT  
TGGCTGTTGCTATGACACAGTGGCCACTGCAGCCGGTCTCTTGGGGAAGGCTGTGTGGGCCAGCCCAGCCATGC  
CTACCCCGTGGGTGCTGCTGCCAGTGGCCATGGCTCTGTGCAGACTGGGCTGCCCGCTGGTACTTCGTTGC  
CTCTGTGGGCAATGTAACCGCTTCTGGTATGGCGGCTGCCATGGCAATGCCAATAACTTTGCCCTCGGAGCAAGA  
GTGCATGAGCAGTGGCCAGGGATCTCTCCATGGGCCCGCTCGTCCCCAGCCTGGGGCTTCTGGAAGGAGCACCCA  
CACGGATGGTGGCGGCAGCAGTCTGCAGGCGAGCAGGAACCCAGCCAGCACAGGACAGGGGCGCGGTGCAGAG  
AAAGCCCTGGCCTTCTGGTGGTCTCTGGCGGAAGACCAACAGCCTGGGCCAGGGGAGGCCCCACACCCAGGC  
CTTTGGAGAATGGCCATGGGGGAGGAGCTTGGGTCCAGGGCCCCCTGGACTGGGTGGAGATGCCGGATCACCAGC  
GCCACCTTCCACAGCTCCTCCTACAGATCTCACTTCCACCTCTCCAGGATTAGCTTGGCAGGTGTGGAGCCCT  
CGTTGGTGCAGGCAGCCCTGGGGCAGTTGGTGCGGCTCTCTGCTCAGACGACACTGCCCCGAATCCCAGGCTG  
CCTGGCAGAAAGATGGCCAGCCCATCTCTGTGACAGGCACAGGCTGCAGTTTCGACGGATCCCTGATCATCCACC  
CCCTGCAGGCAGAGGACGCGGGCACCCTACAGCTGTGGCAGCACC CGGCCAGGCCGCGACTCCCAGAAGATCCAAC  
TCCGATTATAGGGGGTGACATGGCCGTGCTGTCTGAGGCTGAGCTGAGCCGCTTCCCTCAGCCCAGGGACCCAG  
CTCAGGACTTTGGCCAAGCGGGGCTGCTGGGCCCCCTGGGGCCATCCCCCTTTCACACCCACAGCCTGCAACA  
GGCTGCGTTTGGACCAGAACCAGCCCCGGGTGGTGATGCCAGTCCAGGCCAGCGGATCCGGATGACCTGCCGTG  
CCGAAGGCTTCCCGCCCCCAGCCATCGAGTGGCAGAGAGATGGGCAGCCTGTCTCTTCTCCAGACACCAGCTGC  
AGCCTGATGGTCCCTGGTCATTAGCCGAGTGGCTGTAGAAGATGGCGGCTTCTACACCTGTGTGCTTTTCAATG  
GGCAGGACCGAGACCAGCGATGGGTCCAGCTCAGAGTTCTGGGGGAGCTGACAATCTCAGGACTGCCCCCTACTG  
TGACAGTGGCAGAGGGTGATACGCCAGGCTATTGTGTGTGGTAGCAGGAGAAAGTGTGAACATCAGGTGGTCCA  
GGAACGGGCTACCTGTGCAGGCTGATGGCCACCGTGTCCACCAGTCCCAGATGGCACGCTGCTCATTTACAAC  
TGCGGGCCAGGGATGAGGGCTCCTACATGTGCAGTGCCTACCAGGGGAGCCAGGCAGTCAGCCGAGCACCGAGG  
TGAAGTGGTCTCACCAGCACCCACCGCCAGCCAGGGACCTGGCAGGGACTGCCGTCGACCAGCCAGAGCTGG  
CCAACCTGTGATTTGATCCTGCAGGCCCAGCTTTGTGGCAATGAGTATTACTCCAGCTTCTGCTGTGCCAGTGT  
CACGTTTCCAGCCTCACGCTCAGCCCATCTGGCAGTAGGGATGAAGGCTAGTTCAGCCCCAGTCCAAATAGTT  
CATAGGGCTAGGGAGAAAGGAGATGACTCTTGGCTTCTCTCTGGCTGGCAAAGGGAGTTATCTTCTGGAA  
TACATTAGCTCTTTCAAAAACCCACCCAGTGTTAGCCTCAACGGCAGCCAGTTACCAGCTTCTCTGTAGCCT  
TCAGCAGTGTTCATCTCTGACATAACCACAGGCTGCTGTTTTCAAGAAGAGCAATCTGTTTGGATAAGAAAA  
CCTTTACTTTACAGCTTCCCTTTATAATTTGTACACAGGAATAGTTAAATGCATTTGTTTGTGTTTTTGTAG  
ACGGAGTTTCACTCTTGTGGCCAGGCTGGAGGGCAATGGCGGATCTCAGCTCACTGCAACCTCCGCTCCTGG  
GTTCTTGATTCTCCTGTGTGACGCTTCTGAGTAGCTGGGATTACAGATGCCTATCACCATGCCTGGGTAATTTT  
GTATTTTAGTTGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGATGATCTGCC  
GCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACGCCCAGCCATCAATGCATTTTTTTTATTTT  
TTTTTTGAGACAGAGTTTCGCACTTCTTGCCAGGCTGGAGTACAATGGTGCGATCTTGGCTCACTGCAACCTCC  
ACCTCCTGGGTTCAGCGCTTCTCCAGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTATGTGCCACCATGCCT  
GGCTAATTTTGTATTTTGGTGGAGACGGGGTTTCTCCATGTTGGTCAGACTGGTCTTGAACCTCCGACCTCAGG  
TAATCCGCCCCGCTCCGCTCCCAAATGCTGGGATTAGAGGTGTGAGCCACTGTGCCAGCCCATCAATGTGTT  
TTAAAGCTAGCTGTGAGGGTTCCACTTAATTTAAAGCTGGGCAGGGAGATGTGAATGATTTCAAAGTTAACACC  
TGTTTGTCTTCTAAAGGGCATGCCAAGTCTGCTGTATCAGGGAAGTATTCTGTGCTAAAATCAGCGATGGTTCA  
TTGCTCTAGTCTCTCACCCCTTCTAGGCAGTGCATCAGTCAAGTCTAAATCTGGTGCAGAGGGTTAACAGCATA  
ACCCTTGTGGCAAATGGAATAGATGTTAAGACCTCAAATAGGGATTGGGATGAAACAGCTGCAGTTAGCACT  
GTTATCTGAGCATGAAAGAACTGGAACGCTCCTTACGTGAGATGTTGGACCTTGAAGCCCTCCTGAGGCCAAC  
ATGCAAATCTGGCTGTGACGGTTCTCTGACACCTGTGTAAGCTGACCAGCCTGCTCTGTACAGTGACAATGAG  
GAGCCCCCTCTCTTCTTAAGTAGGAATCTGTGAAGCAAAATGTTTGTGCCAAAGACAAATCAGACTGTGAGTCA  
TTAAAAACAGCATTAGCAGGATGAGGATAGCAATGGGGAAGGGTTGTGGGCAATGCAGTAACAGGGAAATGGCT  
CAGAAATGGTTTGAAGTGGAGACAACATTCTTCATCTCTCAGGACTTCTAATTCCTTGATGCTAAAAGAAGAGG  
CATGGATTCTATGAGCTTCCAAGTCCCTTTCCACTTTAACCTTCTACAAATCTTTCAGAGGACTGCCTAGTAGCA  
AAGGTTATTCCTGGACACAGGAAGACGGGCATTACAGGGACCAAAGCTCTGAAAGGTGACTTTTATTACCAACA  
CACTGGCTGGAAGGGACAAACACATCAGGGTGAGTGACTTCTCAGTCTTCTCTACTCATTCAACAAAGG  
AAATGTGGGCTGGGGCAGAGGTCTTTTTCATTTAATACTGGAAAAATTTGAAGAGCATCCATGTTCACTTATG  
GCTGGTTTTGCTATAGAAATTGGAAAATAAGGCCACTTTTTTG

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**FIGURE 50**

MGPVVPSLGLLEGAPTRMVAAAVLQASRNPASTGQGPRCRES PGLLVVSGGKTNSLGQGRPPT  
PRPLENGHGGRSLGPGPLDWVEMPDHQ RHPSTAPPTDLTSHLSRISLAGVEPSLVQAALGQLV  
RLSCSDDTAPESQAAWQKDGQPISSDRHRLQFDGSLIIHPLQAEDAGTYSCGSTRPGRDSQKI  
QLRIIGGDMAVLSEAELSRFPQPRDPAQDFGQAGAAGPLGAIPSSHQPANRLRLDQNPVV  
DASPGQRIRMT CRAEGFPPPAIEWQRDGPVSSPRHQLQPDGSLVISRVAVEDGGFYTCVAFN  
GQDRDQRWVQLRVLGELTISGLPPTVTVPEDTARLLCVVAGESVNIRWSRNLFPVQADGHRV  
HQSPDGTLLIYNLRARDEGSYMC SAYQGSQAVSRSTE VKVVS PAPT AQPRDPGRDCVDQPELA  
NCDLILQAQLCGNEYYS SFCCASCSRFQPHAQPIWQ

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Tyrosine kinase phosphorylation site.**

amino acids 392-400

**N-myristoylation sites.**amino acids 9-15, 50-56, 112-118, 146-152, 173-179, 195-201,  
220-226, 229-235, 280-286, 306-312, 336-342, 397-403**Myelin P0 protein.**

amino acids 153-182

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**FIGURE 51**

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCCGTATCTGC  
TCTCCTGAAATAATTCTGGAGTCAATGCCCTGAAATGCCAGAGGACATGGAGCAGGAGGAAGTTA  
ACATCCCTAATAGGAGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGGCAGAGCTGTACACA  
AAGAATTTTCAGCAGAATAATTGGCATGCAGTTGGCTGTGGTTTCAGAAGAGCAAGACCAAAAT  
TTGAACAGGTTAATCTGTTGGATTCTAATGCAGTTCATCACATCATTTCATGATTTTCAGCCCC  
ATGTTATAGTACATTGTGCAGCAGAGAGAAGACCAGATGTTGTAGAAAATCAGCCAGATGCTG  
CCTCTCAACTTAATGTGGATGCTTCTGGGAATTTAGCAAAGGAAGCAGCTGCTGTTGGAGCAT  
TTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTACAGAGAGGAAG  
ACATACCAGCTCCCCTAAATTTGTATGGCAAACAAAATTAGATGGAGAAAAGGCTGTCTCTGG  
AGAACAATCTAGGAGCTGCTGTTTTGAGGATTCCTATTCTGTATGGGGAAGTTGAAAAGCTCG  
AAGAAAGTGCTGTGACTGTTATGTTTGATAAAGTGCAGTTCAGCAACAAGTCAGCAAACATGG  
ATCACTGGCAGCAGAGGTTCCCCACACATGTCAAAGATGTGGCCACTGTGTGCCGGCAGCTAG  
CAGAGAAGAGAATGCTGGATCCATCAATTAAGGGAACCTTTCAGTGGTCTGGCAATGAACAGA  
TGACTAAGTATGAAATGGCATGTGCAATTGCAGATGCCTTCAACCTCCCCAGCAGTCACTTAA  
GACCTATTACTGACAGCCCTGTCTAGGAGCACAAACGTCCGAGAAATGCTCAGCTTGACTGCT  
CCAAATTGGAGACCTTGGGCATTGGCCAACGAACACCATTTTGAATTGGAATCAAAGAATCAC  
TTTGGCCTTTCTCATTGACAAGAGATGGAGACAAACGGTCTTTCATTAGTTTATTGTGTTG  
GGTCTTTTTTTTTTTTTTAAATGAAAAGTATAGTATGTGGCACTTTTTTAAAGAACAAAGGAAATA  
GTTTTGTATGAGTACTTTAATTGTGACTCTTAGGATCTTTCAGGTAAATGATGCTCTTGCACT  
AGTGAAATTGTCTAAAGAACTAAAGGGCAGTCATGCCCTGTTTGCAGTAATTTTTCTTTTTTA  
TCATTTTGTGTGCTGGCTAAACTTGGAGTTTGTAGTATAGTAAATTATGATCCTTAAATATT  
TGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTTCAGATGAAATTGTTTCATTCTCGTAAC  
CTCCATATTTTCAGGATTTTTGAAGCTGTTGACCTTTTCATGTTGATTATTTTAAATTGTGTG  
AAATAGTATAAAAATCATTGGTGTTCAATTATTTGCTTTGCCTGAGCTCAGATCAAATGTTTG  
AAGAAAGGAACCTTTATTTTTGCAAGTTACGTACAGTTTTTATGCTTGAGATATTTCAACATGT  
TATGTATATTGGAACCTTCTACAGCTTGATGCCTCCTGCTTTTATAGCAGTTTATGGGGAGCAC  
TTGAAAGAGCGTGTGTACATGTATTTTTTTCTAGGCAAACATTGAATGCAAACGTGTATTTT  
TTTAATATAAATATATAACTGTCCTTTTCATCCCATGTTGCCGCTAAGTGATATTTTCATATGT  
GTGGTTATACTCATAATAATGGGCCTTGTAAGTCTTTTCACCATTTCATGAATAATAATAAATA  
TGTAAGTGTGGCATGTAATGCTTAGTTTTCTTGATTTTACTTCTTTTTTTAAATGTAAGGACC  
AAACTTCTAACTAATTGTTCTTTTGTTGCTTTAATTTTTTAAATTAACATTCTTCTGATGTA  
ACATGTGATACATACAAAAGAATATAGTTTAATATGTATTGAAATAAAACACAATAAAATT



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**FIGURE 52**

MPEMPEDMEQEEVNI PNRRVLVTGATG LLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLD  
SNAVHHIIHDFQPHVIVHCAAERRPDVVENQPD AASQLNVDASGNLAKEAAAVGAFLIYISSD  
YVFDGTNPPYREEDI PAPLNLYGKTKLDGEKAVLENNLGAAVLRIPILYGEVEKLEESAVTVM  
FDKVQFSNKSANMDHWQQRFP THVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKYEMAC  
AIADAFNLPSSHLRPITD SPVLGAQRPRNAQLDCSKLET LGIGQRTPF RIGIKESLWPFLIDK  
RWRQTVFH

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 105-127.

**N-glycosylation site.**

amino acids 197-201

**N-myristoylation site.**

amino acids 303-309

**Short-chain dehydrogenases/reductases family proteins.**

amino acids 18-30

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**FIGURE 53**

TGGGCTCCCTCCAGCACTGCTGTTGCCTGCTGCCTAAGATGGGTGACACTTGGGCCAGCTTCCCTGGCCTGGGC  
CACCCACCCAGCAATGCTGCTGATCTCCCTCCTCTTGGCAGCCGGGTTGATGCACTCGGATGCCGGCACCAGCT  
GCCCGTCCCTTTGCACATGCCGTAACCAGGTGGTGGATTGTAGCAGCCAGCGGCTATTCTCGTGCCCCAGACC  
TGCCAATGGACACCCGAAACCTCAGCCTGGCCCAACCCGATCACAGCAGTGCCGCTGGCTACCTCACATGCT  
ACATGGAGCTCCAGTGCTGGATTGCAACAACCTCCTTAATGGAGCTGCCCCGGGCTCTTCTCCATGCCA  
AGCGCTTGGCACACTTGGACCTGAGCTACAACAATTTAGCCATGTGCCAGCCGACATGTCCAGGAGGCCATG  
GGCTAGTCCACATCGACCTGAGCCACAACCCCTGGCTGCGGAGGGTGATCCCCAGGCTTTTCAAGGCTCATGC  
AGCTCCGAGACCTGGACCTCAGTTATGGGGGCTGGCCTTCTCAGCCTGGAGGCTCTTGAAGTGGCTGCGAA  
TGGTGACCCTGCAGATCGGTGGCAATCCCTGGGTGTGTGGCTGCACCATGGAACCCCTGCTGAAGTGGCTGCGAA  
ACCGGATCCAGGCTGTACAGCAGATTCTCAGCTGGCTGAGTGCCGGGGCCCTCCTGAAGTGGGCGCCCCG  
TCTTCTCACTCACTGAGGAGAGCTTCAAGGCTGCCACCTGACCCTGACCCTGGATGATTACCTATTCTGCGT  
TCGTGGGCTTCGTGGTCTCCATTGCTTCTGTGGCCACCAACTTCTCCTGGGCATCACTGCCAAGTGTGCCACC  
GCTGGAGCAAGGCCAGTGAAGAGGAAGAGATCGACATGCCTGCCTCTCATCCCTCCATGCTGCTGACCGCCACA  
GCTGCTGGCCACCAGACGCCCTCCCTGATTGCTCACTCTGGTCCATGGTGACCTGGCTGCCTCAGTCATGGTTC  
AAGCAAGGTGGGACACTCATTGTATGAGCATCTGCTTTGGGCCAGGCGGCACGCTAGGAATTGGGAACATCA  
GATGAAGTCACTCAGTCCCTGCCCTCAAGGCACTTCCCTCTGGTCAAGGAGAGAGATCCAAAACTATTCCCTTT  
AAGACTATATGTCAAGACTCTGAGCAGCTCATTATGGAGGCCAGAGGAGGAGCCATCATCTGTATCTAGCAATG  
TCCATGAGAATTATAAGATTAGAGTGATTGTGAAGTGGGTGATCAGGAAATATCTACTTTGTGAGGTAGGCAAA  
GAAGGTGTCTGCACATGGCAGAGGCCAGAATATGCATAGTGTGCTGTGTGAGAAGAGTGAACAGTTCCTGGTC  
ACTTACTTGTATAGAGGGGTGTGGCACAGAAGTCAACCTACCCCTCACCTCTGACACCAAACTGTCAAGTC  
TCAGCAATGCCAGCACTGCCTACAGGAGTAAGAACACCTCTATGACAGCCCTGGCCTCCTTCCACAGCAGC  
TACCAGGTGAGACCACCTCCAGTGACTGCCCCATATGACCAAAATGTACCAAGTTGGTGAGGTCCAGGCAGCA  
GGCTGAGGATGGACACTTTCATGCCCTTGCTCCTGCTCACTCAAGTTTGTCTCAGAGAGAGAGGCAGGA  
GGCCAGCAACTGGGCGAGCAAGAGTCTGGCACCTTGGGATCCTAATCATGTGACTGTTCTGCCACAGTGCTC  
ATGCCACAGGCTCTACCCAGGAAAGTGACTGTGGGCCACAGACCCACAGCCTGGCAGCACCAGAGCTAAAAGG  
GGCAAAAGGCAGCAGTATGACCATATGAGGCTTGCATTTTCTTCTAAGCAACTTACCCAGCTTAAGCATGA  
GGTGAGAGAGCTATTAAATACTAAGCCCTTGGCAGTGTGAGTACTTTGAAAAGCTCTCTGCACAAACCATTC  
CTTTGACACACACACACAAATCTTTGAGGTGAACCTTGTGTTTCCATTTTACGGATGAGGCAACTAAGGCT  
CAGAGAGGTTAAAGTCACATGCCACTATGAGCAAGATAAAGTCTGTGCTCTTTCTACTGCCCCATCAAGTTGGG  
GAACATCACCATTCCCTCTAGAGTTATATAAATCAAAATCAACTAGAGCTGACAAAGTTCCCTATAAGGTCCAG  
GCACTCCTCTGGGCACTTTTATATCTATTGACTCACTTCTTTCAATTCTCACAGCAACACTGCCTGGTGGTTTTT  
ATTATCCCATTTGACAGATGAATTAATCGTAGAGAGTTGAGTGACTTACCAAGGTTGTCTGGATAAGCCCTAG  
AAGGAAGGCGGTAGGCAGCTCCATTGAGGAAAGTGCATCTAATCAGTCAGTCAAAAAATCAAGTAACCTTACGAG  
CAAAGCACAATTATCATCATCGTGGTCTTCTTCATCAGTTTCGTGAGCAGCATCATTATCTTCCCTATTGTT  
CAGCACCGGATAGTTTATGATATTTTGCATCATTCTCCTGACTTTTACATCCCTGTGAGGAGGTAATCA  
AACATCAGTAATCCTGTTTTACAGATGGGGAAGAGTCTCAAGGTTGGATATGACTTGCTATGTGGCAAGGTTG  
GGGCTCAACCCTAACACAGTTCTCTTTCCAGTGCTTCTCAAGTGCTTGGGGAAGAGAATGCCTCAGAAGGCTGG  
GTAGTGGGCGCTGGAATTCAGCATCCATGAATGCTAGTGGATAAGCTAAATAGAAGGCAGCCAAACCATCT  
GCTGTACAGATTGAAGTATGCTCAGGCTAGGCAAAATGCAAGGCTCTGAAACAGAGACTACACAGGTAACACCTG  
AATAGGAGACTCCTGCTTTACAATGTGTAGATAAAACATCAGCAATGGTGGCCATGGTGGCAGTCATGTGAAAAG  
TAAGATCTTTGGGAATCAAGAAAGGAAGCTGTGTTAACCCTCCTGCTCAAGCCCTGCTGCGTGTGTGCAAGAG  
ATACTAAGAGAGCAAGAAAGCTATAGGTGAGAACCTCTGCAGTTTAGGAGAAGAACATCAAGGCACAGTCCAACA  
TGCTGATAAGTCTGGCCAGGAGGAGAATTAACACAGGGGCTTTCCACACCTCCCTTGGCCCAAGCTCCAGCGGTA  
TTCTATCAGCCCATCCTCCTGGAAAGCTGAAAGGAATGAAGGAGGCTAATAAGTCATCTTCCAGGAAGGCATCC  
CTCACTCGTGCTTCCCTGAGCTAGTCAACCAAAAGAGTCTTCAAGAACTTGTAGACCTGAAGTACTTGAACCT  
GTGTCCCTGAATCTTTTACAACATCTGGGACAAATCCCTGGTCTGTGACATCCGAAGCAGAACTGTGCCCT  
GCTCTCTCCTTCTGTGATGACCAAGGATGGTGAACCTCAAGTTGTTCTCTACAAGCCAGGCCAGCAACCTAAATAC  
TTGGAGAGGAACCTTTAGAACTATAATCCTGACAAATAGAAAAGTTTCCCATAGGGGCATACCATAATACTAT  
AATAACCTCCAGGAACCTATTGTTTGGCAAAATGTAGTTAATATATTTAAGATATATGCTTTTGTGATAGGAC  
TAGAACCAGAAAAGACCAAAATGCCCTTGGACATCAATGTCTTTCTAGTGGGACAATTTGGTCTCCATTAAAT  
GCCAAACCTTTCTGAACAGGATACATGGCTTTTAAAGGACAGATGTTTCTCCTGCTGCTAGAGTTTCTCAGTTT  
ACTAGAGCACAATGAGGAAAGTATTCAACCTCCCTACTGCCAAGGAATCCCTGCTTCTCCCCACCGCCATCAT  
CTGTCCAAGCTATCAGAAGCAACCTTCTAGAGATAATCAACAATCCTGATTAGAATTGCTCCCATATCCCTGG  
TGACCACAGGCTTCAATCAAATTGTCAAACCTGGTTAAACATGTATGTGATGGGGTATCTCTGCATCTGTATGCT  
GTCTGCGAGGTTCTTGTATATTGGCTGTCCGCTGACTTGGGACAGATCTCTCTAGAACTTGGGTTTCACTTCT  
GACATAGTCCACTCAGGCTAGGCTGAGTGGCTAAATATGCATAAATAAGCATGCCTAAATAGGCATATATAGGT  
TGGTGCAAAAGTAATTGCGGTTTTTGGCATTAAAAATGATGGCAAAAAATCCCAATTACTTTTGGCTCAATCTAAT  
ATTACATTGCTGTATAGATTAAAGATGGAATCCACAGGTTTAGGGTAGGACTGGATGCTCAAAAAA

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**FIGURE 54**

MLLISLLLAAGLMHSDAGTSCPVLCTCRNQVVDCCSSQRLFSVPPDLPM DTRNLSLAHN RITAV  
PPGYLTCYME LQVLDLHNNSLMELPRGLFLHAKRLAHL DLSYNNF SHVPADM FQEAHGLVHID  
LSHNPWLRRVHPQAFQGLMQLRDL DLSYGGLAFLSLEALEGLPGLVTLQIGGNPWVCGCTMEP  
LLKWLNRNRIQRCTADSQ LAECRGPPEVEGAPL FSLTEESFKACHLT LTLD DYLFI AEFVGFVVS  
IASVATN FLLGITANCCHRW SKASEEEEEI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation sites.**

amino acids 52-55, 81-84, 107-110

**Tyrosine kinase phosphorylation site.**

amino acids 148-154

**N-myristoylation sites.**

amino acids 11-15, 263-268

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 175-185

**Leucine zipper pattern.**

amino acids 77-98

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**FIGURE 55**

GGCTGCGCCCAGGCCGGCGGGCCCCAGCAGCTGCGAACCGCCGGCGCACACCTGTTTCCGCGC  
CCGGGGACTTCCCCGGCGGGGCTCAGAAGTGTGGGGTCGGTCGCTTGGCTTCCCCTGGCGTCA  
GCGACCCAGGGTAACCTCCTCCACTGCTGCGTGCCGTGCAGGCCTGCCTGTGTGAGAGCCACG  
TGTGCCGCGCTCTGGGCACAGCCTTGGAAGTCAAGACCGCGACGGCAGCAGAGCAGAAACCT  
TACAGAAACATGAAGCCCTCAACCATCTGCTACTCAGTTATTCGGGGCTGACGGCGGCTTCTA  
GAACATCCAGGTGTTCTGCAGATGCGAGAACTCATCTGTAGTCACCAGATGGAGTCCCAAAC  
AGCCAAGCAGATGTAAGGCCTGTGCTGTGGCTCTGAGGCCCTGAATACAGAAGGGTCACCTTC  
TTAGTGGCCAAAGAGCAGTTGTTGACATTGATGTCTAATTATTGAACACGACCAGTCATTTTA  
CTGAGCTGCAGTGAGGAAACACTGACCATAGAAGATCAAGCCAAATGAGGGATTGCAAATTTCT  
CTGATTCTTTTGAATTAGGATTCCAGATGGGGGCTCATTCTACAGCCCCCAACATTCCTAT  
AGCCGTTATCACTGCCATCACCCTGCCACCAGCATCTTCTTGCAGATTCCACCCCTGCTCCC  
CAGAGACTTCCTGCTTTGAAAGTGAGCAGAAAGGAAGCTCTCAGAAAAATCTCTAGTGGTGGC  
TGCCGTCGCTCCAGACAATCGGAATCCTGCCTTCACCACCATGGGCTGGCTTTTTCTAAAGGT  
TTTGTGTTGGCGGGAGTGAGTTTCTCAGGATTTCTTTATCCTCTTGTGGATTTTTGCATCAGTGG  
GAAAACAAGAGGACAGAAGCCAAACTTTGTGATTATTTTGGCCGATGACATGGGGTGGGGTGA  
CCTGGGAGCAAACCTGGGCAGAAACAAAGGACACTGCCAACCTTGATAAGATGGCTTCGGAGGG  
AATGAGGTTTGTGGATTTCCATGCAGCTGCCTCCACCTGCTCACCCTCCCGGGCTTCCTTGCT  
CACCGGCCGGCTTGGCCTTCGCAATGGAGTCACACGCAACTTTGCAGTCACTTCTGTGGGAGG  
CCTTCCGCTCAACGAGACCACCTTGGCAGAGGTGCTGCAGCAGGCGGGTTACGTCACTGGGAT  
AATAGGCAAATGGCATCTTGGACACCACGGCTCTTATCACCCCAACTTCCGTGGTTTTGATTA  
CTACTTTGGAATCCCATATAGCCATGATATGGGCTGTACTGATACTCCAGGCTACAACCACCC  
TCCTTGTCCAGCGTGTCCACAGGGTGATGGACCATCAAGGAACCTTCAAAGAGACTGTTACAC  
TGACGTGGCCCTCCCTCTTTATGAAAACCTCAACATTGTGGAGCAGCCGGTGAACCTGAGCAG  
CCTTGCCCAAGATATGCTGAGAAAGCAACCCAGTTCATCCAGCGTGCAAGCACCAGCGGGAG  
GCCCTTCTGCTCTATGTGGCTCTGGCCACATGCACGTGCCCTTACCTGTGACTCAGCTACC  
AGCAGCGCCACGGGGCAGAAGCCTGTATGGTGCAGGGCTCTGGGAGATGGACAGTCTGGTGGG  
CCAGATCAAGGACAAAGTTGACCACACAGTGAAGGAAAACACATTCTCTGGTTTTACAGGAGA  
CAATGGCCCGTGGGCTCAGAAGTGTGAGCTAGCGGGCAGTGTGGGTCCCTTCACTGGATTTTG  
GCAAACCTCGTCAAGGGGGGAAGTCCAGCCAAGCAGACGACCTGGGAAGGAGGGCACCGGGTCCC  
AGCACTGGCTTACTGGCCTGGCAGAGTTCCAGTTAATGTCACCAGCACTGCCTTGTTAAGCGT  
GCTGGACATTTTTCCAACCTGTGGTAGCCCTGGCCAGGCCAGCTTACCTCAAGGACGGCGCTT  
TGATGGTGTGGACGTCTCCGAGGTGCTCTTTGGCCGGTCACAGCCTGGGCACAGGGTGCTGTT  
CCACCCCAACAGCGGGGCAGCTGGAGAGTTTGGAGCCCTGCAGACTGTCCGCCTGGAGCGTTA  
CAAGGCCTTCTACATTACCGGTGGAGCCAGGGCGTGTGATGGGAGCATGGTGCCTGAGCTGCA  
GCATAAGTTTTCTCTGATTTTTCAACCTGGAAGACGATACCGCAGAAGCTGTGCCCTAGAAAG  
AGGTGGTGCAGGAGTACCAGGCTGTGCTGCCCCAGGTCAGAAAGGTTCTTGACAGACGTCTCCA  
AGACATTGCCAACGACAACATCTCCAGCGCAGATTACACTCAGGACCCTTCAGTAACCTCCCTG  
CTGTAATCCCTACCAAATTGCCTGCCGCTGTCAAGCCGCATTAACAGACCAATTTTTATTCCAC  
GAGGAGGAGTACCTGGAAATTAGGCAAGTTTGTCTCCAAATTTTCAATTTTACCCTCTTTACAA  
ACACACGCTTTAGTTTAGTCTTGGAGTTTAGTTTTGGAGTTAGCCTTGCAATATCCCTTCTGTA  
TCCTGTCCCCCTCCACGCCGACCCGAGAGCAGCTGAGCTGCGCTGGCTCTGGGCAGGGAGTG  
TGCTTAAATGGGAAGCACACGGGCTTGGAGTCAGGCACAGGTGCCAGCTCCAGCTTTTGAAC  
TTGGGCAATTGTTTAACTAACCTGCAAGTTGATTTTGGGGTTAAATAAAGGCATACATGAA  
AATGCCTGGCAACTTTAAAAA

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**FIGURE 56**

MGWLFLKVLLAGVSFSGFLYPLVDFCISGKTRGQKPNFVIILADDMGWGDLGANWAETKDTAN  
LDKMASEGMREVDHFHAAASTCSPSRASLLTGRLGLRNGVTRNFAVTSVGGLPLNETTLAEVLQ  
QAGYVTGIIGKWLGHGSHYHPNFRGFDYYFGIPYSHDMGCTDTPGYNHPPCPACPQGDGPSR  
NLQRDCYTDVALPLYENLNIVEQPVNLSLAQKYAEKATQFIQRASTSGRPFLLYVALAHMHV  
PLPVTQLPAAPRGRSLYGAGLWEMDSL VGQIKDKVDHTVKENTFLWFTGDNGPWAQKCELAGS  
VGPFTGEFWQTRQGGSPAKQTTWEGGHRVPALAYWPGRVPVNVSTALLSVLDIFPTVVALAQA  
SLPQGRRFDDGVDVSEVLFGRSQPGHRVLFHPNSGAAGEFGALQTVRLERYKAFYITGGARACD  
GSMVPELQHKFPLIFNLEDDTAEAVPLERGGAEYQAVLPEVRKVLADVLQDIANDNISSADYT  
QDPSVTPCCNPYQIACRCQAA

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 353-373

**N-glycosylation sites.**

amino acids 117-120, 215-218, 356-359, 397-500

**N-myristoylation sites.**

amino acids 12-17, 33-38, 52-57, 97-102, 101-106, 113-118, 158-163, 328-333, 388-393, 418-423, 435-440, 436-441

**Amidation site.**

amino acids 382-385

**Sulfatases signature 2.**

amino acids 129-138

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**FIGURE 57**

TGGACAAGACACCTCCAGGAGCCCAGCTCACAGCCACCGGTACCTTCTTCCAGGACAAGCTGG  
GGGCTCCATGGGCGCCTGAGGGCCAGGCGCCAGGGCCGTGGGCACGAGT**AT**GGTGAGACACC  
AGCCCCCTGCAGTACTACGAGCCACAGCTGTGCCTCTCCTGCCTCACGGGCATCTACGGCTGCC  
GTTGGAAGCGCTACCAGCGCTCCCATGATGATACCACACCGGGCACAGCGCCATTCTGCATG  
TGGGGGCTGTGGCAGCAGTCACCATGCTCTCCTGGATCGTGGCAGGACAGTTCCGCGCTGCAG  
AGCGGACCTCCTCCCAGGTGACCATTCTCTGTACCTTCTTCACCGTGGTGTTTGCCCTCTACC  
TGGCCCCCTCTACCATCTCCTCTCCCTGCATCATGGAGAAGAAAGACCTCGGCCCCAAGCCTG  
CTCTCATTGGCCACCGCGGGGCCCCATGCTGGCTCCAGAGCACACGCTCATGTCCTTCCGGA  
AGGCCCTCGAGCAGAAGCTGTACGGGCTCCAGGCTGACATTACCATCAGCCTGGACGGCGTGC  
CCTTCCTCATGCATGACACCACCCTGCGGCGCACCACCAACGTGGAGGAGGAGTTCCCGGAGC  
TGGCCCGCAGGCCTGCCTCCATGCTTAACCTGGACCACCCTGCAGAGACTCAACGCTGGCCAGT  
GGTTCCTGAAGACTGACCCCTTCTGGACAGCCAGCTCCCTGTCACCCTCGGACCACAGAGAGG  
CCCAGAACCAGTCCATCTGCAGCCTGGCAGAGCTCCTGGAGCTGGCCAAGGGCAATGCCACAC  
TGCTGCTCAACCTGCGTGACCCGCCCCGGGAGCACCCCTACCGCAGCAGTTTTATCAACGTGA  
CTCTGGAGGCCGTGCTGCACTCCGGCTTCCCCCAGCACCAAGGTATGTGGCTGCCTAGCAGGC  
AGAGGCCCCCTGGTGCGGAAGGTGGCTCCCGGCTTCCAACAGACATCAGGCTCCAAGGAGGCAG  
TCGCCAGCCTGCGGAGAGGCCACATCCAGCGGCTGAACCTGCGCTACACTCAGGTGTCCCGCC  
AGGAGCTCAGGGACTACGCGTCCCTGGAACCTGAGTGTGAACCTCTACACAGTCAACGCACCGT  
GGCTCTTCTCCCTGCTGTGGTGTGCGGGGTCCCATCCGTACCTCTGACAACCTCCACACCC  
TGTCCCAGGTGCCTTCCCCCTCTGGATCATGCCCCCGGACGAGTACTGTCTATGTGGGTCA  
CTGCCGACCTGGTCTCCTTACCCTCATCGTGGGCATCTTCGTGCTCCAGAAGTGCGCCTGG  
GTGGCATAACGAGCTACAACCCTGAGCAGATCATGCTGAGTGTGCTGCGGTGCGCCGGACCAGCC  
GGGACGTCAGCATCATGAAGGAGAAGCTTATTTTCTCAGAGATCAGCGATGGTGTAGAGGTCT  
CCGATGTGCTCTCCGTATGTTTACAGACAACAGTTATGACACATATGCCAACAGCACCGCCACCC  
CTGTGGGCCCCCGAGGGGGTGGCAGCCACACCAAGACCCTCATAGAGCGGAGTGGGCGT**TAGC**  
TGAAGACATGTCTGTCCACCTGTACCTGACACAGAAGCTGGGGAGCCTAGGAGAGCTGGTGG  
AAGTGTGTCTGAACTCGGAGTGTCTGGGAGCGGGCTCCACAGCCTCCTTGTGGGCTCCAGCC  
CCTTGTGTCAGCCGACGCTCTCTGAGGGGGACTCCCTGTCTCCTGAGGCCCAGCTGGGCCAGG  
ACTCCATCCTTTTACAGATGCCCCCTGCAGGCCTGGGGCTCCTTCTGGGAAGTATGGGGCCTAGGG  
CTTGGTCCCCCTCTTCTGAGGGCCCTCTCCTGTATCCCCGACCTGGAAGCTTTGATGGGTATGG  
GCCATGCCATACCCCCTGTGGCAATGGAGTGTGTGGATGCTCACCTGTGCCATCTGTCTCCT  
GTCTGTGCCAGGAGGCACCTGAGTTCTCTGCTGTTATCCTGCCCCAAGGGCCTGGGCGGAGCC  
TCTACCTGAAGCAACTCTGCTCTTCTGTCTCAGTCTCAAAGCACAAAGGAGGTTACAGCCAGGAG  
GAAGCCAGCTGCAATGTGGAGACACGTCTCCTCCCCAACCCACCTCATGCCACCGCCAACCC  
CCTGCCCCAGGAGCGGGCCTGAGCCACGTCCCCTAGGAGCAGCTGGAGATGGCCAAAAGAGTG  
AGCTCAGGACTACTGGATCCCATGCCCAGGTGTCCAGCAGACCTCAAGGCAGAAGGGTCACTT  
AACCAGGAGTCCACAGACTGATGTGACCTCAGGTTCACACATCAGTGGCCACAGGGCAGGGC  
CCACCTGGTAGAAGTGTTCTGGATATGGCCAGGGTGGGTGTGTGGCTAAGTGGGCCTGAACAG  
AGGGAACCTAGGGCCCTTGCCAATGTGATTAAAGCTGCCATCTTGAAA

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**FIGURE 58**

MVRHQPLQYYEPQLCLSLTGIYGCRWKRYQRSHDDTTPGTAPFLHVGAVAAVTMLSWIVAGQ  
FARAERTSSQVTILCTFFTTFVVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGAPMLAPEHTL  
MSFRKALEQKLYGLQADITISLDGVPFLMHD TTLRRTTNVEEEFPELARRPASMLNWTTLQRL  
NAGQWFLKTDFFWTASSLSPSDHREAQNQSICSLAEELLELAKGNATLLLNLDRDPPREHPYRSS  
FINVTLEAVLHSGFPQHQMVLPSRQRPLVRKVAPGFQQTSGSKEAVASLRRGHIQRLNLRYT  
QVSRQELRDYASWNLSVNLYTVNAPWLF SLLWCAGVPSVTS DNSHTLSQVPSPLWIMPPDEYC  
LMWVTADLVSETLIVGIFVLQKWRLGGIRSYNPEQIMLSAAVRRTSRDVSIMKEKLIFSEISD  
GVEVSDVLSVCSDNSYDTYANSTATPVGPRGGGSHTKTLIERSGR

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 47-61, 77-93, 335-350, 380-399

**N-glycosylation sites.**

amino acids 182-186, 217-221, 233-237, 255-259, 329-333, 462-466

**Tyrosine kinase phosphorylation site.**

amino acids 130-139

**N-myristoylation sites.**

amino acids 21-27, 48-54, 294-300, 404-410, 442-448, 473-479

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**FIGURE 59**

CCTGAGCAAACACAGCAGCCCCGAGTGTTCCCAAGGCCAAAATGCTGAGAACGTCCACTCCTAA  
TCTGTGTGGTGGTCTGCATTGCCGGGCCCCCTGGCTCTCTTCTGGCATTCTCTGCCTCTGCCT  
CATATTCTTGTAGGCCAGGTGGGCTTGCTGCAGGGACACCCCCAGTGCCTGGATTACGGGCC  
CCCTTTCCAGCCCCCTCTGCACCTTGAGTTTGTCTCTGACTATGAGTCCTTCGGCTGCTGTGA  
TCAGCACAAGGACCGCCGCATCGCTGCCCGGTACTGGGACATCATGGAATATTTTGATCTGAA  
GAGACATGAGCTGTGTGGAGATTACATTAAAGACATCCTTTGCCAGGAGTGCTCGCCCTACGC  
AGCCACCTCTACGACGCCGAAAACACCCAGACGCCTCTCCGGAATCTCCCGGGCCTCTGCTC  
TGATTACTGCTCTGCCTTCCATTCTAACTGTCACTCAGCCATTTCCCTGCTGACCAATGACCG  
CGGCCTCCAGGAGTCTCATGGAAGGGACGGTACCCGCTTCTGCCACCTCCTGGACCTTCCTGA  
CAAGGACTATTGCTTCCCTAATGTCTGAGGAACGACTATCTCAACCGCCACCTGGGCATGGT  
GGCCCAAGATCCTCAGGGCTGCCTGCAGCTCTGCCTGAGCGAGGTGGCCAACGGGCTGAGGAA  
CCCCGTCTCCATGGTCCATGTGGGGACGGCACCCATCGCTTCTTTGTTGCCGAGCAGGTAGG  
AGTGGTGTGGGTCTACCTCCCTGATGGGAGTCGCCTGGAGCAACCCTTCCTGGACCTCAAGAA  
CATCGTGTTGACCACCCCATGGATCGGGGATGAGAGAGGCTTCTTGGGGTTGGCTTTTCACCC  
CAAATTCGGCCACAATCGCAAGTTCTATATTTATTCGTGCCTGGACAAGAAGAAGGTAGA  
AAAGATCCGAATTAGTGAGATGAAGGTTTCTCGGGCTGATCCTAACAAGCTGACCTGAAATC  
AGAGAGGGTCATCTTGAGATTGAAGAACCAGCCTCAAACCATAATGGCGGACAACCTTCTTTT  
TGGCCTGGATGGCTATATGTACATATTCAGTGGGGACGGGGACAGGCTGGAGATCCCTTTGG  
CCTGTTTGGAAATGCTCAGAACAAAAGTTCCCTGCTGGGAAAAGTTTTAAGGATCGATGTGAA  
CAGGGCAGGCTCACATGGCAAGCGGTACCGAGTCCCTCGGACAATCCATTTGTTTCTGAGCC  
AGGGGCCCCACCCCGCCATCTATGCCTATGGGATCAGGAACATGTGGCGTTGTGCTGTGGACCG  
AGGGGACCCCATCACGCGCCAGGGCCGAGGCCGATATTCTGTGGGGACGTGGGCCAGAACAG  
GTTTGAAGAGGTTGACCTCATTTTGAAGGTGGAACTATGGCTGGAGAGCAAAGGAAGGGTT  
TGCTATGTTATGACAAAAAAGTTTGTCAATGCCTCTTTGGATGATGTTCTGCCAATCTATGC  
TTATGGCCATGCAGTGGGGAAGTCAGTCACTGGAGGTTATGTCTATCGTGGTTGTGAATCCCC  
AAATCTCAATGGCCTGTATATCTTTGGAGACTTCATGAGTGGTCGACTTATGGCTTTGCAGGA  
AGATAGAAAAAACAAGAAATGGAAGAAGCAGGATCTTTGCCTGGGCAGCACCACGTCTGTGC  
CTTCCCAGGGCTGATCAGCACCCATAGCAAGTTCATCATCTCCTTTGCTGAAGATGAAGCAGG  
GGAGCTGTATTTTCTGGCGACCTCTTACCCAAGTGCCATGCACCACGTGGATCTATTTACAA  
GTTTGTGACCCCTCAAGGCGAGCACCCCAAGTGCAAATACAAGCCAGTGCCCGTGAG  
AACCAAGAGTAAGCGGATCCCGTTTCAGACCACTCGCCAAGACAGTCTTGGACTTGCTAAAGGA  
ACAATCAGAGAAAGCTGCTAGAAAATCTTCCAGTGCAACCTTAGCTTCTGGCCCAGCCCAGGG  
TTTGTCTGAGAAAGGCTCCTCCAAGAAGCTGGCTTCTCCTACAAGCAGCAAGAATACATTGCG  
AGGGCCTGGTACAAAGAAGAAAGCCAGAGTGGGGCCCCACGTCCGCCAGGGCAAGAGGAGGAA  
GAGCCTGAAAAGCCACAGTGGCAGGATGAGGCCATCAGCAGAGCAGAAGCGAGCTGGCAGAAG  
TCTCCCTTGAACCTATTGGTCAAGGTGGCCGACAGGGTGACGTGAGAGAGGAGAGCCACCTCAT  
CAAATGAAAGTCACTGCTGAATAAAGACCTTAGAAGTCTGGGAAGCCAGGGTAGAGGTGGGGC  
AGGGCGGTTTTCTCTCCCTGGGAAATCTTGCTGTCTACTGAATAAATAAATGCACCTTCTCT  
GTATGCAGTGCTTCTGTGGGAGACCATATCCCAGATTGCTGGTGCACCTGGGTTATGGTAAGC  
ACTAGTCCATGAGCCTGCTTGAATCACACTGGATGTCTCCGTTTTGTCTTGTAATGCCTAC  
AACCTGAGGTAATAAATCAACATTTGCTCA



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**FIGURE 60**

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGQVGLLQGHQPCLDYGPPFQPPLHLEFCSD  
YESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCDYIKDILCQECSPYAAHLYDAENTQTPL  
RNLPGLCSDYCSAFHSNCHSAISLLTNDRGLQESHGRDGTFRFCHLLDLPDKDYCFPNVLRNDY  
LNRHLGMVAQDPQGCLQLCLSEVANGLRNPVSMVHAGDGTHRFFVAEQVGVVVVYLPDGSRL  
QPFLDLKNIVLTTPWIGDERGFLGLAFHPKFRHNRFYIYYSCLDKKKVEKIRISEMKVSRAD  
PNKADLKSERVILEIEEPASNHNGGQLLFGLDGYMYIFTGDGGQAGDPFGLFGNAQNKSSLLG  
KVLRIDVNRAGSHGKRYRVPSDNPFVSEPGAHPAIYAYGIRNMWRCVDRGDPITRQGRGRIF  
CGDVGQNRFEEDLILKGGNYGWRAKEGFACYDKKLCHNASLDDVLPYAYGHAVGKSVTGGY  
VYRGCESPNLNGLYIFGDFMSGRLMALQEDRKNKKWKKQDLCLGSTTSCAFFGLISTHSEKFI  
SFAEDEAGELYFLATSYPSAYAPRGSYKFDVPSRRAPPGKCKYKVPVVRTKSKRIPFRPLAK  
TVLDLLKEQSEKAARKSSSATLASGPAQGLSEKGSSKKLASPTSSKNTLRGPGTKKKARVGPH  
VRQGKRRKSLKSHSGMRPSAEQKRAGRSLP

**Important features of the protein:****Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 17-36

**N-glycosylation sites.**

amino acids 372-376, 480-484

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 645-649, 699-703

**Tyrosine kinase phosphorylation site.**

amino acids 81-89

**N-myristoylation sites.**amino acids 11-17, 37-43, 156-162, 165-171, 357-363, 365-371,  
368-374, 408-414, 459-465, 548-554, 557-563**Amidation sites.**

amino acids 391-395, 696-700

**Cell attachment sequence.**

amino acids 428-431

**Leucine zipper pattern.**

amino acids 25-47

**FIGURE 61**

CTCCATTAAACCACCACCAGCTCCCCAAGCCACCCCTTCAGCCATGAAGTTCTCTGCTCCTGGT  
CTTGGCAGCCCTCGGATTCCTGACCCAGGTGATCCCAGCCAGTGACAGGTGGGTCAAAATGTGT  
GAGTAACACCCCAGGATACTGCAGGACATGTTGCCACTGGGGGGAGACAGCATTGTTTCATGTG  
CAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTTCCTGCCGAAGCCTGACCTACCACAGCT  
CATCGGTAACCACTGGCAATCAAGGAGAAGAAACACACAAAGGAAAGACAAGAAGCAACAAAC  
GACCGTAACATCATAATATAACCACTGCTATCGCCTCCACCAACTCAGAGAAATATCATTTCCAC  
AGTTCCAATTCCTCCTACATTGCTGAGTACTAGCCAAGGCTCCTCTTTATGGGGCAGATATCT  
ATAGCCAACCCCAAACTTCTGTCTTCTATCATTCTGTCAATTCATCTAGTAACTAATTTGGAG  
TTTGTATCTATCTTACGAGAACAATCATCATGCAGATTTCGTCCACAGGGGATCTGTCACTTTG  
GGTCTCCAAATGAAAAATGTCAAGACAGAATTGGACATGCAAAGATTGACTGGGAGAACAC  
ACCTCTGATGGACAAAGGTGAGACAGAGCAGCCACAGGCAGGGAGAGCCTTCAGACTGCAACG  
CTGGCCTGATACGTGTCAAAGGAGAGAGGGATAGAGGAGGATTGAATAGAAGGAGACTAAGAC  
TGCAGCTCTAAGAAAGTCTCAGCCAAACAGATGGGGAGGCCCAAAGCAAGGCTTGCCCCCTCAG  
AGGAGCTCACGCAGGGCAGGAATAGCCAGGTTCTCATATCCCAGGGGTTTCAGACTTGCGTGAG  
AACAGCCCCTGGAGAACATGGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCCACC  
AACTATCCCCTTGAAGCAAGTTCTCTTGAAAGGAAATCTAAACAGTGCACCCCATGGCTGCC  
ACGGAGTATAAGGAGGGAGAGAAAGGAGCTGAAAGTCTAGGTTTGGCCAGCTAGGTAGACTGA  
CTTGTGAGGTATTTATTTATTTATTTGAGTAACAAAGCAGACAGAATACATAGCCACCATTGG  
TAGTACACCCCAAAAGCAAGGATGGCATGATGCTGGTGACTCAAACGTGCCTACTCATGGTGT  
CAAATTGGCATAATCCTCTTGGAAGCTGTGTGGAATAAGCACAGAGAAGCAGAACTCTAAT  
TGCTTAATCCACTAAACATTACTTCTGGGAATTGGCTCATCATAAATTATCCAAGAGAAAGCA  
CAAAGTTATGGGCACAAAGGTTTTCCATATAATATTATTTAAAATGCTGAGAAAATGAAAAA  
TCTAAATGGTGAAATATATACTAATGCCATCTATAAATACAAACAAATAGAATGTTTATAGAA  
TAATGGAACATAATAACATTATTCAAAATTGCATTTATGCTATAGTTGTCAAAATTGTCTCCT  
TATATGATACAAACTCATGAAAATTATGACTTTTTTGTGGTTGGAAAGCAGAATTATGCA  
TAAATTTCTCTTACAGTTCGATGCCATTAGTTTTATATAACATTTATTTGACACGTACTGA  
CTTCTATCTGAGAAGAACAACCAAAACACTCAGGCCTAAATAATTAAAACGGTCCTAAAAA  
CTAGCAAACCAGATAAGAAAAGATGTTAATGCCCATTCCTTAACCTATGTCTTAGACCAAAAT  
TAATTCTAGATGGTTTTTAAAATGACAGTGTAAGTAAAGTATTAAAAGATTGTGTGGTCAAA  
TATTCAATTTAAGAGCAAGGAAATTCCTATAAATATAACAATAGAGGCAGAACTCATGTAAGA  
ATAAATTGATTAGGTGGTATTAAATATTAAGTTCCTATGTATGTCAAAGATATCATTTTGAA  
ATTCATCCATCTTATTGGGTATTGCAGGAGTTCATTCCTTTTTGTATAAATACTCTTCCGT  
CATATGAATAGTATTCATTTGTATACTGGTTTTGTGATGGACATTGGGTTGTTCCCAGTTTA  
TGGCTATTACAAATAAAGCTTCTATGAACATTTATGTACA

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## **FIGURE 62**

MKPELLLVLAALGFLTQVIPASAGGSKCVSNTPGYCRTCCHWGETALFMCNASRKCCISYSFLP  
KPDLPQLIGNHWQSRRRNTQRKDKKQQTTVTS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 1-22

**N-glycosylation site.**

amino acids 50-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 79-82

**N-myristoylation site.**

amino acids 23-28

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**FIGURE 63**

GCGGAGCGCCTGGGAGAGGAGAAGGAGCCGACCTGCCGAGATGGAGGGCGACCGGCACCTGGGC  
GCTGCTGCTGGCGCTGGCGCTGCTCCTGCTGCTGACGCTGGCGCTGTCCGGGACCAGGGCCCCG  
AGGCCACCTGCCCCCGGGCCACGCCGCTACCACTGCTGGGAAACCTCCTGCAGCTACGGCC  
CGGGGCGCTGTATTCAGGGCTCATGCGGCTGAGTAAGAAGTACGGACCGGTGTTACCATCTA  
CCTGGGACCCTGGCGGCTGTGGTGGTCTGGTTGGGCAGGAGGCTGTGCGGGAGGCCCTGGG  
AGGTCAGGCTGAGGAGTTCAGCGGCCGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGG  
CCATGGGGTTTTCTTCTCCAACGGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCATGCTTGC  
TCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGAGCTGATCCAGGCGGAGGCCCGGTG  
TCTGGTGGAGACATTCCAGGGGACAGAAGGACGCCCATTCGATCCCTCCCTGCTGCTGGCCCA  
GGCCACCTCCAACGTAGTCTGCTCCCTCCTCTTTGGCCTCCGCTTCTCCTATGAGGATAAGGA  
GTTCCAGGCCGTGGTCCGGGCAGCTGGTGGTACCCTGCTGGGAGTCAGCTCCCAGGGGGGTCA  
GACCTACGAGATGTTCTCCTGGTTCCTGCGGCCCTGCCAGGCCCCCACAAGCAGCTCCTCCA  
CCACGTCAGCACCTTGGCTGCCCTCACAGTCCGGCAGGTGCAGCAGCACCAGGGGAACCTGGA  
TGCTTCGGGGCCCCGCACGTGACCTTGTGATGCCTTCTGCTGAAGATGGCACAGGAGGAACA  
AAACCCAGGCACAGAATTCACCAACAAGAACATGCTGATGACAGTCATTTATTTGCTGTTTGC  
TGGGACGATGACGGTCAGCACACCGTCCGGCTATACCCTCCTGCTCCTGATGAAATACCCTCA  
TGTCCAAAAGTGGGTACGTGAGGAGCTGAATCGGGAGCTGGGGGCTGGCCAGGCACCAAGCCT  
AGGGGACCGTACCCGCCTCCCTTACACCGACGCGGTTCTGCATGAGGCGCAGCGGCTGCTGGC  
GCTGGTGGCCATGGGAATACCCCGCACCTCATGCGGACCACCCGCTTCCGAGGGTACACCCT  
GCCCCAGGGCAGGAGTCTTCCCCCTCCTTGGCTCCATCCTGCATGACCCCAACATCTTCAA  
GCACCCAGAAGAGTTCAACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGA  
GGCGTTTCTGCCCTTCTCCTTAGGGAAGCGTGTGCTGCCTTGGAGAGGGCTGGCAAAAGCGGA  
GCTCTTCTCTTCTTACCACCATCCTACAAGCCTTCTCCCTGGAGAGCCCGTGCCCCCGGGA  
CACCTGAGCCTCAAGCCACCGTCAGTGGCCTTTTCAACATTCCCCCAGCCTTCCAGCTGCA  
AGTCCGTCCTGACCTTCACTCCACCACGCAGACAGATGAAGGAAGGCAACTTGAAGTG  
GTGGGTGCCCAGGACGGTGCCTCCAGCCTCAACAGTGGGCATGGACAGGGTTAATGTCTCCAG  
AGTGTAAGTGCAGGCAGCCACATTTACACGCCTGCAGTTGTTTTCCGGAGTCTGTCCCACGG  
CCCACACGCTCACTTGACTCATGCTGCTAAGATGCACAACCGCACACCCATAACAACATAAA  
GGGCCACAAAGCAACTGCTGGGTAGCTTTCCACAGACATAAATATAGTCCATCTGCAATCAC  
AAGCACATAGCCAGGTAACCCACCAACTCCCCTGGATCTGCAGCCCACACGTGGGAGTCTGGC  
TGTCACCTTACAAGCCACAGAAACGGCCACACATGTTACAGCTCACACGCCCTCTCCATT  
ATCGAACTTCTCAGTGTCCCTGTCCCTGGTGCCTGGCACAGGGAACAGCATGCCCCCTCCGGG  
GTCATGCCACCCAGAGACTGTGCTGTCTATGGCCCCAACTCATGCTCCCTCTTGGCTACA  
CCACTCTCCCAGCCTGTGACCACCGATGTCCACACACCCCCAACCACTTGTCCACACAGCTAC  
CCACGTACAACATCGTCCTGGCTCCCCAGAGTATCTTCCCCTGAGACACGCCGCCCCCACAG  
AGGCACAGTCCCCAGCCACCTCTGCAACTGCAGCCCTCAGTCAACCCCTTTTAAAGCACCTGA  
TTCTACCAAATGCAAACACATCTGGGTCTGCGATTATGCACAGAGACTTTGGACATACGAGGA  
CCCTCAGACCGGAGGAACACCTGCCCAACCCCAACACGTGCTTATGTAACCACGTGGAAAGCG  
GCCCCCTGCTGCCCTCCACACACATAACACTCACTGATCTACAGCCCCTGTTCGGCGTCA  
GAGTCCCCACTAGACCCAGTGGAAGGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTCACC  
CTGTAGGGAGTGAGCCGATCTGACGTTCTTGTGACTTAAGGGTCCGGCTTGGGAATTAAA  
GTTTGTCTTGGCCTTTAGCCTAAAAA

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**FIGURE 64**

MEATGTWALLLALALLLLTLALSCTRARGHLPPGPTPLPLLGNLLQLRPGALYSGLMRLSKK  
YGPVFTIYLGPRPVVVLVGQEAAREALGGQAEFFSGRGTVMLEGTFDGHGVFFSNGERWRQ  
LRKFTMLALRDLGMGKREGEEELIQAEARCLVETFOGTEGRPFDPSTLLAQATSNVVCSTLLFGL  
RFSYEDKEFQAVVRAAGGTLLGVSSQGGQTYEMFSWFLRPLPGPHKQLLHHVSTLAAFTVRQV  
QQHQGNLDASGPARDLVDAFLLKMAQEEQNPGTEFTNKNMLMTVIYLLFAGTMTVSTTVGYTL  
LLLMKYPHVQKWVREELNRELGAGQAPSLGDRTRLPYTDAVLHEAQRLLALVPMGIPRTLMRT  
TRFRGYTLPGQTEVFPLLGSILHDPNIFKHPEEFNPDRFLDADGRFRKHEAFLPFSLGKRVCL  
GEGLAELFLFFTTILQAFSLESPPDLSLKTPTVSGLFNIPPAFQLQVRPTDLHSTTQTR

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 294-313

**Glycosaminoglycan attachment site.**

amino acids 99-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 128-132

**N-myristoylation sites.**amino acids 51-57, 109-115, 115-121, 188-194, 207-213, 257-263,  
284-290, 339-345, 370-376, 444-450**Amidation sites.**

amino acids 140-144, 435-439

**Leucine zipper pattern.**

amino acids 32-54, 39-61

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 433-443

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**FIGURE 65**

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC  
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCCCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTCAGTTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATT  
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTGAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCTCCACTAGTCCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC  
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAAGGCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAACTCTGGAGGTGGAGCATCAAGTTCCAGCC  
GGCCCCCTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCCTTGGTGTTGCCTTCTTGCACTCTCCACACATTTCCCTTGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTTTTCACAGGGAAAAAAAAAAAA

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**FIGURE 66**

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIRAVG  
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSDLDPATLSATFQGHMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGASPRGNRSLEFGLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGSPLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCFNLTFGASTGPGYWDQHYLSWSMMLLGVGFPPVDGLSPLVLGIMAVAL  
GAPGLMLLGGGLVLLHHKKYSEYQSIN

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234,  
333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**Casein kinase II phosphorylation sites:**

amino acids 151-155, 249-253, 255-259

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern.**

amino acids 371-393

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FIGURE 67

[illegible]



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**FIGURE 68**

MFPLRALWLWVALLGVAGSCPEPCACVDKYAHQFADCAVKELREVPEGLPANVTTLSSLSANKI  
TVLRRGAFADVTVQVTSWLAHNEVRTVEPGALAVLSQLKNLDLSHNFISFPWSDLRNLSALQ  
LLKMNHNRLGSLPRDALGALPDLRSLRINNRLRTLAPGTFDALSALSHLQLYHNPFHCGCGL  
VWLQAWAASTRVSLPEPDSIACASPPALQGVVYRLPALPCAPPSVHLSAEPPEAPGTPLRA  
GLAFVLHCIADGHPTPRLQWQLQIPGGTVVLEPPVLSGEDDGVGAEEGEGEGDGDLLTQTQAAQ  
TPTPAPAWPAPPATPRFLALANGSLLVPLLSAKEAGVYTCRAHNELGANSTSRVAVAATGPP  
KHAPGAGGEPDGQAPTSEKSTAKGRGNSVLPSKPEGKIKGQGLAKVSILGETETETEPEEDTSE  
GEEAEDQILADPAEEQRCGNGDPSRYVSNHAFNQSAELKPHVFELGVIALDVAEREARVQLTP  
LAARWGPGPGGAGGAPRPGRRPLRLLYLCPAGGGAHVQWSRVEEGVNAYWFRGLRPGTNYSC  
LALAGEACHVQVVFSTKKELPSLLVIVAVSVFLLVLATVPLLGAACCHLLAKHPGKPYRLILR  
PQAPDPMKRIAADFDPRAVSEKSYVAGGEAGGEEPEDVQGEGLDEDAEQGDPSGDLQRE  
ESLAACSLVESQSKANQEEFEAGSEYSDRLPLGAEAVNIAQEINGNYRQTAG

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 587-610

**N-glycosylation sites.**

amino acids 52-55, 121-124, 337-340, 364-367, 474-477, 563-566

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 397-400

**Casein kinase II phosphorylation sites.**amino acids 19-23, 202-205, 289-292, 246-249, 411-414, 431-434,  
433-436, 440-443, 544-547, 583-586, 650-653, 700-703**N-myristoylation sites.**amino acids 15-20, 48-53, 165-170, 296-301, 351-356, 362-367,  
390-395, 419-424, 514-519, 536-541, 557-562, 561-566, 610-615,  
661-666, 716-721**Amidation site.**

amino acids 522-525

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 10-20, 603-613

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**FIGURE 69**

GGCGGCGGGAGCAGCGAAGGGGGCGGCAGGGATCCTCCAGGCTGCCGGCTGGGAAGGCGTGGG  
CGACCCGGTGTGTGGCGCGCCCAGAGCCCCGCGTTTCAGCCCTAGGGAAGGAAGCCAGTTGAG  
GGAAGTTCTCCATGAATGTACGTACAAATGATGATGACCGACCAAATCCCTCTGGAAGTGGCA  
CCATTGCTGAACGGAGAGGTAGCCATGATGCCCCACTTGGTGAATGGAGATGCAGCTCAGCAT  
GTTATTCTCGTTCAAGTTAATCCAGGTGAGACTTTTACAATAAGAGCAGAGGATGGAACACTT  
CAGTGCATTCAAGGACCTGCTGAAGTTCCCATGATGTCACCCAATGGATCCATTCTCTCCCAT  
CATGTGCCTCCAGGTTATATCTCACAGGTGATTGAAGATAGTACTGGAGTCCGCCGGGTGGTG  
GTCACACCCAGTCTCCTGAGTGTTATCCCCAAGCTACCCCTCAGCCATGTCTCCAACCCAT  
CATCTCCCTCCCTATCTGACTCACCATCCACATTTTATTATAACTCACACACGGCTTACTAC  
CCACCTGTTACCGGACCTGGAGATATGCCGCCTCAGTTTTTTTCCCAGCATCATCTTCCCCAC  
ACAATATATGGTGAGCAAGAAATTATACCATTTTATGGAATGTCAAGCTACATCACCCGAGAA  
GACCAGTACAGCAAGCCTCCGCACAAAAAAGTGAAGACCGCCAGATCGATCGCCAGAACCGC  
CTCAACAGCCCTCCTTCTTCTATCTACAAAAGCAGCTGCACAACAGTATACAATGGCTATGGG  
AAGGGCCATAGTGGTGGAAAGTGGCGGAGGCGGCAGCGGTAGTGGTCCCGGAATTAAGAAAACA  
GAGCGACGAGCAAGAAGCAGCCCAAAGTCGAATGATTCAGACTTGCAAGAATATGAGTTGGAA  
GTAAAGAGGGTGCAAGACATTCTTTCGGGAATAGAGAAACCACAGGTTTCTAATATTCAGGCA  
AGAGCAGTTGTGTTGTCTGGGCTCCCCCTGTTGGACTTTCCTGTGGACCCACAGTGGTCTT  
TCCTTCCCCTACAGTTACGAGGTGGCCTTATCAGACAAAGGACGAGATGGAAAATACAAGATA  
ATTTACAGTGGAGAAGAATTAGAATGTAACCTGAAAGATCTTAGACCAGCAACAGATTATCAT  
GTGAGGGTGATGCCATGTACAATTCCGTAAAGGGATCCTGCTCCGAGCCTGTTAGCTTCACC  
ACCCACAGCTGTGCACCCGAGTGTCTTTCCCCCTAAGCTGGCACATAGGAGCAAAAGTTCA  
CTAACCTTGCAAGTGGAAAGGCACCAATTGACAAACGGTTCAAAAAATCACCAACTACCTTTTAG  
TGGGATGAGGGAAGAAAGAAATAGTGGTTTTCAGACAGTGCTTCTTCGGGAGCCAGAAGCAGTGC  
AAGTTGACAAAGCTTTGTCCGGCAATGGGGTACACATTACAGGCTGGCCGCTCGAAACGACATT  
GGCACCAGTGGTTATAGCCAAGAGGTGGTGTGCTACACATTAGGAAATATCCCTCAGATGCCT  
TCTGCACCAAGGCTGGTTTCGAGCTGGCATCACATGGGTACGTTGCAGTGGAGTAAGCCAGAA  
GGCTGTTTACCCGAGGAAGTGATCACCTACACCTTGGAATTCAGGAGGATGAAAATGATAAC  
CTTTTCCACCCAAAATACACTGGAGAGGATTTAACCTGTACTGTGAAAAATCTCAAAGAAGC  
ACACAGTATAAATTCAGGCTGACTGCTTCTAATACGGAAGGAAAAAGCTGTCCAAGCGAAGTT  
CTTGTTTGTACGACGAGTCCTGACAGGCCTGGACCTCCTACCAGACCGCTTGTCAAAGGCCCA  
GTTACATCTCATGGCTTTAGTGTCAAATGGGATCCCCCTAAGGACAATGGTGGTTCAGAAATC  
CTCAAGTACTTGCTAGAGATTACTGATGGAAATCTGAAGGTGAAGTTTTTGGCAATTGTTTT  
ATTCAAATCCAAATAGCAAGCTCTGTTTTCTAATATAGTAAATGTCTTTATAGTAATAGTGAGT  
AATCATTAATTCATAAGATAGAATTATTATTACAATAAACAACTTTAGTCACATATTGGCAG  
TTTTTCTATTTCAAACACAGCACCAGAGATCAGAGTCTACTTGAACTTACATTTGTGTTATT  
TAACAATTTTTCTGTATCTTTTTTCATTGGTGTGTTTTGTTTTGTTTTATCTTTGTTTTGTTTTCT  
TTGGTTTTGGTTTTGTTTTGTTTTGTTTTGAGATACGATCTCTGTACACAGGCTGGAGGGC  
AGTGGCACAGACATGGCCCATTCAGTCTCAGACTCCTGGGCTTAAGTGACTCTTCTGCCACA  
GAAGATGAGGAAGAATACATTTTTCATAGTGATGGGGTCTCACTATGTTATCTAGGCTGGTCT  
CAAACCTCCTGGCCTCAAGCAACCCCTCCACCTTGCCCTCCCAAAGTGCTGGGACTATAGACATG  
AATCACCACACTCAGCTTCCATGTCTTTTATGAACTAGGGTTCCTAATTAATCAGATAAATT  
TGGTATTTTCATCTCCTAACTTGCCATATGTTTTCTGGAAATCTTATAAGCAGCCGAGAGTG  
GTGGCTCACGCTGTAGTCCCAGCACTTTGGGAGGCTGAGGTGGGTGGTCAGGAGATCAAGACC  
ATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTG  
GCAGGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGAAGAATTGCTTGAACCCAGCAG  
GCGGAGGTTGCAGTGAGCTGAGATTGCACCACTGCCTCCAGCCTGGTGACAGAGTGAGACTC  
TGTCTCAAAAAAAAAAAAA

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**FIGURE 70**

MMMTDQIPLLELPPLLNGEVAMMPHLVNGDAAQHVLVQVNPGETFTIRAEDGTLQCIQGPAEV  
PMMSPNGSIPPIHVPPGYISQVIEDSTGVRVVVTPQSPECYPPSYPSAMSPTHHLPPLYLTHH  
PHFIHNSHTAYYPPVTGPGDMPPQFFPQHHLPHITYGEQEIIPFYGMSSYITREDQYSKPPHK  
KLKDRQIDRQNRNLNSPPSSIIYKSSCTTVYNGYGKGHSGSGGGGSGSGPGIKKTERRARSSPK  
SNDSDLQEYELEVKRVQDILSGIEKPQVSNIQARAVVLSWAPPVGLSCGPHSGLSFPYSYEVA  
LSDKGRDGKYKIIYSGEELECNLKDLPATDYHVRVYAMNSVKGSCSEPVSFTHTHSCAPECP  
FPPKLAHRSSSLTLQWKAPIDNGSKITNYLLEWDEGKRNSGFRQCFFGSQKHCKLTKLCPAM  
GYTFRLAARNDIGTSGYSQEVVVCYTLGNIPQMPSAPRLVRAGITWVTLQWSKPEGCSPEEVIT  
YTLEIQEDENDNLFHPKYTGEDLTCTVKNLKRSTQYKFRLTASNTEGKSCPSEVLVCTTSPDR  
PGPPTPLVKGPVTSHGFSVKWDPPKDNGGSEILKYLLEITDGNSEGEVFGNCFIQIQ

**Important features of the protein:****N-glycosylation sites.**

amino acids 69-73, 254-258, 401-405

**Glycosaminoglycan attachment sites.**

amino acids 229-233, 234-238, 236-240

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 416-420, 535-539

**Tyrosine kinase phosphorylation site.**

amino acids 319-326

**N-myristoylation sites.**amino acids 52-58, 227-233, 228-234, 230-236, 231-237, 232-238,  
235-241, 239-245, 402-408, 610-616**Amidation site.**

amino acids 414-418

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 290-301

**ATP/GTP-binding site motif A (P-loop).**

amino acids 546-554

**CUB domain proteins profile.**

amino acids 294-301

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**FIGURE 71**

AAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGATGTCAGCTCTTCTGGCTCCTTCTCAGCCTTGTT  
GCTGTAAGTGTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTGGACAAGTTAACCACGAAGCCGAA  
GACCTGTTCTATCAAAGTTCATTGCTTCTTGGAAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATG  
AATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAATGTATCCACTACAAGAA  
ATTGAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCAGAAGACAAG  
AGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAAACCCAGATAAT  
CCACAAGAAATGCTTATTACTTGAACCAGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTC  
TGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGAAA  
AATGAGATGGCAAGAGCAAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGACTATGAAGTAAATGGGGTA  
GATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGGAAACATACCTTTGAAGAGATTAAACCATATAT  
GAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCTATATCAGTCCAATTGGATGCCTC  
CCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGACTCTTGACAGTTCCTTTGGACAG  
AAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAG  
AAGTTCTTTGTATCTGTTGGTCTTCTTAATATGACTCAAGGATTCTGGGAAAATCCATGCTAACGGACCCAGGA  
AATGTTTCAGAAAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACA  
AAGGTGACAATGGACGACTTCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCA  
CAACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCA  
GCCACACCTAAGCATTAAATCCATTGGTCTTCTGTCAACCCGATTTTCAAGAAGACAATGAAACAGAAATAAAC  
TTCTGTCTCAACAAGCACTCAGATTGTTGGGACTCTGCCATTACTTACATGTTAGAGAAGTGGAGGTGGATG  
GTCTTTAAAGGGGAAATTCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGGGGTG  
GTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGTTTCTGATGATTACTCATTC  
ATTGATATATACACAAGGACCTTTACCAATTCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGC  
CCTCTGCACAAATGTGACATCTCAAACCTCAGAGAAGCTGGACAGAACTGTTGTAAAGAAATACCTCAAAATGTT  
GAACCTCTCCTAGTATTTCAGTATTACTCATTCCATGCCATGGTTTGTATTGATTCTTTGTTCTAAAAAGAAA  
ATTTTATGGCCTCAAAATGTCTCATTTACAAACCAAAACATTTAATTTGTGGTCAGACAGGAACCTAGACCATA  
AACAATTGGGTGGGCCACCTCTTTCTCCCTATCATACTACAGCCCTCTCTTCTGGTAATTGGAAGGAAAGAG  
CGGTTTAGGGTGGAAATATATCTGTTAATATGCATTCTTTCTTATCTGCCAGAAGCAAAATTTAGCCAGTCAAA  
AGAAGAAACCATAGATCATAGATGTAATATATGTACATCTGGAACCCCTCAAAGGCCCTGAACCCCTTTTTT  
TGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCTGGACCCCTAGCATTGGAAAATGTTGTAGGAGCAAGAA  
CATGAATGTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTT  
TGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCCAAAGCATCAAAGTGAGGATAAGCCTAAATCAGCTC  
TTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATGAGGC  
AGTACTTTTTAAAGTAAAAATCAGATGATTCTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCA  
GAATCTCCTTTAATTTCTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGG  
CCATCAGGATGTCCCGGAGCCGATCAATGATGCTTTCCGCTGAATGACAACAGCCTAGAGTTTCTGGGGATAC  
AGCCAACTTTGGACCTCCTAACAGCCCTGTTTCCATATGGCTGATTGTTTTGGAGTTGTGATGGGAGTGA  
TAGTGGTTGGCATTGTCTCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAGCAAGAGTGGAG  
AAAACTCTTATGCCCTCCATCGATATTAGCAAAGGAGAAAAATAATCCAGGATTCAAAACACTGATGATGTTTCA  
CCTCCTTTTAGAAAAATCTATGTTTTCTCTTGAAGTGATTTGTTGTATGTAATGTTAATTTTATGGTATAG  
AAAATATAAGATGATAAGATATCATTAAATGTCAAACTATGACTCTGTTTCAAAAAAAATTTGTCCAAAGACA  
ACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTTCAATATTTTCTGCTCTGATTTGACTTCTGTT  
CTGTTTCTTAATAAGGATTTTGTATTAGAGTATATTAGGGAAAGTGTGATTTGGTCTCACAGGCTGTTTCAAGGA  
TAATCTAAATGTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTGGATCT  
TGTATGGAATATGGATGGATCACTTGTAAAGGACAGTGCCTGGGAACTGGTGTAGCTGCAAGGATTGAGAATGGCA  
TGCATTAGCTCACTTTTCAATTAATCCATTGTCAAGGATGACATGCTTTCTTCAAGTAAGTCAAGTACTA  
TGGTATTTGCTTACAGTATGTTTGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATC  
CAGGGAACAGGTAGAGGACATTGCTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAAAACCTA  
GAGCCAGGGCCCTCCGTGAACCTCCAGAGCATGCCTGATAGAACTCATTCTACTGTTCTTAAGTGTGGAGT  
GAATGGAATTTCAACTGTATGTTTCAACCTCTGAAGTGGGTACCCAGTCTCTTAAATCTTTTGTATTTGCTCACA  
GTGTTTGAAGCAGTGTGAGCACAAGCAGACACTCAATAAATGCTAGATTTACAAAA

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**FIGURE 72**

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSSLASWNYNTNITEENVQNMN  
NAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTI  
YSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE  
MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY  
PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFQKPNIDVTDAMVDQAWDAQRIKFAEKFF  
VSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGGH  
IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLK  
QALTIVGTLPTFTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLF  
HVSDDYSFIRYYTRTLYQFQFQEQALCQAAKHEGPLHKCDISNSTEAGQKLL

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 53-57, 90-94, 103-107, 322-326, 432-438, 546-550

**N-myristoylation sites.**

amino acids 260-266, 286-292, 395-401

**Cell attachment sequence.**

amino acids 204-207

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 371-381

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**FIGURE 73**

CCCACGCGTCCGAGCGGGGTGGACAAGTGGCGTGTGTGCTGCGACCCCGAGGGAAGATGAACG  
GGACGCGGAACCTGGTGTACCCTGGTGGACGTGCACCCAGAGGACCAGGCGGCGGGCAGGA  
AGACCTATGCCATGGTGTCCAGCCACTCAGCTGGTCATTCTCTGGCTTCAGAACTGGTGGAGT  
CCCATGATGGACATGAGGAGATCATTAAGGTGTACTTGAAGGGGAGGTCTGGAGACAAGATGA  
TTCACGAGAAGAATATTAACCAGCTGAAGAGTGAGGTCCAGTACATCCAGGAGGCCAGGAAC  
GCCTACAGAAGCTCCGGGAGGATATAAGTAGCAAGCTTGACAGGAACCTAGGAGATTCTCTCC  
ATCGACAGGAGATACAGGTGGTGTAGAAAAGCCAAATGGCTTTAGTCAGAGTCCCACAGCCC  
TGTACAGCAGCCCACCTGAGGTGGACACCTGTATAAATGAGGATGTTGAGAGCTTGAGGAAGA  
CGGTGCAGGACTTGCTGGCCAAGCTTCAGGAGGCCAAGCGGCAACACCAGTCAGACTGTGTGG  
CTTTTGAGGTCACACTCAGCCGGTACCAGAGGGAAGCAGAACAAAGTAATGTGGCCCTTCAGA  
GAGAGGAGGACAGATGTCCAGAGTGAATTGGAGAATGTCCTGGGGGAATGAAGTTCCTTCCACA  
AACACAGCTCAGTTCTTAGCAACAACTGTTTGTCTTTCTACTTGCTCCATCTGCAGCCTACG  
CTGCCCTGGCCTCCTGCAGACAGATAGTGGGGTTACCTGGCAAGGCCTGGTGAGAGCCAGTGA  
ACCTAAGCTTTGACTGGGTGGCCTTGTCTTTCTGGGGAGGAGGGAATGTACATTCAGGGAGTA  
GCCTTTTGCGGAAAAATTCTCTAGGGCTACAGACAGTCATGTGTGACTTCTCTCTGCTGTGAA  
AACTCCCAGAGTCTCTTTAGGGATTTTCCCTAAGGTGTACCACCAGGCACACCTCAGTCTTCT  
TGACCCAGAGCCTGAAAACCTGTTTTCACTGGGTTCACCAGTCCCAGCAAAATCCTCTTTGTA  
TTTATTTTGCTAAGTTATTGGTGGTTTTGCTTACATCTCATGATTGATATAATACCAAAGTTC  
TATAGCCTTCTCTTGAGTATTTGGATTGCTTGAAACCGGGAAAACTGTTCCCATTAGGCTT  
GTTAATGTCAGAGTGACACTATTATGAATCTTTCTCTCCCTTTCCTCTGCCTGTTTCTTCTCT  
CTTTCTCCTTCAAACCTTGCTCTGCAGCTAAGGAAGGTGAGTCTACTTTCCTGAGGCTTTGGG  
GTCAGAGTATATGTTGTTTGGAGAAAGAGGGCAATCAGGACTCTTCTGGGACCCAGATGAGTT  
CTTCACTAGCCCTTCTGAACCCCTTGCTCCATAATTGGTCTTTTATCCTGGCTCTGAATGACC  
CTGCAGGTCATCATGGTTTTCTTTTTTTTATTGTTTTTTTTTTTCTGAGACAGAGTCTCACT  
CTGTCAACCAGGCTGGAGTGCAGTGGCGGATCTCAGCTCACTGCAACCTCTGCCTCCCGGAT  
TTAAGCGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGTGCCACCACGCCTG  
GCTGATTTTTGTATTTTTTAGTAGAGATGGGGTTTACCATACTGGCTAGGCTGGTCTCGAATT  
CCTGACCTCAGGTGATCCACCCACCTCGGCTTCCCAAAGTGCTAGGATTATAGGCTTGAGCTA  
CTGCGCCCGGCCCATGGTGTTTTTCTTTAGGGCTCTTCCCTACAGCCTTGAGAAGTAGATAGGC  
ATCAGAGTATGGTACTATAGGAATCAGAAAAATTCAAACAAATGTGGATTAAAGTGTTTAGGC  
TCTATGTGGCTCACGCAGCCAGAATCCTTAAGTCTGTGTGTTTCTGTGTCTCAAGACTGGGCT  
CACATTCTGGCTTTGTCCATAACAATGCTCTGGGATTTTCAGGGAGTTCCTCATTTGTAAAAT  
GAGGGGGTCAGAGCAGGTGATATCCATGTTTCTTCCCTTTCTGATATTGTTGTCTGTGGCATA  
TTCTTTGTATGGCGAATTTAATAAATTATATTAATGTGTCA

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## **FIGURE 74**

MNGTRNWCTLVDVHPEDQAAAGRKTYAMVSSHSAGHSLASELVESHGHEEIIKVYLKGRSGD  
KMIHEKNINQLKSEVQYIQEARNCLQKLREDISSKLDRLGDSLHRQEIQVVLEKPNGFSQSP  
TALYSSPPEVDTCINEDVESLRKTVQDLLAKLQEAQRHQSDCVAFEVTLSTRYQREAEQSNVA  
LQREEDRCPE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-39

**N-glycosylation site.**

amino acids 2-6

**Amidation site.**

amino acids 21-25

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**FIGURE 75**

GCTTGACACATGGCTCCGGAGGCTCCGGTTGCCCATCCGAGCCCCCTGCCAGGCTCTAACGTTCCCAACTGACAA  
CACCAGTAACTAAATATAGGAGCAGATGGTGGGGACGGGCTGTGCGAGCGGCTCCTTTGCAGAGGTCTCCGGACT  
GCAGATAAGGCTCAGGCCCTTTTGTGAGAAGCAGACCAGCCTGGGGGCTGGCGGCAGGACACCTGTGTCTGCATG  
CTGAAGAAGATGGGTGAGGCCGTGGCCAGAGTAGCAAGGAAGGTCAACGAGACGGTGGAGAGCGGCTCTGACACT  
CTGGACCTGGCCGAGTGCAAGCTGGTCTCCTTTCCCATTTGGCATCTACAAGGTCTGCGGAATGTCTCTGGCCAG  
ATCCACCTCATCACCTGGCTAACAACGAGCTTAAGTCCCTCACCAGCAAGTTCATGACCACATTAGTCAGCTC  
CGAGAGCTCCACCTGGAGGGGAACCTTCTACACCGCCTCCCCAGCGAGGTCAAGTCCCTGCAGCACCTCAAGGCC  
ATTGACCTGTCCCGGAACCAAGTTCAGGACTTCCCTGAGCAGCTTACCGCCCTGCCGGCGCTGGAGACCATCAAC  
CTGGAGGAGAACGAGATCGTAGATGTGCCGTGGAGAAGCTGGCCGCCATGCCAGCCTTGGCGAGCATCAACCTC  
CGCTTCAACCACTCAACGCCGAGGTGCGCGTGATCGCCCCGCCGCTCATCAAGTTTGACATGCTCATGTCTCCG  
GAAGGCGCAAGAGCCCCCTACCTTAGGCCACCCTCCTCATGCCACCCAGCAAGGGACAGAGGCCACAGGCCCTG  
GAACCTTGAAGGGAGGGAGGCCCATGGGAGGCCAAGCCTGGGGGCTGGGGGCGGGTGGGCGAGCAGCAGTGG  
TGGGTGGGGTGCAGCTGGTCTGGATAGATAGCTTACAGCAGTAGTGGGCTCTGGAATGCCCAAGGGAAGAGGCAA  
GGTGGGGCCTGCAGCCTGGACTCGGCACCTCAGAGCTGTGTGCAAACTCAGGCAGATCTCCTGCCCTCTCTGAGC  
CTTGTCACTTGAAAAAACAGGACCCTTTCCCTCCTTTGGGCTCCCTGGAGGTTTTTAAGCAGTACGTGCCCTCA  
AGTTACCTCCAGATCAGCAGGCACAGGTGGGCATTGCCAGGTATTTTCTGAGCCCTGCCGGTTTGAGGCCCTGT  
TTTTAGTGCTGAGAGCCAGTTGCTGCCCTGAGAAGAGAAGACAACCTCCATCTATTTATTGCTTCCTGAGAACTG  
ACCTGGATGCGGCCCTCTGCAGGGCCAGTCTTCAGTCTGTGGTCCCTGGACTGGTGGGAACCTGAAGTAGGAG  
TCCTGGGAGAGCTGTGGTGGGAATATGGGCTGGCAGCTGTGCAGGGCAAGAACATTATGTAGGAGCCCGAGGAC  
CANCANGCTGGGAATGGGGAGCAAGTCAGTCAGTCTGTCTATTCCCCACAGTTAACAATTTGCCGGGTGGGAA  
GTCTGAGTGCTCCGTCCCTCTAGCATCACTCCTGAGCTGCGGGAGAGGTGGCCAGAGAACAGCAGAGTCAGTT  
ACACCTGCAGCTCTTGTCTAAAGTGATTAGATGGCCACCCTCACCAGTGTCCAGTCCAGCAGCAGCCTGGCTGCC  
TTGTCTATGGCCTCTTGGGGCAGAAAGCGATGTGGACCACGGGATTGTAGCCAGCCAGCTCCCAGGCCAACGCC  
CAAAGCCCTGATGACCTGGTTCTTCTGAGGCCCTCAACCTGGCATCTTAGGGTATGGTCAGGCAACAGGGTGACC  
AGCTGTCTGGTTTCCCAGGACATGGAACCTTCAATGCTAAACTGGGACATTACCCAGCAAGTGGGGATGGGTG  
GTCCCTACCAGGAGAGGGCCTGGGGCTCTTGCTTCCCGAGAACGCTGTGGCTTGAAGAACCTTGACTGCTTGG  
TCCTCAGGTATCTACCTCCCACCTTCTCCTCATCTGTGGAGCAAGCCAACTCAGTGGCCAGACCCACCTGATC  
TGATCTTTTGTGCTCCAGAGACACCTGAGGCCAGAGCTTGAGGCAAAGCCAGGCCGTCCAAATCCTGTGTG  
CCGTGGACGAGTGGCCACTTTACTACTCCTAAGGCTAAGATGTTGAGAGCTCAGACCACTGCTCAGAGCAGTAAT  
CCCTGCTCAGATGCTCCAGTTCCTCGTCCCTGCCAGGTCTCTGTCTCTTGGGAAGGAAGTATAGGTGGG  
GCCATTGTTGGGCCATCACTGAGCGCTCAGTATCTCAAGAGACTCTGTTTATTCTGCTCGTATCCCAAGGCCCTGG  
TTGGTCAAACCTCTGGGCAAAGGGTTTTTCAAGATGAGGAGGTCAAGACAGGATGTCCAGAGCTACCGAGTTCATCT  
GTGGGTGTTGGGGCAAGTGGGGCTGAAGTCCCTGTGCAGGCTGCGCTGGCCCCACCTGCCTTGTGCCCTGGAGT  
GGGGTTTCTCCTTGTGGAAGAGAGGCATCCTTCTCTGATGTGCACAAACACAATGTATGACCAGAGCCTTGCAA  
CTCAAAGTGTGGTCTGTGGACCAGCAGCGGCAGTGACACCTGGGAGCTTGTAGGAATGCAGAGTCTAGGCCCTCA  
CCCTATACCTCCCGACTCAGACCCTGCATTTTAGCAAGACCCCAAGCTGATTCTATAAGCACTTTAGAGTTTGA  
GAAGCAAGGACCTAGGCTGGGGATGTCTCCGAGCAGAGGGTGAAGTTTCTCTCAGTTCTCTCCCTGCCACTTCC  
AGGGATCTGAGCCTGTGTTGAGCCTCCTCCCTAACCACCCCTGGGAGACACTTGGCCTGTTAGATTGTTCCAGAG  
TCTGCATGGCACTCCTGAAGAAGGGAGTGTGACCTGCAGTACCAGGAGATGAGGGTTAGGTGTGCCAGCCCTC  
CAGACCCGGCTTTCTGGTTAACCCTGCATGCCAAGCTGCCTGCTGCCCCAGGTCTCACCTCAGGCCTTTGAA  
GGGGCAGCTTCTGGAAGTTGTTTTCTCCTCTGCTTGGAGAGTTTGGCCTTGTCTGTCTTGGAAAGTGTGGGCAGC  
CACAGATGCCCCAAATCAGAGCTCACAGTGAGTGGAGCCCTAAGCTTCAGTCTGCAATAAAGAATGCATTGGTT  
TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 76**

MLKKMGAEAVARVARKVNETVESGSDTLDLAECKLVSFPIGIYKVLNRNVSGQIHLITLANNELK  
SLTSKFMTTFSQLRELHLEGNFLHRLPSEVSALQHLKAIDLSRNQFQDFPEQLTALPALETIN  
LEENEIVDVPVEKLAAMPALRSINLRFNPLNAEVRVIAPPLIKFDMLMSPEGARAPLP

**Important features of the protein:**

**N-glycosylation sites.**

amino acids 17-21, 47-51

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**FIGURE 77**

CACCAACAAGCAATCGTTTCATGAGAAAGCCGTGCACCCGCTGCAGTTGGGCCATGTGGTCCGCATCGTATTCAC  
TAGGTCCCCATTGTACACCAAGTACTGTCCCGGCGTCTCCAGCAGATGCCTGCAGCCTTCCACCTTCTCAAGCAG  
GGTGGTGTGAGTGCGCTGCTTTCCTTCTCGCTGGACCGGAGCCGTGCGGGGAGGCACCCCGGGGGTGGAGAA  
AAAGCCGGCCTGGCCTCGGAGGTGGTCTCGGCCCGCCCGCCACCGACTCCCTCCTCCCTCCAGAGGCGGCGGC  
GGCTCCGGCGGCAGCAGCGGCAGGCAGCAACGTAAGCGGGATGCTCTCCAGGCTGCTTTTCTGCTCGGTACAGAA  
ATGGCTGAGCTGGTACATCTCGCTCTCCAGGTAGGAGATCTCGCGGGCCGTCTCTATGAACTGCCGGTAGTTCTG  
GTAGACGTTGCGCTTCAGGTTCTGCGCCGTCTCCTCCGCCAGCGCTGGATGCGCTGCCGGTGTCTCTGGAGGTC  
CCGGTCCCCATCCGACTGCTGCGAGAGCTGCTTACGTACAGCCGCGCCTCAAAACCCCTGACTCCAGCTGCCG  
ACGCAGGCGGCTCGCCCCACTGTCCGACATCGCCATCGCCATTTCTCTCCGGGTCTCAGCCTACTGTCACTA  
TCGGCGCCGAGCCGCGCGGCTGTCTAGACCCACCCAAGGCCAACCAGGCTCCTGGGCTGAGGAAGCAGGAATG  
GGAACGAGACGAGTACGCTGCGCCGGGTCTGAGCGTCAGACACTGCGCCTGCGCAAGTGGGCGGAGCGCAGACA  
TTGCGCTGCGCAGCAATGCCATCGGTTAAAGCGCATGCGCAAGATGAGCTATTGCGGAAGTGAAGGAGGGAGA  
GGCCGAGAGAAATTTTCGTACTGCGCATGAACCGAGCGTGACGTTGAGGTTTGAATAACCGGCAAGAGTAAAG  
GCTGAACTAGCTTCTGAAAGCTTCGTAGGGCCCGAGCCCTGTGAGCCAGGTTCTGCGCCCACTAGGAGGTGT  
CATGCTGACTGCTTTTTTAAAGCCCTAGAATCCTTGGCTTCGGCGTTTGGGGTAAGCTCCGTTCTCGTCTCAA  
GCGCGTTTCCGCGAATCTCGCGGGATGACGGGCGCTCTCGAGAGCCGGCATCTCTAGGAGCTAGTCTCTGGT  
CTCGCTAGGCGGCTTGGGGTCCGCGCGTAAGTGGGGAGCCAGCCTGACGCGGCGGACCCCGCTGTGATCCTG  
GCAACGATGATGATGACTTGATGTTGGCACTGCGGCTCAGGAGGAGTGGAAGTTCAGGAGGCGGAGCGCGAT  
CATGCCAGGAGTCCCTGTGCTAGTGGACGCGCTCGTGGGAGTTGGTGGACCCACACCGGACTTGCAGGCACTG  
TTGTTTCACTTTAACGACCAATTTCTTGGGGCCAGCTGGAGGCGCTCGAGGTGAAGTGGAGCGTGCGAATGACC  
CTGTGTGCTGGGATATGCAGCTATGAAGGGAAGGTTGAATGTGTCCATCCGTCTCAGCGAACCCCTTTTGAAG  
TTGAGGCCAAGAAAGGATCTTGTAGAGACCTCTGCAATGAAATGATACATGCCTATTTATTTGTCACTAATAAC  
GACAAAGACCGAGAAAGGCATGGTCCAGAATTTGTAACATATGCATCGCATCAACAGCCTGACTGGAGCCAAAT  
ATAACGGTATACCATACTTTTACGATGAGGTGGATGATGAAATGATACATGCCTATTTATTTGTCACTAATAAC  
CAGCACAGGCCACCGTATTACGGTATGTCAAACGAGCTACTAACAGGGAACCCCTCTGCTCATGACTTTGGTGG  
GCTGAGCACCAGAAAACCTGTGGAGGCACTTACATAAAAAATCAAGGAACAGAGAATTACTCAAAAAAAGGCAAA  
GGAAAGGCAAACTAGGAAAGGAACAGTATTGGCCGAGAGAATAAAGGTACCTTCGTGTATATTCTTCTGATT  
TTTATGTGACCATAGCTATGATGTAAGACAATACTGTCTCAGAGAACTGGTATTAAGATAAACTTAAGGATC  
GTTTCTGGTGTAGAAGTCTTCAAGTGTAGACTTAAGGAAAAATCCCACTGTCCATGAAATGATGGTAGGAAAAC  
AGACTTTGCTCTGTACAGAAGTAAGTAAAAGTAGGAATAGTTCCATGGATATTTTATTTTATTAATCTTTT  
CAGTTTCTTTTATTCAAAGAAAACAAATCTCTGATAATATTTGAGGTAAAGTTCCCTTCCCTATCTTGA  
CTCACTGAGTTATTAGGAAACAGAAAGGCAAAAGATTGTCAAAATAAAACAATAATTCAAGTAACATGCCCGG  
AATATACGTCCTAATACTACCCCTTCTATCAGCTGGATTCTATCCAAGTGAATCTATTGATGTATGTATGTTCA  
TTCAAAGAAATGGGAAAAGGATATGACATATATTTGCCAGTACTTCACTTCAAGATTTACCCTTTTCCCTGTGAAG  
TTCAGAGTTACTGAAGATGCTTCTTCCCTTGGGAAGTTGTTGACCCAAGAACATAGGTTATATTTCCCAATCTT  
TAATTATTGAGTGAAAGAGCTATAGATGAATGATATGGAAAGACCGTATCTTCAATTTTCTGAGTAGAAGGAAA  
GATAAGAAATGAGGCAGCAGATTTTCCCTCCTGGAATTACACATAAAGGACACTAAGCAATTTTCAAGGTAAATGT  
TGCTTGTGTTGGTCTTTGGCATGATAAGATTCTTTATTTAAATATGAGAGAATTTTTTTTATCCTTTATATT  
CTCTCAATATCAGAACTCCTGAATCTGAAGATTGCCCTCCTCCCATTAATAGGATTGTATGGATGAAGATGGA  
ATAAAATACTAGTTCTTCAATTTTGAAGAACTGTACATTAGTTAATGTTTGTACTGTATTTCTTTTGAAGTTGA  
GGCACTTACATAACAATCTTCTTGGCTTTTGGCAGATAAACCAACAGAGGTGAGGCCCAGCTAGTAATCCCT  
TTAGTGGGAAAGGATATGTTCTAGGAGAAACAAGCAATTTACCTTACCTGGGAACTGATCACTTCAATGCC  
ATTAATAAAACCAAGATCTTTTAAATCAAAACCATTACGCAATGCTGTAAGACCTAATCTAAAAACAAGGTG  
AAATTTGAACAGAATGGTTCAAGTAAAAATCTCATCTGGTCTCCCTGCTGTTAGTAACAGTCAACAAATGTT  
CTAAGCAACTACTTTCTAGAGTATCATTTGCCAACCAAAAGGCTTTTCAAGGTGTGAATGGATCTCCAAGGATA  
AGTGTAAACAGTTGGCAACATCCCTAAAACTCAGTCTCTTCTAGTTCTCAGAGAAGGGTTTCTCTTAAGATA  
TCCCTAAGAAATTTCTCAAAAGTAACGGAATCAGCATCTGTGATGCCATCCAGGATGTGAGTGGGTCTGAAGAT  
ACATTCCCAATAAACGACCTAGGCTAGAAGATAAAAAAAA

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## **FIGURE 78**

MDDDLMLALRLQEEWNLQEAERDHAQESLSLVDASWELVDPTPDLQALFVQFNDQFFWGQLEA  
VEVKWSVRMTLCAGICSYEGKGGMCSIRLSEPLLKLRPRKDLVETLLHEMIHAYLFVTNNDKD  
REGHGPEFCKHMRINSLTGANITVYHTFHDEVDEYRRHWWRCNGPCQHRPPYYGYVKRATNR  
EPSAHDYWWAEHQKTCGGTYIKIKEPENYSKKGKGKAKLGKEPVLAENKGTFFVYILLIFM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**N-glycosylation sites.**

amino acids 148-151, 217-220

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 184-187

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 121-124, 154-157, 187-190, 192-195

**Tyrosine kinase phosphorylation site.**

amino acids 211-218

**N-myristoylation sites.**

amino acids 59-64, 85-90, 146-151

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 108-117

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**FIGURE 79**

CGGACGCGTGGGTGGCAACCAGGAGAAGCCAAACTTGGTCCCCCGGCTCGCGGAGTGCCTGCG  
AGCGGTGCTCATGGCGCTCTATGAGGTCTTCTCTCACCCGGTCGAGCGCAGTTACCGCGCGGG  
GCTCTGCTCCAAAGCCGCGCTGTTCCCTGCTGCTGGCCGCTGCGCTCACGTACATCCCGCCGCT  
GCTGGTGGCCTTCCGGAGCCACGGGTTTTGGCTGAAGCGGAGCAGCTACGAGGAGCAGCCGAC  
CGTGCGCTTCCAACACCAGGTGCTGCTCGTGGCCCTGCTCGGACCCGAAAGCGACGGGTTCCT  
CGCCTGGAGCACGTTCCCCGCCTTCAACCGGCTGCAAGGGGATCGCCTGCGCGTCCCGCTCGT  
TTCGACTAGAGAAGAAGACAGGAACCAGGATGGGAAGACGGACATGTTACATTTTAAGCTGGA  
GCTTCCCCTGCAGTCCACGGAGCACGTTCTCGGTGTGCAGCTCATCCTGACTTTCTCCTATCG  
ATTACACAGGATGGCGACCCCTCGTGATGCAGAGCATGGCGTTTCTCCAGTCCTCCTTTCTGT  
CCCGGATCCCAGTTATACGTGAACGGAGACCTGAGGCTGCAGCAGAAGCAGCCGCTGAGCTG  
TGGTGGCCTAGATGCCCGATACAACATATCCGTGATCAACGGGACCAGCCCCCTTGCCTATGA  
CTACGACCTCACCCATATTGTTGCTGCCTACCAGGAGAGGAACGTTACCACCGTCCTGAATGA  
TCCCAACCCCATCTGGCTGGTGGGCGAGGCGCAGATGCTCCATTTGTGATTAATGCTATCAT  
CCGATACCCCTGTGGAAGTCATTTCTTATCAGCCAGGATTCTGGGAGATGGTAAAGTTCGCCTG  
GGTACAGTATGTCAGCATCCTGCTTATCTTCTCTGGGTGTTTGAAAGAATCAAGATCTTCGT  
GTTTCAGAATCAGGTGGTGACCAACCATTCCTGTGACAGTGACGCCCCGGGGAGACTTGTGTAA  
GGAGCACTTATCCTAGAAAGGCCATTTCTGAAGACTCAGCAGGACCGTGGCTGCCTCATTGTC  
ATCTTCTGGGAACATCTTAGGACCTTTTGAAAGAGCCCGAGCGGACACCTGCGGGCTTGTGTGC  
TTTTCCCTCAGAGACAACGGTTCTTTCCGGTTTTGCTCTACACAGTCCGTATCTTCAGAGCT  
CCTGCAGAATTGTCAGGGACTAGTTTGTGGAAAGGTCTGAGAGTTCCTGGAGGTATAATTAG  
CTTTTTGGGTTTTCTTCTTTGCCTTAGCGTTGAATTTTCAGGAGAAAATTGCAGTCAGTTAG  
ACATCTTGGAAGAGTCCCATCTCTGGTCAAGCAGAGACTTTTCTCTGTTGAAGTGAAGAAC  
ACACTGTGCATTTCTTCTTCTGTTGTGAGCCACTCTTACTCTTTTCAGGGCTCTCTTGTGAC  
AAACATGCCAATCACTAGCACTTTGCACCCCTGGGCTTCTCCATTTCCCATTCACAGCTTTGA  
TTTCCAGAGCTGAGGCCCTTAACTGGAGACCTGGAGGGGCGAGGGCCCAAGGGCAAGGGCCGCA  
TTAGCACAGGCAATCAGGGAGGGCCGCTGAAGGACACTTGGACCGTCCACCTGCCCCAGCCCA  
ACAGTCAGTCATCTGTATCAGCTCAGCTGAGCAGCCCTGGATCTTTGCCGTACTGTGACTGG  
GCTCTTTGCCCTATTTTTCCCTCTGTCTGTGCCCCCTGGATGGCAGGCTGAAGTCAGAGGGGCT  
GTTTCATTCTCAGCCCCCTCAGCAGCACTGGGGGAAGAAAGCATTGTCACAACAGGTTCTTTC  
TGGCCCTCACCCAACAGCCTGGGCACTTGGCCCTCCTCCTTGCAGCCCTCCCCCTTCTCT  
GCAAAGGACAGGGGCGACAGGGGTTGGTGTGGGATTGGCTCCCGCTGCCTGACAACCACAAG  
TTTATTTTGAAGGCTAGCGGGAAGCCAGCGGCTGGCGTTTCCCTTGACTAAGGAACAGGGTG  
CCCATCAGAGTGGGGCGGGCAGCTTTGGGAAGGACACAAGAAGCAGTAAGAGTGTAAGAGGA  
TGCTGGCCTGGGCGAGGCCAGTCCAGCCTGGCCACTAGCAGAATACCAAGCAGTCCAGTGGATT  
ACCCTCGTGGCTAAGCAAGTGTCTGCAGGAGCAGAGATGGCTGGAAGGGGCTCTGCACACGG  
AAGATGGCTTGTTTCAGCCCATTACCTCCTGAGGATGTGGGCAGTCTCCTCCAAGAACACATG  
GAGCTGCTTCTGATCCCAAGCAGGTCAATTGCCACTGGAAGGACATGGCCCCGGTGATCCATG  
CTTCATGCCCACCCAGAAACACACCCCTCAGTGTGTGCTCAGTTTACTTTGGAGATCAGTTG  
TCGTTTTTAGTGCTCCTTTAGGCTTACTAAAACAGTTTTGGAAACAAAGCTATTTTGAAGTAT  
TCAAGCAGAGGAATTCCTAACAAGTACCCCCCTTGCTTTTTTTTAAATATTCAGGCTGTTTTAT  
ATGCCTAAATTTTTTCTTAAGATCTAAACGAAAAATAGTTTCTTGTAAATTACATAAGG  
CAATGAGATATGGAAGATGACAAGATACGTATAAACATTGGTTTGCATCTTATTAAATTATT  
CTAATGCAATCTTGTATAAAGAACCCATGATGTTTTGTAACCTTCTAATTAAATGTTCAA  
ATGAG

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## **FIGURE 80**

MALYEVFSHPVERSYRAGLCSKAALFLLAAALTYIPPLLVAFRSHGFWLKRSSYEEOPTVRF  
QHQVLLVALLGPESDGFLAWSTFPAFNRLQGDRLRVPLVSTREEDRNQDGKTDMLHFKLELPL  
QSTEHLVGLVQLILTFSYRLHRMATLVMQSM AFLQSSFPVPGSQLYVNGDLRLQKQPLSCGGL  
DARYNISVINGTSPFAYDYDLTHIVAAYQERNVTTVLNDPNPIWLVGRAADAPFVINAIIRYP  
VEVISYQPGFWEMVKFAWVQYVSILLIFLWVFERIKIFVFQNQVTTIPVTVTPRGDLCKEHL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 268-284

**N-glycosylation sites.**

amino acids 194-198, 199-203, 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 51-55

**Tyrosine kinase phosphorylation site.**

amino acids 250-259

**N-myristoylation site.**

amino acids 187-193

**Cell attachment sequence.**

amino acids 307-310

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**FIGURE 81**

GCCGGGAGCTTCCCTGATGTCGCCGCCGCTCCGAGCCGGGGAGGAGCTGCCAGGGGCCAGCTGGGCAGGAGCCT  
GGGTCCGCTGCTGCTGCTCCTGGCGTTGGGACACACGTGGACCTACAGAGAGGAGCCGGAGGACGGCGACAGAGA  
AATCTGCTCAGAGAGCAAAATCGCGACGACTAAATACCCGTGTCTGAAGTCTTCAGGCGAGCTCACCACATGCTA  
CAGGAAAAAGTGCTGCAAAGGATATAAATTTGTTCTTGGACAATGCATCCCAGAAGATTACGACGTTTGTGCCGA  
GGCTCCCTGTGAACAGCAGTGCACGGACAACCTTGGCCGAGTGTGTGTACTTGTATCCGGGATACCGATATGA  
CCGGGAGAGACACCGGAAGCGGGAGAAGCCATACTGTCTGGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT  
GTGTGCCACATCTGCATCAATACCTTGGGCAGCTACCGCTGCGAGTGCCGGGAAGGCTACATCCGGGAAGATGA  
TGGGAAGACATGTACCAGGGGAGACAAATATCCCAATGACACTGGCCATGAGAAGTCTGAGAACATGGTGAAAGC  
CGAACTTGCTGTGCCACATGCAAGGAGTTCTACCAGATGAAGCAGACCGTGTGAGCTGAAGCAAAAGATTGC  
TCTGCTCCCCAACAAATGCAGCTGACCTGGGCAAGTATATCGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT  
TCCAGGACCTCCTGGCCTGCCTGGGGGCCAGGGCCCTCCCGCTCACCAGGACCAAGGGAAGCCAGGCTTCCC  
CGGTATGCCAGGCCCTCCTGGGCAGCCCGGCCACGGGGCTCAATGGGACCCATGGGACCATCTCCTGATCTGTC  
CCACATTAAGCAAGGCCGGAGGGGCCCTGTGGGTCCACAGGGGCACCAGGAAGAGATGGTTCTAAGGGGGAGAG  
AGGAGCGCCTGGGGCCAGAGGGTCTCCAGGACCCCTGGTTCTTTCGACTTCTGCTACTTATGCTGGCTGACAT  
CCGCAATGACATCACTGAGCTGCAGGAAAAGGTGTTCCGGGCACCGGACTCACTCTCAGCAGAGGAGTTCCCTTT  
ACCTCAGGAATTTCCAGCTACCCAGAAGCCATGGACCTGGGCTCTGGAGATGACCATCCAAGAAGAACTGAGAC  
AAGAGACTTGAGAGCCCCAGAGACTTCTACCCATAGCACATCCCAACACCGTCACGCCAAAGGAAGAGAAAGAT  
CAACTCACCTGCAGTTAAACCATCTAAAGAGAAGAAAGACCACTGGAGACCTAGAAAACATACATTTTTCTCTTC  
TCTTCTCCTGACGTCTCTCCACTCCTCTCTTCCAAATACGATGCTATTTTCAGAGTCCCTCCTAGGCCTGCAG  
ACATGAGGGAGTGAATGATTGATTACCTGCTTCTCACTAAGAGTCCATTGGGGTGGTTTGCATTGTAACTTTTT  
TTTTACATCCTATTTTTCCAGGAACCTTGGATTAAAGTACTCTCACAGTGTCTTAAATCATAAATCTTGAAGTT  
AAATTTGGCAGAGTATCAAAAGGGGAAAATGACAAAGTGAAGTCTAAGAAAATGTGAGGCTACTTCTAAGATGT  
GTGTTCACAATAGACCATAACTCCTCTAGTATCAAAATTTGGGGCTCTTCAGTTAAAAAGGGGTGGGGAGGACAAA  
CGTGTGATGTGCTTTGGTGGAGAATTTTTCTTGTGCTTCTAGTAGACTTTAAATATTGTATCCCTTTGTCAA  
ACCTTGTTTTCCCAAATTCAATTAAGAGAGGAGAGAATTGAATGGCGTTAGAGAAGATAGAAAAGAATCACAGT  
CATATATTTACTGTTATATAGATTGCCACATTCTAAAATTCAAATACGGTGCTTAAGGTTTCATGCCATGCTTAT  
CTGTAAGTATCCTATTTAGGGAAGAGATTAACTCTCTTTTCAAAAAACAAAGTGAAATGCCTGGATTACAT  
TAAACAATGGGCTCTCGTTTGCTATAATATTTTAAAGCTGTTTAAATCAACAGTGGAGTCTGCTCTATAAATATA  
GATTATTTTGTTCATAAACTGGCTGAGCTTAGAGAGAGGTGCAGAATTCCTGGTCTGAGCAGGTGCCCAGAAGG  
TACCATTAGGTGCCATGATCCAGGCTGAACCAATATACAGTGGGGCTGAAGTCTGCAAGGAGGTTGCTGGCTTGG  
GCTGACCTCACTAATGCCATCAGCAGCGGTAGGTAAATTTTTCTCCTTGGGTATTACAAGTTTTTGTCTGGAGC  
CAACCAAGCTTGCCACCAACATATTGAGAGTAATACACTATTGAAAGTTATCTTGGATGGGGAGAAAAAAAATA  
GTGGTTTTCTTGTGTTGCAAAAACCTCCTTCTTCTCATTTTTTCTTAATTTTCTTAATTTAGTCCAAGTTC  
CAGTTCTTTTAGGCCTTCTCTTGATTATTTTTCCCTGCATGTGAGAAGCAGTTTCAGAAAAAGGTCTATATCTC  
CACCTCCTAGTGAGTTAGAGTGTCTCTCAGAGCACCTCTGGGTGGCAAAGGGAAGCATGTTCTGCAAGGTTT  
GCTGTGGATTGAGAAGCACCAGGAGCAAGAGACCAGAAGGATGATCTGCTCCTTTGTAACGTTGTTGAGGGCCCT  
CTTGTTTCCAAATGAGCAGCTTATAGGTTACTCACAGTCCACTTCTCACTGGACACACAAAGTGGCTCTTTATCT  
ACCTTTGCGGGAGATTTTCACTCTCCTGCAAAATGATCGTTCTCACTCATATTAGCTCATGTTGGAATTTCCCA  
TCCTGCCATGTCCTTTCCCATTTCTTTTTGGCTTTTTGCCTCCACCTTTTAGCCACATCATTTAACTCCACTA  
CTGTGAAAGCTGTCTTAAAGAAAATCCCTCTTGGCCGGGTGTGGTAGCCACGCCTCTAATCCCAGCACTTTGGG  
AGGCTGAGGCGGGGAGATCACAAGGTGAGGAGATCGAGACCAGCCTGACCAACATGGTGAAACCCTGTCTCTACT  
AAAAATACAAAAATTAGCTGGGCGTGTGGCACACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA  
TTACTTTAACCTGCGGGGGGAGCCTAGATTGCGCTACTGCACTCCAGCCTAGGCAACAGAGGGAGACTCTGTCTC  
ATTAAAAA

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**FIGURE 82**

MVPPPPSRGGAARGQLGRSLGPLLLLLALGHTWTYREEPEDGDREICSESKIATTKYPCLKSS  
GELTTCYRKKCKCKGYKFVLGQCIPEDYDVCAEAPCEQQCTDNFGRVLCTCYPGYRYDRERHRK  
REKPYCLDIDECASSNGTLCALHICINTLGSYRCECREGYIREDDGKTCTRGDKYPNDTGHEKS  
ENMVKAGTCCATCKEFYQMKQTVLQLKQKIALLPNNAADLGKYITGDKVLASNTYLPGPPGLP  
GGQGPPGSPGPKGSPGFPGMPGPPGQPGPRGSMGPMGSPDLSHIKQGRRGPVGPFGAPGRDG  
SKGERGAPGPRGSPGPPGSFDFLLMLADIRNDITELQEKVFGHRTHSSAEFPLPQEFPSYP  
EAMDLGSGDDHPRRTETRDLRAPRDFYP

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites.**

amino acids 142-148, 182-188

**Tyrosine kinase phosphorylation site.**

amino acids 125-132

**N-myristoylation sites.**

amino acids 10-16, 143-149, 155-161, 196-202, 250-256

**Amidation site.**

amino acids 299-303

**Aspartic acid and asparagine hydroxylation site.**

amino acids 150-162

**Cell attachment sequence.**

amino acids 176-179

**Clq domain proteins.**

amino acids 247-280

**Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 144-165

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**FIGURE 83**

ATCTGAGTGAGCTAACTGACACAATGAAACTGTCAGGCATGTTTCTGCTCCTCTCTCTGGCTC  
TTTTCTGCTTTTTTAACAGGTGTCTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGTTCCAGG  
ACCCAAGGTCTACTGCACTCGGGAATCTAACCACACTGTGGCTCTGATGGCCAGACATATG  
GCAATAAATGTGCCTTCTGTAAGGCCATAGTGAAAAGTGGTGGAAAGATTAGCCTAAAGCATC  
CTGGAAAATGCTTGAGTAAAGCCAATGTTTCTTGGTGACTTGCCAGCTTTTGCAGCCTTCTTT  
TCTCACTTCTGCTTATACTTTTGCTGGTGGATTCCCTTTAATTCATAAAGACATACCTACTCTG  
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGATTCACTTGTCAATAAAGTACATTC  
TGCAAAAGCAAAA



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**FIGURE 84**

MKLSGMFLLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNPHCGSDGQTYGNKCAFCCK  
AIVKSGGKISLKHGPGKC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 26-32, 52-58, 56-62, 69-75

**Kazal serine protease inhibitors family signature.**

amino acids 40-63

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**FIGURE 85**

GGAGCAGACACACAGACCCGGGCGGAGGCCCTCTTCTAGCCCTGCGGGAACCGGACAGTTC  
CCCAACTGGGGACTCTGGAACCACAGCTCCTAAATCATCAAATTCTCAAGCTTTTTTTTTTCC  
TCTCTTCGTCCCAGCCATCCAGTCTTCTTCTTTTTTTTTTTTTTAAGTTATTGTTTTTT  
TCGCTCCTGTCATTATGAAAGTGGTCACGCCATTCAATATTAAGACTTGGAGGGAATTGGGGA  
AAGAAAAGAAAGAATCTAAAAGAAGAGAAGCGACCGGTGCTTTTAAGGGTGTCTAATTTTCAA  
AAGAGACGTCTGGGAGTATTTTGCTCTGGGCGTTTGGAGCAACTTCGCGGACAGCGGAGCTCG  
CCCAGCATGGATGTTCCAGGTTACAGGCGCCTTTCTTCTGAGAACGACCCTGGCCTTGAACG  
TCAGAGCCGGGACGAAGGCCCCCGGAGGCTGCTGCGAGCTCCGCGCGTTCTTCGCGCCCTT  
CCGCGCCGCTCGCGCCGGCGCCGGCCTCCACCCCGCGCGCCGCTCCACAGTCCCGATGC  
AGGCGCCCGGCGGGGGCCACTCGGGCTGCGGCTGATGATGCCCGGGCGCGGGGGGCGCTGC  
GCGAGCCTGGCGGCTGCGGATCCTGCCTGGGGGTGGCGCTGGCCCTGCTGTTGCTGCTACTGC  
CCGCTGCTGCCCCGTGCGGGCGCAGAACGACACGAGGCCATCGTGCTGGAGGGCAAGTGCC  
TGGTGGTGTGCGACTCCAGCCCGTCGGCGGACGGCGCCGTACCTCCTCCCTAGGCATCTCCG  
TGCGCTCCGGCAGCGCCAAGGTGGCCTTCTCCGCCACGCGGAGCACCACGAGCCGTCCG  
AGATGAGCAACCGCACCATGACCATCTATTTTCGACCAGGTATTAGTAAATATTGGCAACCACT  
TTGATCTTGCTCCAGTATATTTGTAGCACCAGAGAAAAGGGATTTATAGCTTCAGCTTCCACG  
TGGTCAAAGTGATAACAGACAAACCATCCAGGTGAGTTAATGCAGAATGGCTACCCAGTGA  
TCTCGGCCTTTGCAGGAGACCAGGATGTCACCAGAGAAGCTGCTAGCAATGGCGTGCTGCTGC  
TCATGGAAAGGGAAGACAAAGTGCATCTCAAACCTTGAGAGAGGCAACCTCATGGGGGGCTGGA  
AATACTCCACATTCTCGGGCTTCTTGGTGTTCCTCTATAAACACAGAGCCCCCTAGATGGTG  
GGGAATGGCAAACCTGGACCCAGGACTCCGCCCTTTAAACACCCCTGAACCTACTGGAATTGG  
ACACCTTGTTTCCAACCTCCGTCAGACTGTTGCACTAGAAGAATGATTTCCCTTTGAAACCTCC  
AGTACTTTTGTGTTTTGTTTTTGGAACTAGTACAAATTCCTCGGGAACCTGGCCTCTAATTAGT  
TTTAGATGACAAGGTCTTAAGGAGAAATGAAATTATCGATTTGAGCAATTTGTACCTGTGATT  
GTAAAGTCAATATCGGATTTTATTGTTGGGACCATGGACCTCTTTTGTGTTGTATGTTGTATTG  
TCGTCCCAACGGAAGGAGAGCTCCTGACTCCAGGATGGGCTGCAGGTTGCAGTCAGGGCTTGA  
AGTAGGAGCCCAGCAAAGAACCACCTGCTGGACAGTCCTTGACATGTGTTCTGTGTGTGCTG  
TATAGCCTTAAGAAAAAGAATGGCTTCACTTTTATTCTGTATTCTTCCCCCACCATGTGGCT  
GGGAGGACTTGGGAGGGGGATGGGGACATTGGGAACCTGTCAAGAAGTGCTTTATCCAGAGAA  
GCAAATTTTGCACGATTGGACTGCAATTTTGTGTTTGTATTGTTTGTGTTTTTCTTGAAAAG  
CTTTACTTTTCTTCCACACTCAGCTCTCCCTCCTCAACCCCACTTTTATTTTTCTTGCTGGG  
GTTGAGGAGAGAAAATATAGAATTCCTGGATAAGACCAAACAAAACAAACATTAAAATACCT  
GTATGTTTTGTTTTAGACGAGACCAAACCTAAACAAAAGTATCTGTTTATCAAAGTAAAAGTA  
ACACAATGGACAATTTCTGCTTATTCTCTCAAAGAGATTCTAAGATGCACCTTTAGAACTATTA  
ATAGCAACCTGCATTTTTTTTTTAATTTATACTTCAGAATCCTTTAAGAACCTGGTGTTCCTGA  
GTGGTCCCTGAATCATATAAGTTGGTAATGGAAGCTGTAATGACCAAGTCCCTAAACATACTA  
TGTCTTTGCCACGTGTGCTGTGACTTCTCTGTGGGTGATTTAATTTATTTGGATCCACCTCTG  
AGTGAGCGCACAGTGATCAGGTGCTTCAAAGCCAACAGACCAGCTCCTCTTCCCTCCGGATCCT  
CTTTTGATCTGCCCAGGAAAGGGATGCATTGACACTCTCCTGCATGCACCTGGCGAGAAGCCA  
CCTGAAAGTCACTGTGGTTAAAGATATTGGTGGAGGTACCCAGGAGCACTGTTACAAATCCT  
TCTTGTTTTGGCATCTCGTACAACATTATTAAGACACAGCTGAGAGTTGATGGGTGTGTAATG  
CATATGCCAAGGAAATGTCATAATCCCAAAGCAATCAAAAAGGAGACCTCAAACCAGATGTT  
AATTTGTTCTTTGTGTAACAATGTAACCAAAATATTGATGATAAAAGTCATAATTTAAGATT  
AGAATAAATGGGTTTGATGTCTGGCAAAAAAAAAAAAAA

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## **FIGURE 86**

MQAPGRGPLGLRLMMPGRRGALREPGGCGSCLGVALALLLLLPACCPVRAQNDTEPIVLEGK  
CLVVCDSPPSADGAVTSSLGISVRSWSAKVAFSATRSTNHEPSEMSNRTMTIYFDQVLVNIGN  
HFDLASSIFVAPRKGIIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQDVTREAASNGVL  
LLMEREDKVHLKLERGNLMGGWKYSTFSGFLVFPL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-48

#### **N-glycosylation sites.**

amino acids 53-57, 110-114

#### **N-myristoylation sites.**

amino acids 26-32, 27-33, 29-35, 33-39, 76-82, 205-211

#### **Amidation site.**

amino acids 16-20

#### **Clq domain signature.**

amino acids 117-148

#### **Clq domain proteins.**

amino acids 115-149

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**FIGURE 87**

AGGGCCCCGCGGGTGGAGAGAGCGACGCCCGAGGGGATGCGGGCAGCGTCCCGGAGCGCCTCTG  
GCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGGCTCCGGCGTCTTCC  
AGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGCCTTGCGAGC  
CCGGCTGCCGGAATTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTCTGCTCGCCCCGAC  
CCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCGGGACG  
ACAGTAGCGGGCGGGGGCGCAACCCTCTCCAAGTGCCTTCAATTTACCTGGCCGGGTACCT  
TCTCGCTCATCATCGAAGCTTGGCACGCGCCAGGAGACGACCTGCGGCCAGAGGCCTTGCCAC  
CAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGAGAACTGGTTAT  
TGGATGAGCAAACCAGCACCCCTCACAAGGCTGCGCTACTCTTACCGGGTCATCTGCAGTGACA  
ACTACTATGGAGACAACTGCTCCCGCCTGTGCAAGAAGCGCAATGACCACTTCGGCCACTATG  
TGTGCCAGCCAGATGGCAACTTGTCTGCTGCGCGGTTGGACTGGGGAATATTGCCAACAGC  
CTATCTGTCTTTCCGGGCTGTCTGAACAGAATGGCTACTGCAGCAAGCCAGCAGAGTGCCTCT  
GCCGCCAGGCTGGCAGGGCGGCTGTGTAACGAATGCATCCCCACAATGGCTGTGCGCCACG  
GCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGGCCTGTTTTGTGACC  
AAGATCTCAACTACTGCACCCACCACTCCCATGCAAGAATGGGGCAACGTGCTCCAACAGTG  
GGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTGGACTGTGAGCTGGAGC  
TCAGCGAGTGTGACAGCAACCCTGTGCGAATGGAGGCAGCTGTAAGGACCAGGAGGATGGCT  
ACCACTGCCTGTGTCTCCGGGCTACTATGGCCTGCACTGTGAACACAGCACCTTGAGCTGCG  
CCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAACCAGGGGGCCAATATGCTT  
GTGAATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAGAAAGTGGACAGGTGCACCAGCA  
ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGCATGTGCCGCTGCCGTC  
CTGGATTACGGGCACCTACTGTGAATCCACGTCAGCGACTGTGCCCGTAACCTTGCGCCC  
ACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTGCACCTGCCCTGCCGGCTTCTCTG  
GCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTGCCTCGAGTCCCTGCTTCAACAGGG  
CCACCTGCTACACCGACCTCTCCACAGACACCTTTGTGTGCAACTGCCCTTATGGCTTTGTGG  
GCAGCCGCTGCGAGTTCCCCGTGGGCTTGCCGCCAGCTTCCCCTGGGTGGCCGTCTCGCTGG  
GTGTGGGGCTGGCAGTGCTGCTGGTACTGCTGGGCATGGTGGCAGTGGCTGTGCGGCAGCTGC  
GGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCCATGAACAACTTGTCCGACTTCCAGAAGG  
ACAACCTGATTCTGCGCCCGAGCTTAAAAACACAAACCAGAAGAAGGAGCTGGAAGTGGACT  
GTGGCCTGGACAAGTCCAAGTGTGGCAAACAGCAAAACCACACATTGGACTATAATCTGGCCC  
CAGGGCCCCTGGGGCGGGGGACCATGCCAGGAAAGTTTCCCCACAGTGACAAGAGCTTAGGAG  
AGAAGGCGCCACTGCGGTTACACAGTGAAAAGCCAGAGTGTGGATATCAGCGATATGCTCCC  
CCAGGGACTCCATGTACCACTGTGTGTGTTGATATCAGAGGAGAGGAATGAATGTGTCAATTG  
CCACGGAGGTATAAGGCGAGGAGCCTACCTGGACATCCCTGCTCAGCCCCGCGGCTGGACCTTC  
CTTCTGCATTGTTTACA

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**FIGURE 88**

MAAASRSASGWALLLLVALWQORAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCLK  
HFQAVVSPGPCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG  
DDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSTLRLRYSYRVICSDNYYGDNCSRLCK  
KRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGRCLNE  
CIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTCTCRPG  
YTGVDCELELSECDSPCRNNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCR  
ERNQGANYACECPPNFTGNSNCEKKVDRCTSNPCANGGQCLNRGPPSRMCRCPGFTGTYTELV  
SDCARNPCAHHGGTCHDLENGLMCTCPAGFSGRRCEVRTSIDACASSPCFNRTATCYTDLSTDTF  
VCNCPYGFVGSRCFPPVGLPPSPFWVAVSLGVGLAVLLVLLGMVAVAVRQLRLRPDDGSREA  
MNNLSDFQKDNLI PA AQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTMPGK  
FPHSDKSLGEKAPLRLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIATEV

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 530-552

**N-glycosylation sites.**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

**Glycosaminoglycan attachment site.**

amino acids 96-100

**Tyrosine kinase phosphorylation site.**

amino acids 340-347

**N-myristoylation sites.**amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,  
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

**Aspartic acid and asparagine hydroxylation site.**

amino acids 339-351

**EGF-like domain cysteine pattern signature.**amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,  
388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,  
449-470

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**FIGURE 89**

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGAC  
TTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGC  
CGCCCAGTCCCGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCCTGTTTTACTCC  
TCCTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCC  
GAGCGTGGAAGAAATGGGGTTCCCTCGGGACCGGCACTTGGAATTCTGGTGTTAGTGCTCCCGATT  
CAAGCTTTCCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCA  
GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAACATATCCT  
CCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTGATAACTTGAACTGCTAAAGGCA  
ATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT  
AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGATTATGACTCT  
ACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG  
ACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC  
AGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA  
GCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAAC  
AATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA  
GAGAAAGTGAATCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA  
GTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGAC  
AACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAA  
AAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG  
ATGATGGTGAAATATGGAACAATATCTECAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGAT  
GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAATGCTACTGACAATATAAGCAAG  
CTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT  
AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAAGATGATAACTCAACCCAGGA  
GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGCCATCAGAAAAAATATT  
GAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGA  
GACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC  
GAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAAC  
TGTTTCAGAAAACATAATATAGCTTAAAACACTTCTAATTCTGTGATTAAATTTTTTGACCC  
AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAACATAGC  
TTTCTTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 90**

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK  
PGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSG  
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL  
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNT  
LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK  
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEK  
EYGLKDKSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDL SKMRDFIN  
KQADAYVEKGILDKEEAIAIKRIYSSL

**Important features:****N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390**N-myristoylation sites:**

amino acids 143-148, 239-244

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**FIGURE 91**

TGCATCAGTGCCCAGGCAAGCCCAGGAGTTGACATTTCTCTGCCCAGCCATGGGCCTCACCCCT  
GCTCTTGCTGCTGCTCCTGGGACTAGAAGGTCAGGGCATAGTTGGCAGCCTCCCTGAGGTGCT  
GCAGGCACCCGTGGGAAGCTCCATTCTGGTGCAGTGCCACTACAGGCTCCAGGATGTCAAAGC  
TCAGAAGGTGTGGTGCCGGTTCTTGCCGGAGGGGTGCCAGCCCCTGGTGTCTCAGCTGTGGA  
TCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGGGGCCTGCTGCAGGT  
GGAAATGGTTACCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGGCCAG  
GGGGCCCCAGATTTTGCACAGAGTCTCTCTGAACATACTGCCCCCAGAGGAAGAAGAAGAGAC  
CCATAAGATTGGCAGTCTGGCTGAGAACGCATTCTCAGACCCTGCAGGCAGTGCCAACCCTTT  
GGAACCCAGCCAGGATGAGAAGAGCATCCCCTTGATCTGGGGTGCTGTGCTCCTGGTAGGTCT  
GCTGGTGGCAGCGGTGGTGCTGTTTGCTGTGATGGCCAAGAGGAAACAAGAATCCCTCCTCAG  
TGGTCCACCACGTCAGTGACTCTGGACCGGCTGCTGAATTGCCTTTGGATGTACCACACATTA  
GGCTTGACTCACCACCTTCATTTGACAATACCACCTACACCAGCCTACCTCTTGATTCCCCAT  
CAGGAAAACCTTCACTCCCAGCTCCATCCTCATTGCCCCCTCTACCTCCTAAGGTCCTGGTCT  
GCTCCAAGCCTGTGACATATGCCACAGTAATCTTCCCGGGAGGGAACAAGGTGGAGGGACCT  
CGTGTGGGCCAGCCCAGAATCCACCTAACAATCAGACTCCATCCAGCTAAGCTGCTCATCACA  
CTTTAAACTCATGAGGACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTA  
GGATCCTTAGGATATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCCTAACTTTACT  
AGGGAAAGTGACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCC  
CCCACTGGTTCTTCTACCATTACACACTGGGCTAAATAAACCTAATAATGATGTGCAAAAAA  
AA



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**FIGURE 92**

MGLTLLLLLLLLGLEGGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQPLV  
SSAVDRRAPAGRRFTLTDLG GLLQVEMVTLQEEDAGEYGCMVDGARGPQILHRVSLNILPPE  
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFAVMAKRKQ  
ESLLSGPPRQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 161-181

**N-myristoylation sites.**

amino acids 17-23, 172-178

**Amidation site.**

amino acids 73-79

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**FIGURE 93**

GGCGGCGTTGCCGGGCTCTCCGGAAGGAGACGTGGCGGCGGTTGGGCGGTTGATACCCGGGCG  
CTTTATAGTCCC GCCCCTCCTCCTCCACCTCCTCCTCCTCCTCCTCCTGCGGCGAGAG  
GAGGTTGTGGCGGTGGCTGGAGAAAGCGGCGGCGGAGGATGGAGGAAGGAGGCGGCGGCGTAC  
GGAGTCTGGTCCCGGGCGGGCCGGTGTTACTGGTCCTCTGCGGCCTCCTGGAGGCGTCCGGCG  
GCGGCCGAGCCCTTCTCAACTCAGCGATGACATCCCTTTCCGAGTCAACTGGCCCGGCACCG  
AGTTCTCTCTGCCACAACCTGGAGTTTTATATAAAGAAGATAATTATGTCATCATGACAACCTG  
CACATAAAGAAAAATATAAATGCATACTTCCCTTGTGACAAGTGGGGATGAGGAAGAAGAAA  
AGGATTATAAAGGCCCTAATCCAAGAGAGCTTTTGGAGCCACTATTTAAACAAAGCAGTTGTT  
CCTACAGAATTGAGTCTTATTGGACTTACGAAGTATGTCATGGAAAACACATTCGGCAGTACC  
ATGAAGAGAAAGAACTGGTCAGAAAATAAATATTCACGAGTACTACCTTGGGAATATGTTGG  
CCAAGAACCCTTCTATTTGAAAAAGAACGAGAAGCAGAAAGAAAGGAAAAATCAAATGAGATTC  
CCACTAAAAATATCGAAGGTGAGATGACACCATACTATCCTGTGGGAATGGGAAATGGTACAC  
CTTGTAGTTTGAACAGAACCGGCCCGAGATCAAGTACTGTGATGTACATATGTCATCCTGAAT  
CTAAGCATGAAATTCTTTAGTAGCTGAAGTTACAACCTGTGAATATGAAGTTGTCATTTTGA  
CACCCTCTTGTGCAGTCATCCTAAATATAGGTTTCAAGCATCTCCTGTGAATGACATATTTT  
GTCAATCACTGCCAGGATCTCCATTTAAGCCCTCACCCTGAGGCAGCTGGAGCAGCAGGAAG  
AAATACTAAGGGTGCCTTTTAGGAGAAATAAAGAGGGTGTGCGTTGGTGGAAATATGAATTCT  
GCTATGGCAAACATGTACATCAATACCATGAGGACAAGGATAGTGGGAAAACCTCTGTGGTTG  
TCGGGACATGGAACCAAGAAGAGCATATTGAATGGGCTAAGAAGAATACTGCTAGAGCTTATC  
ATCTTCAAGACGATGGTACCCAGACAGTCAGGATGGTGTACATTTTATGGAAATGGAGATA  
TTTGTGATATACTGACAAACCAAGACAGGTGACTGTAAACTAAAGTGCAAAGAATCAGATT  
CACCTCATGCTGTTACTGTATATATGCTAGAGCCTCACTCCTGTCAATATATTCTTGGGGTTG  
AATCTCCAGTGATCTGTAAATCTTAGATACAGCAGATGAAAATGGACTTCTTTCTCTCCCCA  
ACTAAAGGATATTAAAGTTAGGGGAAAGAAAAGATCATTGAAAGTCATGATAATTTCTGTCCC  
ACTGTGTCTCATTATAGAGTTCTCAGCCATTGGACCTCTTCTAAAGGATGGTATAAAATGACT  
CTCAACCACTTTGTGAATACATATGTGTATATAAGAGGTTATTGATAAACTTCTGAGGCAGAC  
ATTTGTCTCGCTTTTTTTTCATTTTTGTGTGTCTTATAAACTGACTGTTTTTCTTTGCTTGGA  
TACTGTGATTCCAAAATAAATCTCATCCAAGCAAGTTAGAGTCCAGCCTAATCAAATGTCATA  
ATTGTTGTACCTATTGAAAGTTTTTAAATAATAGATTTATTATGTAAATTATAGTATATGTAA  
GTAGCTAATGAAGTAAAGATCATGAAGAAAGAAATTGATAGGTGTAAATGAGAGACCATGTAA  
AATATGTAAATTCTAGTACCTGAAATCCTTTCAACAGATTTTTATATAGCAACTGCTCTCTGC  
AAGTAGTTAAACTAGAACTGGGCACATGGTAGAGGCTCACATGGGAGTTGTCCTCACCCTTG  
TTAATCTCAAGAACTCTTATTTATAATAGGTTGCTTCTCTCTCAGAACTTTTATCTATTACT  
TTTTTCTTCTTATGAGTATGTTTACTCTCAGAGTATCTATCTGATGTAGACAGTTGGTGATGC  
TTCTGAGACTCAGAATGGTTTACTCTAACAAAACACTGTGCTGTCTATCCCTTGTACTTGCCCT  
ACTGTAATATGGATTTCACTTCTGAACAGTTTACAGCACAATATTTATTTTAAAGTGAATAAA  
ATGTCCACAAGCAAAAA

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**FIGURE 94**

MEEGGGGVRS LVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGVLYKE  
DNYVIMTTAHKEKYKCILPLVTSGDEEEEEKDYKGNPRELLEPLFKQSSCSYRIESYWTYEVC  
HGKHIRQYHEEKETGQKINIHEY YLG NMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMT PYY  
PVGMGNGTPCSLKQNRPRSSTVMYICHPE SKHEILSVAEVTTC EYEVVILTPLLCSHPKYRFR  
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVFRRNKEGVGWKYEFCY GKHVHQYHEDK  
DSGKTSVVVGTWNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYNGD IC DITDKPRQVTV  
KLKCKESDSPHAVTVYMLPHSCQYILGVESPVICKILDTADENGLLSLPN

**Important features of the protein:****Signal peptide:**

amino acids 1-30

**Glycosaminoglycan attachment site.**

amino acids 28-32

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 337-341

**N-myristoylation sites.**amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,  
196-202**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 54-60

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**FIGURE 95**

TTCCGTTTCTGGGAGGAGTGAGGGGCAACGGGTCTGGAGAAAAAGGAAAAAGAAGGGCTCAGC  
GCCTCCCCGCCGGGCGGTGGACAGAGGGGCACAGTTTCGGCAGGCGGGTGAGGTCGCTGAGGG  
CCCGCCGGAGATGTTTTTCTTGTGCGAGCACGGTGCAACCCAGGTTACAGTTCCTCTGAGTCA  
TCTCATCAATGCCTTCCATACACCAAAAAACACTTCTGTTTCTCTCAGTGGAGTGTGAGTTTC  
TCAAACCCAGCATCGAGATGTAGTTCCTGAGCATGAGGCTCCAGCAGTGAACCTTCACTTAA  
CTTAAGGGACCTTGGATTATCTGAACTAAAAATTGGACAGATTGATCAGCTGGTAGAAAATCT  
ACTTCCTGGATTTTGTAAGGCAAAAAACATTTCTTCCCATTGGCATAACATCCCATGTCTCTGC  
ACAATCCTTCTTTGAAAATAAATATGGTAACCTTAGATATATTTAGTACATTACGTTCCCTCTTG  
CTTGATCGACATCATTCAAGAGCTCTTCAAAGCATTTGTTTCAGATCTTCAGTACTGGCCAGT  
TTTCATACAGTCTCGGGGTTTTAAAACTTTGAAATCAAGGACACGACGTCTCCAGTCTACCTC  
CGAGAGATTAGCTGAAACACAGAATATAGCGCCATCATTCGTGAAGGGGTTTTCTTTTGCAGGA  
CAGAGGATCAGATGTTGAGAGTTTGGACAAACTCATGAAAACCAAAATATACCTGAAGCTCA  
CCAAGATGCATTTAAAACTGGTTTTGCGGAAGGTTTTCTGAAAGCTCAAGCACTCACACAAAA  
AACCAATGATTCCCTAAGGCGAACCCGTCTGATTCTCTTCGTTCTGCTGCTATTCCGCATTTA  
TGGACTTCTAAAAAACCCATTTTTATCTGTCCGCTTCCGGACAACAACAGGGCTTGATTCTGC  
AGTAGATCCTGTCCAGATGAAAAATGTCACCTTTGAACATGTTAAAGGGGTGGAGGAAGCTAA  
ACAAGAATTACAGGAAGTTGTTGAATTCTTGAATAATCCACAAAAATTTACTATTCTTGGAGG  
TAAACTTCCAAAAGGAATTCTTTTAGTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCG  
AGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTATGCTTCTGGATCCGAATTTGATGAGAT  
GTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAGCAAAGGCGAATGCTCC  
TTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCAATGCA  
TCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATGA  
AGGAGTTATCATAATAGGAGCCACAACTTCCAGAGGCATTAGATAATGCCTTAATACGTCC  
TGGTCGTTTTTGACATGCAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTGCAACAGAAATTTT  
GAAATGGTATCTCAATAAAATAAAGTTTGTATCAATCCGTTGATCCAGAAATTATAGCTCGAGG  
TACTGTTGGCTTTTCCGGAGCAGAGTTGGAGAATCTTGTGAACCAGGCTGCATTAAAAGCAGC  
TGTGATGGAAAAGAAATGGTTACCATGAAGGAGCTGGAGTTTTCCAAAGACAAAATTCTAAT  
GGGGCCTGAAAGAAGAAGTGTGGAATTGATAACAAAAACAAAACCATCACAGCATATCATGA  
ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT  
CATGCCACGGGGGCCAACACTTGGACATGTGTCCCTGTTACCTGAGAATGACAGATGGAATGA  
AACTAGAGCCCGAGCTGCTTGACAAAATGGATGTTAGTATGGGAGGAAGAGTGGCAGAGGAGCT  
TATATTTGGAACCGACCATATTACAACAGGTGCTTCCAGTGATTTTGATAATGCCACTAAAAT  
AGCAAAGCGGATGGTTACCAAATTTGGAATGAGTGAAAAGCTTGGAGTTATGACCTACAGTGA  
TACAGGGAACTAAGTCCAGAAACCAATCTGCCATCGAACAAGAAATAAGAATCCTTCTAAG  
GGACTCATATGAACGAGCAAAACATATCTTGAAAACCTCATGCAAGGAGCATAAGAATCTCGC  
AGAAGCTTTATTGACCTATGAGACTTTGGATGCCAAAGAGATTCAAATTGTTCTTGAGGGGAA  
AAAGTTGGAAGTGAGATGATAACTCTCTTGATATGGATGCTTGCTGGTTTTATTGCAAGAATA  
TAAGTAGCATTGCAGTAGTCTACTTTTACAACGCTTTCCCTCATTTCTTGATGTGGTGTAATT  
GAAGGGTGTGAAATGCTTTGTCAATCATTTGTACATTTATCCAGTTTGGGTATTCTCATT  
TGACACCTATTGCAATTAGCATCCCATGGCAAATATATTTGAAAAATAAAGAATATCAG  
GATTGAAAACAAAAA

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**FIGURE 96**

MFSLSSTVQPQVTVPLSHLINAFTPKNTSVSLSGVSVSQNQHRDVPPEHEAPSSEPSLNLRD  
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFFENKYGNLDIFSTLRSSCLYR  
HHSRALQSICSDLQYWPVFIQSRGFKTLKSRTRRLQSTSERLAETQNIAPSFVKGFLLRDRGS  
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDSLRRTRLILFVLLFGIYGLL  
KNPFLSVRFRTTTGLDSAVDPVQMKNVTFEHVKGVEEAKQELQEVVEFLKNPQKFTILGGKLP  
KGILLVGPPGTGKTLLARAVAGEADVPFYYASGSEFDEMFGVGASRIRNLFREAKANAPCVI  
FIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKPNEGVIIGATNFBREALDNALIRPGRF  
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPEIIARGTVGFGAELENLVNQAALKAADV  
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAIAYYTKDAMPINKATIMPR  
GPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITTGASSDFDNATKIAKR  
MVTKFGMSEKLGVMTYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEAL  
LTYETLDAKEIQIVLEGKKLEVR

**Important features of the protein:****Transmembrane domain:**

amino acids 238-259

**N-glycosylation sites.**amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,  
623-627**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

**Amidation site.**

amino acids 387-393, 709-713

**ATP/GTP-binding site motif A (P-loop).**

amino acids 322-330

**AAA-protein family proteins**

amino acids 315-336, 343-386, 405-451

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**FIGURE 97**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCCAA  
ACAAGTTTGTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCAGTGAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACCTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAATAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 98**

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR  
ILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTELRKISSLANSELTIKKDLRLC  
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAADVVKALGELDILLQWMEETE

**Signal sequence:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 107-110, 140-143

**N-myristoylation site.**

amino acids 51-56

**Interleukin 10:**

amino acids 9-176

**FIGURE 99**

[illegible]



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## **FIGURE 100**

MRLLEWFLLLFGPWLLRKAVSAQIPESGRPQYLGLRPAAAGAGAPGQQLPEPRSSDGLGVGR  
AWSAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLLVTG  
KIVDHVNGTF SVYFRHNSSSLGNLSVSIVPPSKRVEFGGVWLPGPVPHPLQSTLALEGVLPGL  
GPPLGMAAAAAGPGLGGSLLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHRPCLYD  
PSQVCFTHTQSQAAWLCAKPFKVICIFVSFLSFDYKLVQKVC PDYNFQSEHPYFG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 273-288

**N-glycosylation sites.**

amino acids 72-76, 133-137, 143-147, 149-153

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,  
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230

**Cytochrome b/b6 Qo site signature.**

amino acids 5-11

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**FIGURE 101**

AATGCCCCATGCGCACCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTTCCTCCGATG  
GCGTCCGGCCTCAGCCCTCTTCTCCCCATCAGGGGCAGTGCCACGTCTTTGGAGCTGCAGC  
GAGGGACGGATGGCGGAACCCTCCAGTCCCCTTCAGAGGCGACTGCAACTCGCCCGCCGTGC  
CTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCTGGGAATAGGACTGTGG  
ACCTCTTCCCAGTCTTACCGATCTGTGTCTGTGACTTGACTCCTGGAGCCTGCGATATAAATT  
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTTCTCCTTCTGCCTTCCAG  
GCAGCGTAAGGTCTTCAAGCTGGGTTTGTGTAGACAACTCTGTTATCTTCAGGAGTAATTCCC  
CGTTTTCTTCAAGAGTTTTTCATGGATTCTAATGGAATCAGGCAGTTTTGTGTCCATGTGAACA  
ACTCAAACCTTAACTATTTCCAGAAGCTTCAAAGGTCAATGCAACCAACTTCCAGGCCCTGG  
CTGCAGAGTTTGGAGGCGAATCATTCACTTCAACATTCCAACTCAATCACCACCATCTTTTT  
ACAGGGCTGGGGACCCATTCTTACTTACTTCCCCAAGTGGTCTGTAATAAGCTTGCTGAGAC  
AACCTGCAGGAGTTGGAGCTGGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTTCCTAGAGA  
GTAAAAGTACAACCTGCACTCGTTTTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTTCAG  
CCCTCAATGCTGCCTCTTACTATAACTTCACAGTCTTAAAGGTTCCAAGAAGCATGACTGATC  
CACAGAATATGGAGTTCAGGTTCTGTAATACTTACCTCACAGGCTAATGCTCCTCTGTTGG  
CTGGAAACACTTGTGAGAATGTAGTTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTT  
TTGGAATCCAGAAAGTTTTCTGTCAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTT  
CCTTACAGCAACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCA  
CCAGTCCTAGAAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATG  
ATATAAGTTACTCAATGACCCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTTAAAAGAC  
ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAGACT  
GCAGCCACTTGCAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCAGACCAGAGTATGTTG  
CCATCTTTGGTAATGCTGACCCAGCCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGCACT  
GCAGCATTTTCAGCTATAAACTGTACTTCCTGCTGTCTCATACCAGTTTCCCTGGAGATCCAGG  
TATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTATCAGGAGTTTCGATTCC  
TATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAGTATCTTTGACAACCTCTTG  
TGAACCTTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGGGCCAACCCTAAATGGACTGGA  
AATGGCCATTTCGACTTCTTTCCCTTCAAAGTGGCATTTCAGCAGAGGAGTATTCTCTCAAAAAT  
GCTCAGTCTCTCCCATCCTTATCCTGTGCCTCTTACTACTTGAGTTCTCAACCTAGAGACTA  
TGTGAAGAAAAGAAAATAATCAGATTTTCAGTTTTCCCTATGAGAACTCTGAGGCAGCCACTT  
ATCTTGGCTAAATAGAACCTCACCTGCTCATGACCAGAGAGCATTTAGGATAATAGATGACCT  
AACTGAAGGAATCCTTGTATATGAAAGGAGTATTTTAGAAAAGCAATAAAAATATTTTATTC  
ATCNTAAAAAAAAA

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**FIGURE 102**

MRTPLQALLQVFFLVFPDGVPRQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRPVPG  
PTVVPTLVTPSAPGNRTVDLFPVLPICVCDLTPGACDINCCDRDCYLLHPRTVFSFCLPGSV  
RSSSWVCVDNSVIFRSNSPFPSRVFMDNGIRQFCVHVNNNSLNLYFQKLQKVNATNFQALAAE  
FGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS  
TTCTRFFKNLASSCTLDSALNAASYNFTVLKVP RSMTDPQNMEFQVPVILTSQANAPLLAGN  
TCQNVVSQVTYEIETNGTFGIQKVSVSEGQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP  
RSGNPGYIVGKPLLALTDDISYSMTLLQSQNGSCSVKRHEVQFGVNAISGCKLRLKKADCSH  
LQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW  
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTTLVNFDITQKPQPPRGQPKMDWKWP  
FDFFPFKVAFSRGVFSQKCSVSPILILCLLLLGVNLNLETM

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 484-505, 581-600

**N-glycosylation sites.**amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,  
410-414, 487-491**N-myristoylation sites.**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 420-431

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**FIGURE 103**

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGGAGCCATGTGGGAT  
TAAGAAGTGATAGGAGAGCTTGCTGTCTGTCTCTGCTCTCCACTGTGTGAGGATACAACAGGA  
AGACAGCCATCTGGTGAGGAAGAGAGGGCCCTCGCCAGATAACCGGACCTGCTGACACCTTGAT  
CTTGGA CT TCCCATCTTCCAGGAAGGCCTGACCTCAGTTGTTCCAGGGTAAAGAATTTGGGCA  
GTGCCCACACCCACGCTGTTGGATAACATTTCTTCACCATAACCAGTGAGGGTGAATGTGTACA  
CGCCCAGCTTCCTGCCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG  
TGCGCCTTCTTTTGTTCCTGCTGTTGCTACTAATAGCCTTGAGATCATGGTTGGTGGTCACT  
CTCTTTGCTTCAACTTCACTATAAAAATCATTTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGC  
AGGTCTTCTTGAATAAAAATCTTTTCCCTTCAGTACAACAGTGACAACAACATGGTCAAACCTC  
TGGGCCTCCTGGGGAAGAAGGTATATGCCACCAGCACTTGGGGAGAATTGACCCAAACGCTGG  
GAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTG  
ATCCTTCCACTCTGCAAGTCGAGATGTTTTGTCAACGTGAAGCAGAACGGTGCACTGGTGCAT  
CCTGGCAGTTCCGCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGA  
CAGTAATTAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAA  
AGTATTTTCAAGGAAGCTCTCAAAGGGAGACTGCGATCACTGGCTCAGGGAATTCTTAGGGCACT  
GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACCTAGAGGTGATACCACGGCGGCGCAG  
AGTTGTTACCTGTGGTCCTCGATCGCTGACAGCCTTGCTCCCACTGCTGTGTGTTCCCTGA  
GTCAAGTGGAGGCGGAGCCTGCAATGAGCGGAGATCGCGCCTCTGCATTCCAGTCTTGGAAC  
AGAGCAAGACTCCGTCTCAAAAAAAAAAATTTTTTTTTCAGTACATATTTTTTAAAGATAGG  
GCTGGGCACAGCAGCTCACATCTATAATCCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC  
TTGAGCCCAGGAATCTGAAGCTGCAGTGAGCCTTTGCTCGTGAGATTGTGGACCTATGATCCT  
ACCACCAGCCCACCTGGTTCTAACACCCCCTCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG  
AGGGAGAAAAGAGAGATAAGCAAAGAACAGAGAGGAAAAATGGAAAATAAGAGGAAATTGGGG  
GAATTAAACAGAGGGGAGGGCATGGATCCCCGGGAGTTAGAAGAGTAGCAGCTTGTGGATTAC  
TACGCAGTGGAGGAAGAAGAGTTGTTGGAAATTATTTGAGAGGTAGTATAATCATTTGTGAGG  
CAGTTTTCTGCATTCACCATTTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTCACA  
TTACACTGAAATTCTTCCCTAATACATCATTTGCATTGGAATAAAGTACGGTTTTTCAAACAAC  
CTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTCTTTGTTTGT  
TGTTTGTTTTTTTTGGAGACAGAGTCTCACTCTATCTCCAGGCTGGAGTGTAGTGGTGCATCC  
CGGCTCACTGCAACCTCGATCTCCAGGCTCAAGCGATTCCCCTGCCTCAGCCTCCTGAGTAG  
CTGGGATTACAGGCATGAGCCACCACGCCCCGCTAATTTTTGTATTTTTAGTAGAGACGGGGT  
TTCACCCTGTTGGCCAGGCTGGTCTCGAACTACGGACCTCAGGTGATCTGCCCCCTCAGCCT  
CTCAAAGTGCTGGGATTATAGCATGAGCCACTGAGCCCAGACACAAGTAGTTCTTTCTGATAA  
ACACTTTAACA CTGAATGCA

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## **FIGURE 104**

MRRISLTSSPVRLLLFLLLLLLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKNLFLQ  
YNSDNNMVKPLGLLGKKVYATSTWGELTQTLGEVGRDLRMLLCDIKPQIKTSDPSTLQVEMFC  
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGDC  
DHWLREFLGHWEAMPEPTGRRST

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 11-30 (possible type II protein)

**N-glycosylation site.**

amino acids 36-39, 154-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-5, 182-185, 209-212

**Casein kinase II phosphorylation site.**

amino acids 86-89, 93-96, 142-145, 185-188

**N-myristoylation site.**

amino acids 46-51

**Amidation site.**

amino acids 77-80, 207-210

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**FIGURE 105**

TTTTCCGAGTGACCTTCTTGATGCTGGCTGTTTCTCTCACCGTTCCCCTGCTTGGAGCCATGA  
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTTCAAAGAACCCCCGCTCTTGCTTG  
GTGTTCTGCATCCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTTGAAAATCAACTTGTTG  
GACCGGAGTCCATAGCACATATTGGGGATGTGATGTTTACTGGGACAGCAGATGGCCGGGTCTG  
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCCGGTTTGGTTCGGGCCCCTTGCAAACCC  
GAGATGATGAGCCTGTGTGTGGGAGACCCCTGGGTATCCGTGCAGGGCCCAATGGGACTCTCT  
TTGTGGCCGATGCATACAAGGGACTATTTGAAGTAAATCCCTGGAAACGTGAAGTGAACTGC  
TGCTGTCCTCCGAGACACCCATTGAGGGGAAGAACATGTCCTTTGTGAATGATCTTACAGTCA  
CTCAGGATGGGAGGAAGATTTATTTACCGATTCTAGCAGCAAATGGCAAAGACGAGACTACC  
TGCTTCTGGTGATGGAGGGCACAGATGACGGGCGCCTGCTGGAGTATGATACTGTGACCAGGG  
AAGTAAAAGTTTTATTGGACCAGCTGCGGTTCCTGAATGGAGTCCAGCTGTCTCCTGCAGAAG  
ACTTTGTCCTGGTGGCAGAAACAACCATGGCCAGGATACGAAGAGTCTACGTTTCTGGCCTGA  
TGAAGGGCGGGGCTGATCTGTTTGTGGAGAACATGCCTGGATTTCCAGACAACATCCGGCCCCA  
GCAGCTCTGGGGGGTACTGGGTGGGCATGTCGACCATCCGCCCTAACCCTGGGTTTTCCATGC  
TGGATTTCTTATCTGAGAGACCCTGGATTAAAAGGATGATTTTTAAGCTCTTTAGTCAAGAGA  
CGGTGATGAAGTTTGTGCCGCGGTACAGCCTCGTCTAGAACTCAGCGACAGCGGTGCCTTCC  
GGAGAAGCCTGCATGATCCCGATGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG  
ATGGGCACCTGTACCTGGGCTCTTTAGGTCCCCCTTCCTCTGCAGACTCAGCCTCCAGGCTG  
TTTAGCCCTCCCAGATAGCTGCCCTGCCACGCAGGCCAGGAGTCTTCACACTCAGGCACCAG  
GCCTGGTCCAGGAGGAGCTGTGGACACAGTCGTGGTTCAAGTGTCCACATGCACCTGTTAGTC  
CCTGAGAGGTGGTGGGAATGGCTGCTTCATTCCTCGAGGATGCCCGGGCCCCACCTGGGCTTG  
TCTTTCTGTTTAGAGGGAAGTGTAACATATCTGCCATGAGGAACATAAATTCATGTAAAGCCA  
TTTTCTCTTAAACAAAACAAAACCTTTCTAAGTACAATCAATTCTCTAGGATTGGGAAGCTCCT  
TGCACTTGGAACAGGGCTCAGGTGGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG  
CGGCCCTGTCTGCGGCCTCAAAGTTCTTCTTTACTATATATAACGTGCGGTCATACCTTTCT  
TCGTTGTGGTGGGGATGGAAGAGCAGAGGGAGCATGGCCCAGGGGTGTTGAGGCCAGCGGTGA  
GAGCCGTGTTAGCCAAGACATGGAAGTGTGTTCTCAAGGGTTATGTGGGGCGTGGGCTCTCCA  
TAGTGTGTATGAAAAGCTTGTTGACTCTAGCGGCTCAGAGAGGACTTTGCTGGGTTTCTTTCT  
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTCGGGACCTACTGCAG  
GGGTCCGTTTAGTAACGTCTTGTCTGTGATCTTTGTTCTTGACCTCTAGACCCCAAGATGTGA  
ACAGTGCACGTGTTAATGTCATCTTTGCTCATGTGTTATAAGCCCCAAGTTGCTGTATATTTT  
CACAAGTATGTCTACACACTGG

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**FIGURE 106**

MLAVSLTVPLLGAMMLLESPIDPQPLSFKEPPLLLGVLHPNTKLRQAERLFENQLVGPESIAH  
IGDVMFTGTADGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNTLFVADAYK  
GLFEVNPWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG  
TDDGRLLLEYDTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGADL  
FVENMPGFDPNIRPSSSGGYWVGMS TIRPNPGFSMLDFLSERPWIKRMIFKLFSQETVMKFVP  
RYSLVLELSDSGAFRRSLHDPDGLVATYI SEVHEHDGHL YLG SFRSPFLCRLSLQAV

**Important features of the protein:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 1-21 (possible type II)

**N-glycosylation sites.**

amino acids 116-119, 152-155

**Casein kinase II phosphorylation sites.**

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

**N-myristoylation sites.**

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

**Amidation site.**

amino acids 164-167

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**FIGURE 107**

AACGAAGCGTGCGCGCTTTGGTAACCGGCTAGAAATCCCGCACGCGCGCCTGCCTCCTCTCCC  
CAGGCCTGAGCTGCCCCCTCCCACTGCCTTTCCTTCTTCCCGCAGCTCAGAAGCTTCGCGAGGG  
CCCAGAGAGGCGGTGGGGTGGGCGACCCCTACGCCAGCTCCGGGCGGGAGAAAGCCCACCCTCT  
CCCGCGCCCCAGGAAACCGCCGGCGTTTCGGCGCTGCGCAGAGCCATGGGAATTCTCCTGGCTGG  
AGACGCGCTGGGCGCGGCCCTTTTACCTGGCGTTCGTGTTCTGCCTGGCCCTGGGGCTGCTGC  
AGGCCATTAAGCTGTACCTGCGGAGGCAGCGGCTGCTGCGGGACCTGCGCCCCCTTCCCAGCGC  
CCCCACCCACTGGTTCCTTGGGCACCAGAAGTTTATTTCAGGATGATAACATGGAGAAGCTTG  
AGGAAATTATTGAAAAATACCCCTCGTGCCCTTCCCTTTCTGGATTGGGCCCTTTCAGGCATTTT  
TCTGTATCTATGACCCAGACTATGCAAAGACACTTCTGAGCAGAACAGATCCCCAAGTCCCAGT  
ACCTGCAGAAATTCTCACCTCCACTTCTTGGAAGGACTAGCGGCTCTAGACGGACCCAAGT  
GGTTCCAGCATCGTCGCTACTAACTCCTGGATTCCATTTTAAACATCCTGAAAGCATACTTG  
AGGTGATGGCTCATTCTGTGAAAATGATGCTGGATAAGTGGGAGAAGATTTGCAGCACTCAGG  
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTCTGGATATAATCATGAAATGCG  
CTTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAAGCCATAT  
TTGAACTCAGCAAAATCATATTTACCGCTTGTACAGTTTGTGTATCACAGTGACATAATTT  
TCAAACCTCAGCCCTCAGGGCTACCGCTTCAGAAGTTAAGCCGAGTGTTGAATCAGTACACAG  
ATACAATAATCCAGGAAAGAAAGAAATCCCTCCAGGCTGGGGTAAAGCAGGATAAACTCCGA  
AGAGGAAGTACCAGGATTTTCTGGATATTGTCTTTCTGCCAAGGATGAAAGTGGTAGCAGCT  
TCTCAGATATTGATGTACACTCTGAAGTGAGCACATTCTGTTGGCAGGACATGACACCTTGG  
CAGCAAGCATCTCCTGGATCCTTTACTGCCTGGCTCTGAACCTGAGCATCAAGAGAGATGCC  
GGGAGGAGGTGAGGGGCATCCTGGGGGATGGGTCTTCTATCACTTGGGACCAGCTGGGTGAGA  
TGTCGTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCTGCAGTCCCGTCCATTT  
CCAGAGATCTCAGCAAGCCACTTACCTTCCCAGATGGATGCACATTGCCTGCAGGGATCACCG  
TGGTTCTTAGTATTTGGGGTCTTCACCACAACCCTGCTGTCTGGAAAAACCCAAAGGTCTTTG  
ACCCCTTGAGGTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCTACTTACCATTCT  
CAGCTGGATCAAGGAAGTGCATTGGGCAGGAGTTTGCCATGATTGAGTTAAAGGTAACCATTG  
CCTTGATTCTGCTCCACTTCAGAGTGACTCCAGACCCACCAGGCCTCTTACTTTCCCAACC  
ATTTTATCCTCAAGCCCAAGAATGGGATGTATTTGCACCTGAAGAACTCTCTGAATGTTAGA  
TCTCAGGGTACAATGATTAAACGTACTTTGTTTTTCGAAGTTAAATTTACAGCTAATGATCCA  
AGCAGATAGAAAGGGATCAATGTATGGTGGGAGGATTGGAGGTTGGTGGGATAGGGGTCTCTG  
TGAAGAGATCCAAAATCATTTCTAGGTACACAGTGTGTGCTAGCTAGATCTGTTTCTATATACT  
TTGGGAGATTTTCAGATCTTTTCTGTAAACTTTCCTACTATTAATGCTGTATACACCAATA  
GACTTTCATATATTTTCTGTTGTTTTTAAATAGTTTTTCAGAATTATGCAAGTAATAAGTGCA  
TGTATGCTCACTGTCAAAAATTCCCAACACTAGAAAATCATGTAGAATAAAAAATTTTAAATCT  
CACTTCACTTAGCCGACATTCCATGCCCTGACCAATCCTACTGCTTTTCTTAAAAACAGAATA  
ATTTGGTGTGCATTCTTTTCAGACTTTTTCCTATACATTTTATATGTAGAAATGTAGCAATGTA  
TTTGTATAGATGTGATCATTCCCTATATTGTTATTGATTTTTTTTCACTTAATAAAAATTCACCT  
TATTCCTTAAAA



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**FIGURE 108**

MEFSWLETRWARPFYLA FVFCLALG LLQA IKLYLRRQRLRLRPF PAPP THWELGHQKFIQD  
DNMEKLEEIIEKYPRAFPFWIGPFQAF FCIYDPDYAKTLLSRTDPKSQYLQKFSPPLL GKGLA  
ALDGPKWFQHRRLLT PGFHFNILKAYIEVMAHSVKMMLDKWEKICSTQDTSVEVYEHINSMSL  
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLSPQGYRFQKLSR  
VLNQYTDTI IQERKKSLQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDIDVHSEVSTFLL  
AGHDTLAASISWILYCLALNPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCR LI  
PAVPSISRDL SKPLTFPDGCTLPAGITVVL SIWGLHHNPAVWKNPKVFDPLRFSQENS DQRHP  
YAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLK  
KLSEC

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 310-330, 397-413, 459-473

**N-glycosylation site.**

amino acids 206-210

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 265-269, 504-520

**N-myristoylation sites.**

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

**Cytochrome P450 cysteine heme-iron ligand signature:**

amino acids 447-457

**Cytochrome P450 cysteine heme-iron ligand proteins.**

amino acids 444-475

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**FIGURE 109**

GGCGTTCGGGGCCTCAACTTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC  
AGCAATTTTGCTTCTTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCCTGGATTCTGAGAT  
CCAGACCAGCTCCTCCCAGACCTCTCCAGAAGAAGCCATGGGAACCCCTCGTATCCAGCATTT  
GCTGATCCTCCTGGTCCTAGGAGCCTCCCTCCTGACCTCGGGCCTAGAGCTGTATTGTCAAAA  
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTTAACTGGACCACAGAGGAAGT  
GGAGACTTGTGACAAAGGGGCACCTTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA  
GACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGAAGGGGAGGAGGCCATAACAATTGTCCA  
GCACTCTTACCTCCCGGCCTGATCGTGACCTCCTACAGTAACTACTGTGAGGATTCCCTTCTG  
TAATGACAAAGACAGCCTGTCTCAGTTTTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTC  
AACAACCCTCCATTGTCCAACCTGTGTGGCTTTGGGGACCTGTTTCAGTGCTCCTTCTCTTCC  
CTGTCCCAATGGTACAACCTCGATGCTATCAAGGAAAACCTTGAGATCACTGGAGGTGGCATTGA  
GTCGTCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTT  
AGCAGTAGGACCCATGTTTGTGAGGGAAGCGTGCCACATCAGCTGCTCAACCTCGAAA  
GACTGAAAATGGGGCCACCTGTCTTCCCATTCCTGTTTGGGGGTACAGCTACTGCTGCCATT  
GCTGCTGCCATCATTTATTCACCTTTCCTAAGGAAGGCACTTCTGGGCCTGGGTCTGAGGACAT  
CTTTTTTGAAGTGGGAGCCTTCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT  
GAGGGAGAATACAGAGATACTATGAACGTATTTGACATTTTAAATAACAATTTCTGCTATAATT  
TTTGTATGCAGTAGGCGTTACTAATAAACATTTCTGCTGTGA

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**FIGURE 110**

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVETCDKGALCQET  
ILIIKAGTETAILATKGCIPEGEEAITIVQHSSPPGLIVTSYSNYCEDSFCDKDSLSQFWEF  
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMI  
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVWGLQLLLPLLLPSFIHFS

**Important features of the protein:****Signal peptide:**

amino acids 1-23.

**Transmembrane domain:**

amino acids 184-201

**N-glycosylation sites.**

amino acids 45-49, 159-163

**N-myristoylation sites.**amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,  
175-181

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**FIGURE 111**

CGAGAAGAGGACAGAGGAGACTGAGCAAAGGGGGTGGGCTCCAGGCGACCCCTAGCCCAATTCTGCCCTCCAT  
CCCAAGGGGCGAGAGAAATTGTCTTTCTTTGCTGACTCCTACGAGGAAAAAAAAAAAAAAAAAAAAAACCATTAA  
AGGGAAAGATAAACGAGACGGAGGAAAGGTGGCAGCCAGATTACTTAGAGAGGCACAGAGGAGAGATCGGGG  
TGAGTCGCCCATGGGACTCCCAGGGCCAGCACCCGCCCTCCCCAGCTGCTGTTCTTAATTCTGCTGAGCTGT  
CCCTGGATCCAGGGTCTGCCCCCTGAAGGAGGAGGAGATATTGCCAGAGCCTGGAAGTGAGACCCCCACGCTGGCC  
TCTGAGGCCCTGGCTGAAGTGTCTATGGGGCCCTGCTGAGGAGGGGCCAGAGATGGGCTACCTGCCAGGATCT  
GATCCGGACCCACGCTAGCCACCCCTCCGGCCGGCCAGACTCTCGCAGTGCCCTCCCTGCCACGGGCCACTGAG  
CCGGGGACAGGGCTCTGACAACAGCCGTACCCCTAACGGGGTCAAGGGGGCAGGCCCCACTGCGCCAGAACTG  
CTGACCCCGCCCCAGGAACCACAGCCCCACCCCAACCCAGCCCTGCCCTCCCCAGGGCCTCCCCTTGGGCTGAG  
GGAGGAGAGGAGGAGACGACGACCACCATCATCACGACAACCTGTACCCTACGCTGACGAGCCAGTTCTG  
TGTAATAACAACATCTCCGAGGGCGAAGGGTATGTGGAGTCTCCAGATCTGGGGAGCCCCGTAGCCGACCCCTG  
GGGCTCCTGGACTGCACTTACAGCATCCATGTCTACCCTGGCTACGGCATTGAGATCCAGGTGCAGACGCTGAAC  
CTGTACAGGAAGAGGAGCTCCTGGTGTGGCTGGTGGGGATCCCAGGCCTGGCCCCCGACTCCTGGCCAAAC  
TCATCCATGCTTGAGAAGGACAAGTCTTCCGGAGCCCAACCAACCGGCTGCTTCTGCACTTCCAGAGCCACGG  
GTCCCAAGGGCGGTGGCTTCAGGATCCACTATCAGGCCTACCTCCTGAGCTGTGGCTTCCCTCCCGCCGGCC  
CATGGGGACGTGAGTGTGACGGACCTGCACCCCTGGGGGCACTGCCACCTTCACTGTGATTGGGGTACCAGCTG  
CAGGGAGAGGAGACCTCATCTGCCTCAATGGCACCCGGCCATCCTGGAACGGTGAAACCCCCAGCTGCATGGCA  
TCCTGTGGTGGCACCATCCACAATGCCACCCCTGGGCGCATCGTGTCCCCAGAGCCTGGGGGAGCCGTAGGGCCC  
AACCTCACCTGCCGTTGGGTGATTGAAGCAGCTGAGGGGCGCCGGCTGCACCTGCACTTTGAAAGGGTCTCGCTG  
GATGAGGACAATGACCGGCTGATGGTGGCTCAGGGGGCAGCCCCCTATCCCCGTGATCTATGATTGCGACATG  
GACGATGTCCCCGAGCGGGGTCTCATCAGTGACGCCCAGTCCCTCTACGTGGAGCTGCTGTGAGACACCTGCC  
AATCCCTGCTGTGAAGCCTTCGATTTGAAGCCTTTGAGGAGGATCGCTGCTTCGCCCCCTTCTGGCACATGGA  
AATGTCACTACCACGGACCCCTGAGTATCGCCAGGGGCACTGGCAACCTTCTCGTGCCTCCCAGGATATGCCCTG  
GAGCCCCCTGGGCCCCCAATGCCATCGAATGTGTGGATCCACAGAACCCCACTGGAACGACACAGAGCCGGCC  
TGCAAAGCCATGTGTGGAGGGGAGCTGTGGAACAGCTGGCGTGGTCTCTCTCCGACTGGCCCCAGAGCTAT  
AGCCCGGGCCAAGACTGCGTGTGGGGCGTGACGTCCAGGAAGAGAAGCGCATCTTGCTCCAAGTTGAGATATTG  
AATGTGCGGGAAGGGGACATGCTGACGCTGTTGACGGGGACGGTCCCAGCGCCGAGTCTTGGCCCCAGCTGCGG  
GGACCTCAGCCGCGCCGCGCCTTCTCTCTCTGGGCCCCGACCTCACACTGCAGTTTCAGGCACCGCCCCGGGCC  
CCAAATCCAGGCCTGGGCCAGGGCTTCGTATTGCACTTCAAAGAGGTCCCAGGAACGACAGTGCCTCCGAGCTG  
CCACCTCCGGAGTGGGGCTGGAGAACGGCATCCACGGGGACCTGATCCGGGGCAGGTGCTCACCTACCACTGC  
GAGCCTGGCTACGAGCTGCTAGGCTCCGACATTCTCACTTGCCAGTGGGACCTGTCTTGGAGCGCCGCGCCG  
GCCTGCCAAAAGATCATGACTTGTGCTGACCCTGGCGAGATTGCCAACGGGCACCGCACCGCCTCGGACGCGCG  
TTCCCCGTTGGCTCCCAGCTCCAGTACCGCTGCCCTGCCAGGGTACAGCCTCGAGGGGGCAGCCATGCTCACCTGC  
TACAGCCGGGACACAGGCACACCCAAGTGAGCGATAGGGTCCCCAAATGCGCCTTGAAGTACGAGCCGTGCCTG  
AACCCGGGGGTTCCCAGAATGGCTACCAGACGCTGTACAAGCACCACTACCAGGCGGGCAGTCTCTGCGCTTC  
TTCTGCTATGAGGCTTTGAGCTTATCGGCGAGGTACCATCACCTGTGTGCCCGGCCACCCCTCCCAGTGAGC  
AGCCAGCCCCACTCTGCAAAGTGACCCAGACCACAGATCCATCACGGCAGCTGGAAGGGGGGAACCTGGCCCTG  
GCCATCCTGCTGCTCTAGGCTTGGTCATTGTCTCGGCAGTGGCGTTTACATCTACTACACCAAGCTTCAGGGA  
AAGTCCCTTTTCGGCTTCTCGGGCTCCCACTCCTACAGCCCATCACCGTGGAGTGGACTTCAGCAACCCGCTG  
TATGAAGCTGGGGATACGCGGGAGTATGAAGTTTCATCTGAACCCCAAGACTACAGCTGCAGGACCCAGGACGC  
CCCTCCCTCCTCATTCGGGCAGAGGGAAATACGGGACCCGGTCTCTGCCTCCTGGCTGCCCTCCTCCTGGCTG  
TGTAATAGTCTCCCTATCCACAGAGGGGGCTTGTATGGCCCTGGAGATCCTACAGTAAATAAACCAGCATCCTG  
CCGCCAAAAA

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**FIGURE 112**

MGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEEEILPEPGSETPTVASEALAE LLHGALLRRG  
PEMGYLPGSDPDPTLATPPAGQTLAVPSLPRATEPGTGPLTTAVTPNGVRGAGPTAPELLTTP  
PGTTAPPPSPASPGPPLGPEGGEEETTTTIIITTTT VTTTSPVLCNNNISEGEGYVESPD  
GSPVSRTLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAPRLLANSSMLG  
EGQVLRSPNTNRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGGTATFH  
CDSGYQLQGEETLICLNGTRPSWNGETPSCMASCGGTIHNATLGRIVSPEPGGAVGPNLTCRW  
VIEAAEGRRLLHLHFERSLDEEDNDRLMVRSGGSPLSPVIYDSMDDDVPERGLISDAQSLYVEL  
LSETPANPLLLSLRFEAFEDRCFAPFLAHGNVTTTDP EYRPGALATFSCLPGYALEPPGPPN  
AIECVDPTEPHWNDTEPACKAMCGGELSEPAGVVLSPDW PQSYSPGQDCVWGVHVQEEKRILL  
QVEILNVREGDMLTLFDGDGPSARVLAQLRGPQRRRLSSGPD LTLQFQAPPGPPNPGLGQG  
FVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGT VLT YQCEPGYELLGSDILTCQWDLWS  
AAPPACQKIMTCADPGEIANGHRTASDAGFPVGS HVQYRCLPGYSLEGAAMLT CYSRDTGTPK  
WSDRVPKCALKEYEPCLNPGVPENGYQTLYKH HYQAGESLRFFCYEGFELIGEV TITCVPGHPS  
QWTSQPPLCKVTQTTPDSRQLEGGNLALAILLPLGLVIVL GSGVYIYYTKLQKSLFGFSGSH  
SYSPITVESDFSNPLYEAGDTREYEVSI

**Important features of the protein:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 842-864

**N-glycosylation sites.**amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,  
473-477, 517-521, 641-645**Tyrosine kinase phosphorylation site.**

amino acids 61-69

**N-myristoylation sites.**amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,  
235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,  
626-632, 665-671, 775-781, 842-848**Amidation site.**

amino acids 384-388

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**CUB domain proteins profile.**

amino acids 202-218, 376-392, 553-569

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**FIGURE 113**

GCCGCGGGCGGAGCTGCCTGCCGGTCCCGCGCGCGCTCCGCACTCCTCGGCCCTCGGGCGGTTCGATGGGACGG  
GGCGCCGCGGAGCAGGAGGCGCGCCCGTCCGGGTGCTCGGGCCGCGGGAGCCCACTGTGGGGCTCGGGCATG  
GCGGGCCGCGAGGACCTGAGCTCTCCTCAGGGGAGCGGGAGGCAGCTGCTGGCCGGCGATGGGGACGGAGTGGGG  
CCGTCGCCGCGCGCGCGAGCCGTGAGCGCCGAGCCACCGCCGCGCTACCTCAGCCCTTCGCGAAGCGCCGGGCA  
GCTCGGGAACATGGCCCTGGAGCGGCTCTGCTCGGTCTCAAAGTGTGTTAATAACAGTACTGGTAGTGGAAGG  
GATTGCCGTGGCCCAAAAAACCAAGATGGACAAAATATTGGGAATCAAGCATATTCCTGCAACCCAGTGTGGCAT  
TTGGGTTCGAACCAGCAATGGAGGTCAATTTGCTTCGCCAAATATCCTGACTCATATCCACCAACAAGGAGTG  
TATCTACATTTTGAAGCTGCTCCACGTCAAAGAATAGAGTTGACCTTTGATGAACATTATTATATAGAACCATC  
ATTTGAGTGTGCGTTTGATCACTTGGAAGTTTCGAGATGGGCCATTTGGTTTCTCTCCTCTTATAGATCGTTACTG  
TGGCGTGAAGCCCTCCATTAATTAGATCAACAGGGAGATTTCATGTGGATTAAAGTTTAGTTCTGATGAAGAGCT  
TGAAGGACTGGGATTTTCGAGCAAAATATTCATTTATTCAGATCCAGACTTTACTTACCTAGGAGGTATTTTAAA  
TCCCATTCAGATTGTGCTGAGTCTCGGAGCTGATGGAATAGTGGCTCTAGTCAGGTAGAACAAGAGGA  
GAAACAAAACAGGCCAAGCCGTTGATGTCATCTGGACCATTAAGCCACTCCAAAAGCTAAGATTTATTTGAG  
GTTCTAGATTATCAATGGAGCACTCAATGAATGCAAGAGAACTTCGTTGCAGTCTATGATGGAAGCAGTTC  
TATTGAAAACCTGAAGGCCAAGTTTTCAGCACTGTGGCCAAATGATGTAATGCTTAAACAGGAATTGGAGTGAT  
TCGAATGTGGGCAGATGAAGGTAGTCGGCTTAGCAGGTTTCGAATGCTCTTACTTCCTTTGTGGAGCCTCCCTG  
CACAAGCAGCACTTTCTTTGCCATAGCAACATGTGCATCAATAATTCTTTAGTCTGTAATGGTGTCCAAAATTG  
TGCATACCCTTGGGATGAAAATCATTGTAAAGAAAAGAAAAGCAGGAGTATTTGAACAAATCACTAAGACTCA  
TGGAACAATTATTGGCATTACTTCAGGGATTGTCTTGGTCTCTCATTATTTCTATTTTAGTACAAGTGAAACA  
GCCTCGAAAAAAGGTCATGGCTTGCAAAACCGCTTTTAAATAAAACCGGGTTCCAAGAAGTGTGATCCTCCTCA  
TTATGAACTGTTTTCACTAAGGGACAAAGAGATTTCTGCAGACCTGGCAGACTTGTGGAAGAATTGGACAATA  
CCAGAAGATGCGGCGCTCTCCACCGCTCCCGCTGCATCCAGCACCACCTGTGGGTGCGAGGCCCTCCAGCGT  
CAACAAAAGCAGGACCAACCTCAGTTCATGGAACCTCTTTCCGAAATGACTTTGCACAACCACAGCCAATGAA  
AACATTTAATAGCACCTCAAGAAAAGTAGTTACACTTTCAAACAGGGACATGAGTGCCCTGAGCAGGCCCTGGA  
AGACCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTTCAGGGGGCGAGAAGATTCTGCACAAGCATCCATATC  
CATTGACTTCTAATCTCTGCTAATGGTGATGTGAATCTTAGGGTGTGTACGTACGCAGCCTCCAGGGCACCAT  
ACTGTTTCCAGCAGCCAACCTTTTCTCCCATCACAACCTACGAAGACCTTGATTTACCCTTAACCTATTGTATGG  
TGATGTTTTTATTCTCTCAGGCAGTCTATATATGTTAAACCAATCAAGGAACCTACTCTATTTCAGTGGAACAAT  
AATCATCTCTATTGCTTGGTGTCATTTATAGGAAGCACTGCCAGTTAAGAGCATTAGAAGAGGTGGTTGGATGG  
AGCCAGGCTCAGGCTGCCTCTTCGTTTAGCAACAAGAACTGCTCTTGACTGATAACAGCTCTGTCAATATTT  
TGATGCCACAATAAACTTGATTTTTTTTACATTCCTTTTATTTTTCTTTCTCTAAATTTAATTTGTTTTATAA  
GCCTATCGTTTTTACCATTTCAATTTCTTACATAAGTACAAGTGTTAATGTACCACATACTTCAGTATAGGCATT  
TGTTCTTGAGTGTGCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGTTGTATTTACCCCATCTGTTTCT  
TCTTGGCTAATCTCTGTACTTCTGCCTTTTAAATTAAGTGGGCCCTTATTCCTTATTTCTGTGAGAAATAATAGAT  
GATATGATTTATTACCTTTCAATTATATTTTTCTCAGTTATACTAGAAAATTTCAATCCTGGGATATATGTAC  
CATGTGCAGCTATGACTAAAATTTGAAAAGATAAAAATTTCTAGCAAGCCTTTGAAGTTTACCAAGTATAGTC  
ACATTTCAGTGACAGCCATTTCATTCAGTAAAGAAATCATTTTCACTTTGGGAGAGGCTATAATTACATTTA  
TTTGCAATGTTTCTCTCGCTAGATTGTTACATAGCTCCCATCTGTGTGGTTTTGCTTACAGCATATGGTAACCA  
AGGTTAGATGCCAGTTAAAATTCCTTAGAAATTGGATGAGCCTTGAGATTGCTTCTTAAGTGGGACATGACATTT  
TTCTAGCTCTTATCAAGAATAACAACCTCCACTTTTTTTTAACTGCACCTTTGACTTTTTTTATGGTATAAAAA  
CAATAATTTATAACATAAAAGCTCATTGTGTTTTTACACTTTTGATATTATTTGATACTGTACAACTTTATT  
AAATCAAGATGAAAGACCTACAGGACAGATTCCTTCAGTGTTACATCAGTGGCTTTGTATGCAAAATATGCTGT  
GTTGGACCTGGACGCTATACTTATGTAAAGACCTTGGAATGTGGACATAAGCTCTTTCTTTCTTTTGTAC  
TGTATTTAGTTTGTGATAAAATTTTCACTGTGTGATTTTATGCTCTAAATCACTACACAAATCCCATATTTAAA  
TATACATTGTACCTGAAAAAAA

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**FIGURE 114**

MALERLCSVLKVLLITVLVVEGIAVAQKTQDGQNIGIKHIPATQCGIWVRTSNGGHFASPNYP  
DSYPPNKECIYILEAAPRQRIELTFDEHYIEPSFECRFDHLEVRDGPFGFSPOLIDRYCGVKS  
PPLIRSTGRFMWIKFSSDEELEGLGFRAKYSFIPDPDFTYLGGINPIPDQFELSGADGIVR  
SSQVEQEEKTKPGQAVDCIWTIKATPKAKIYLRFLDYQMEHSNECKRNFVAVYDGSSSIENLK  
AKFCSTVANDVMLKTGIGVIRMWADEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV  
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIGITSGIVLVLLIISILVQVKQPRKKVM  
ACKTAFNKTGFQEVFDPPHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHC  
SQASSVKQSRTNLSSMELPFRNDFAPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEI  
PCEIYVRGREDQAQASISIDF

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 348-369

**N-glycosylation sites.**

amino acids 311-315, 385-389, 453-457, 475-479

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 426-430, 479-483

**N-myristoylation sites.**amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,  
348-354, 352-358, 441-447

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**FIGURE 115**

GGTCTCTGTCCTTGGCTGTGGCTCCTGCGCTCTGGCTGAGCCATGTTTCCTTCTCCTCGCCCTC  
CTCACTGAGCTTGGAAGACTGCAAGCCCACGAAGGTTCTGAAGGAATATTTCTGCATGTCACA  
GTTCCACGGAAGATTAAGTCAAATGACAGTGAAGTTTCAGAGAGGAAGATGATTTACATCATT  
ACAATTGATGGACAACCTTACACTCTACATCTCGGAAAACAATCATTCTTACCCCAGAACTTT  
TTGGTTTATACATATAATGAACTGGATCTTTGCATTCTGTGTCTCCATATTTTATGATGCAT  
TGCCATTACCAAGGATATGCTGCCGAATTTCCAAATTCATTTGTGACACTCAGTATATGTTCT  
GGTCTCAGGGGATTTCTCCAGTTTGAAAATATCAGTTATGGAATTGAACCAGTAGAATCTTCA  
GCAAGATTTGAGCATATAATTTATCAAATGAAAAATAATGATCCAAATGTATCCATTTTAGCA  
GTAAATTACAGTCATATTTGGCAGAAAGACCAGCCCTACAAAGTTCTTTAAACTCACAGATA  
AAAAATCTTTCAAACTATTACCCCAATATCTGGAAATATACATTATAGTGGA AAAAGCTTTG  
ATGTTTACCCAGTTCAAATTGACTGTTATACTGTCTTCCTTGGAATTGTGGTCAAATGAAAAC  
CAGATTTCCACCAGTGGGGATGCTGATGATATATTACAAAGATTTTTGGCATGGAAACGGGAC  
TATCTCATCCTACGGCCCCATGACATAGCATACTTACTTGTTTACAGGAAACATCCTAAATAT  
GTGGGAGCAACATTTCTGGCACCGTATGCAATAAAAGCTATGATGCAGGTATTGCTATGTAT  
CCAGATGCAATAGGTTTGGAGGGATTTTCGGTTATTATAGCTCAACTGCTTGGCCTTAATGTA  
GGATTAACATATGATGACATCACTCAGTGTTTCTGTCTGAGAGCTACATGCATCATGAATCAT  
GAAGCAGTGAGTGCCAGTGGTAGAAAGATTTTAGCAACTGCAGCATGCACGACTATAGATAT  
TTTGTTC AAAATTTGAGACTAAATGCCTTCAGAAGCTTTCAAATTTGCAACCATTACATCAA  
AATCAACCAGTGTGTGGTAATGGGATTTTGGAAATCCAATGAAGAATGTGACTGTGGTAATAAA  
AATGAATGTCAATTTAAGAAGTGCTGTGATTATAACACATGTAACTGAAGGGCTCAGTAAAA  
TGTGGTTCTGGACCATGTTGTACATCAAAGTGTGAGTTGTCAATAGCAGGCACTCCATGTAGA  
AAGAGTATTGATCCAGAGTGTGATTTTACAGAGTACTGCAATGGAACCTCTAGTAATTGTGTT  
CCTGACACTTATGCACTGAATGGCCGTTTGTGCAAGTTGGGAACTGCCTATTGCTATAACGGA  
CAATGTCAAACACTACTGATAACCAGTGTGCCAAGATATTTGGAAAAGGTGCTCAAGGTGCTCCA  
TTTGCCTGTTTTAAAGAAGTTAATTCTCTGCATGAAAGATCTGAAAACCTGTGGTTTTAAAAAT  
TCACAACCATTACCTTGTGAACGGAAGGATGTTCTCTGTGGAAAATTAGCTTGTGTTTCAGCCA  
CATAAAAATGCTAATAAAAGTGACGCTCAATCTACAGTTTATTTCATATATTCAAGACCATGTA  
TGTGTATCTATAGCCACTGGTTCCCTCCATGAGATCAGATGGAACAGACAATGCCTATGTGGCT  
GATGGCACCATGTGTGGTCCAGAAATGTACTGTGTAAATAAAACCTGCAGAAAAGTTCATTTA  
ATGGGATATAACTGTAATGCCACCACAAAATGCAAAGGGAAAGGGATATGTAATAATTTTGGT  
AATTGTCAATGCTTCCCTGGACATAGACCTCCAGATTGTAAATTCCAGTTTGGTTCCCCAGGG  
GGTAGTATTGATGATGGAAATTTTCAGAAATCTGGTGACTTTTATACTGAAAAGGCTACAAT  
ACACACTGGAACAACCTGGTTTATTCTGAGTTTCTGCATTTTTCTGCCGTTTTTCATAGTTTTTC  
ACCACTGTGATCTTTAAAGAAATGAAATAAGTAAATCATGTAACAGAGAGAATGCAGAGTAT  
AATCGTAATTCATCCGTTGTATCAGAAAGCGATGACGTGGGACATTAATATTGCACAGAACCTT  
CCATAGCAAATAACCTAAAGGAACGAATGTGCTTTATTTATAACCTTACGTTATCCCCAATGC  
ATTGTAAATGTCAAACCTTTTGGAAAATAAAGCCTGCGTGCCCTCCC



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**FIGURE 116**

MFLLLALLTELGRQLQAHEGSEGIFLHVTVPRIKISNDSEVSEKMIYIITIDGQPYTLHLGKQ  
SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFNSFVTLSSICSGLRGFLQFENISYG  
IEPVESARFEHIIYQMKNNDPNVSILAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY  
IIVEKALMFTQFKLTIVILSSLELWSNENQISTSGDADDILQRFLAWKRDYLILRPHDIAYLLV  
YRKHPKYVGATFPGTVCNKSYDAGIAMYPDAIGLEGFSVIAQLLGLNVGLTYDDITQCFCLR  
ATCIMNHEAVSASGRKIFSNCSMHDYRYFVSKFETKCLQKLSNLQPLHQNPVCGNGILESNE  
ECDGKNKNECQFKKCCDYNTCKLKGSVKCGSGPCCTSKCELSIAGTPCRKSIDPECDFTEYCN  
GTSSNCVPDTYALNGRLCKLGTAYCYNGQCQT TDNQCAKIFGKGAQGAPFACFKEVNSLHERS  
ENCGFKNSQPLPCRKDVLCGKLACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG  
TDNAYVADGTMCGPEMYCVNKTCKRVHLMGYNCNATTKCKGKGICNNFGNCQCFPGHRPPDCK  
FQFGSPGGSIDGDNFQKSGDFYTEKGYNTHWNNWFILSFCIFLPFFIVFTTVIFKRNEISKSC  
NRENAEYNRNSSVVSESDDVGH

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 665-684

**N-glycosylation sites.**amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,  
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706**Casein kinase II phosphorylation sites.**amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,  
376-380, 415-418, 499-502, 639-642, 708-711**Tyrosine kinase phosphorylation site.**

amino acids 243-249

**N-myristoylation sites.**amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,  
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,  
616-621, 634-639**Amidation site.**

amino acids 328-331

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**FIGURE 117**

CCCACGCGTCCGCGGACGCGTGGGGCTCAGTGGGCGTCGCGCGAAGGCTAAGGGAGTGTGGCG  
GGCGGCTCCGGGAGCCAACATGCCTCGGTATGCGCAGCTGGTCATGGGCCCCGCGGGCAGCGG  
GAAGAGCACCTACTGTGCCACCATGGTCCAGCACTGTGAAGCCCTCAACCGGTCTGTCCAAGT  
TGTAACCTGGATCCAGCAGCAGAACACTTCAACTACTCCGTGATGGCTGACATCCGGGAAGT  
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTCCGTCCCAACGGAGGATTGGT  
ATTTTGCATGGAGTACTTTGCCAATAATTTTGACTGGCTGGAGAACTGTCTTGGCCATGTAGA  
GGACGACTATATCCTTTTTGATTGTCCAGGTCAGATTGAGTTGTACACTCACCTGCCTGTGAT  
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTTCGAGTCTGTGGAGTTTTTCTTGTTGA  
TTCTCAGTTCATGGTGGAGTCATTCAAGTTTATTTCTGGCATCTTGGCAGCCCTGAGTGCCAT  
GATCTCTCTAGAAATTCGCAAGTCAACATCATGACAAAAATGGATCTGCTGAGTAAAAAGC  
AAAAAAGGAAATTGAGAAATTTTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG  
TGACTTAAGAAGCAAAAAATTCAAGAACTGACTAAAGCTATATGTGGACTGATTGATGACTA  
CAGCATGGTTCGATTTTTACCTTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA  
GCATATTGATTTTGCCATTCAATATGGAGAAGACCTAGAATTTAAAGAACCAAAGGAACGTGA  
AGATGAGTCTTCCTCTATGTTTGACGAATATTTTCAAGAATGCCAGGATGAATTGAAGAGTTTA  
CTAAAAGTAACCATCTAAAGAGCTTGTGGCCAAACCAGCAGAACATTCTTCTCTTCAAAGGAT  
GCAATAGTAGAAAGCTACTTATTTTAATGAAAAAAGTAAACTTCGTTCTTTATCAGCCTCA  
TGCCTGAATCAAATTTTAAATTATTCTGAAACTGCTGCTGTTTAAAGTGAATCTTTTAGTAT  
TATAACAGCATCACTTTAGATTTTGTAAGTCAAAATTGAAATGAATGCACATAGATTTATATA  
TAAATTAGCACCTGAGCTAAGGTTAAGGCCGGTCTAACTTATTTTCACTTTTTGTATTATTT  
TTGAGATGCAGGAATTACTGTAACAAAATATGTATGTCCGAAGGGAAAAAGCTGCAAGGATAT  
ATATAAGACCACTGCTTATCTGTATCTTCCCATTTTCCCTATATTGAAAATGTATATTATTTAT  
ATAACTTAAAAAGTAAAAATAACTATGTTTTGAGAT

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**FIGURE 118**

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV  
MEDDSLRFPGPNGGLVFCMEYFANNFDWLENCLGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ  
LEQWEFRVCGVFLVDSQFMVESFKFISGILAAALSAMISLEIPQVNIMTKMDLLSKKAKKEIEK  
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRELPYDQSDEESMNIVLQHIDFAI  
QYGEDLEFKEPKEREDESSSMFDEYFQECQDE

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 151-170

**N-glycosylation sites.**

amino acids 31-35, 47-51

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 212-216

**Tyrosine kinase phosphorylation site.**

amino acids 189-197

**N-myristoylation sites.**

amino acids 13-19, 76-82, 154-160

**ATP/GTP-binding site motif A (P-loop).**

amino acids 10-18

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**FIGURE 119**

GGGCGCTGGGAGACACCGGACGCCCGCTCGGCTGCGCTGCGGCTCAGGCCCCCGCTCGGGCCC  
GACCCGCTCGGTCACCGCCGGCTCGGGCGCGACCTGCCGGCTGCGGGCCCAGGGCCATGCGG  
AGGCCACAGGAGGCCGGCGGCCACGCGCATCCCGTAGCCCAGGTGGCCCAGGTCTGCACCG  
CGGCGGCCCTCGGCGCCATGGAGCCCCCGTATTCGCTGACGGCGCACTACGATGAGTTCCAAGA  
GGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGCGCGCGGGGCTCCCTGCCCCCGGGCTT  
CCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCCGGTCCGGGCTGCCGCGCTGGAACCGGCG  
CGAGGTGTGCTGCTGTCGGGGCTGGTGTTCGCCGCCGGCTCTGCGCCATTCTGGCGGCTAT  
GCTGGCCCTCAAGTACCTGGGCCCCGGTCGCGGCCGGCGGCGCGCCTGTCCCAGGGGCTGCC  
TGAGCGCAAGGCCTTCGCGCGCGCCGCTCGCTTCCTGGCCGCCAACCTGGACGCCAGCATCGA  
CCCATGCCAGGACTTCTACTCGTTTCGCTGCGGCGGTTGGCTGCGGCGCCACGCCATCCCCGA  
CGACAAGCTCACCTATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG  
CCTGCTGGCGCGGCCCGGGGGTGGGCTGGCGGCGCGGCCAGCGCAAGGTGCGCGCCTTCTT  
CCGCTCGTGCCTCGACATGCGCGAGATCGAGCGACTGGGCCCCGCGACCCATGCTAGAGGTCT  
CGAGGACTGCGGGGGCTGGGACCTGGGCGGCGCGGAGGAGCGTCCGGGGGTGCGGGCGCATG  
GGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCCGCGCGCTCTTCTCGCT  
CACGGTCAGCCTGGACGACAGGAACCTCCTCGCGCTACGTTCATCCGCATTGACCAGGATGGGCT  
CACCTGCCAGAGAGGACCTGTACCTCGCTCAGGATGAGGACAGTGAGAAGATCCTGGCAGC  
ATACAGGGTGTTCATGGAGCGAGTGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGC  
CCAAGAGATCCTGCAAGTGGAGCAGCAGCTGGCCAACATCACTGTGTGTCAGAGTATGACGACCT  
ACGGCGAGATGTCAGCTCCATGTACAACAAGGTGACGCTGGGGCAGCTGCAGAAGATCACCCC  
CCACTTGCGGTGGAAGTGGCTGCTAGACCAGATCTTCCAGGAGGACTTCTCAGAGGAAGAGGA  
GGTGGTGCTGCTGGCGACAGACTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCCA  
CCGGGTCCTGCACAACTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCCC  
GCCATTCCGTGAGGCACTGCACGAGCTGGCAGGATGGAGGGCAGCGACAAGCCACAGGA  
GCTGGCCCCGGTCTGCTTGGGCCAGGCCAATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTT  
TGACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGCAGCAGCTAGTGGAACAGACATCAA  
GTACATCCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGGCTGCTGC  
TCGGGCCAAGCTCCAGTACATGATGGTGATGGTTCGGCTACCCGGACTTCCTGCTGAAACCCGA  
TGCTGTGGACAAGGAGTATGAGTTTGGAGTCCATGAGAAGACCTACTTCAAGAACATCTTGAA  
CAGCATCCCCTTCAATCCAGCTCTCAGTTAAGAAGATTCGGCAGGAGGTGGACAAGTCCAC  
GTGGCTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCAGATGGTGT  
CCCCGCGGGCATCCTGCAGCCACCCCTGTACGACCCTGACTTCCACAGTCTCTCAACTACGG  
GGGCATCGGCACCATCATTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGCCAGTA  
TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCCTCCTACAGCCGCTTCTGCGAAA  
GGCTGAGTGCATCGTCCGTCTCTATGACAACTTCACTGTCTACAACCAGCGGGTGAACGGGAA  
ACACACGCTTGGGGAGAACATCGCAGATATGGGCGTCTCAAGCTGGCCTACCACGCCTATCA  
GAAGTGGGTGCGGGAGCACGGCCCAGAGCACCCACTTCCCCGGCTCAAGTACACACATGACCA  
GCTCTTCTTCATTGCCTTTGCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCATCTACCT  
GCAGGTGCTGACTGACAAGCATGCCCCCTGAGCACTACAGGGTGTGGGCGAGTGTGTCCCAGTT  
TGAGGAGTTTGGCCGGGCTTTCCACTGTCCCAAGGACTCACCCATGAACCCTGCCCACAAGTG  
TTCCGTGTGGTGAACCTGGCTGCCCCGCTGCACGCCCCCACTGCCCCCGCACGAATCACCTCC  
TGCTGGCTACCGGGGCAGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCACCACCTGCCTTCC  
AGCCCCCTCAGGACCCGGTCCCCCTGCTGCCCCCTCACTTCAGGAGGGGCTGGAGCAGGGTGA  
GGCTGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGG  
CCAGACCTCTGCCAGGCTGGATTGTACGGGCCCACTTCGCTGTGTTCTTGCTGCAAAGTC  
TGGTCAATAAATCACTGCACTGTTAAAAA

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**FIGURE 120**

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPPGFPLGAARSVTGARSGLPWRNRREVCLL  
SGLVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPEKAFARAARFLAANLDASIDPCQDF  
YSFACGGWLRRAIPDDKLTGTIAAIGEONEERLRLLARPGGGPGGAAQRKVRAFFRSCLD  
MREIERLGPRPMLEVEDCGGWDLGGAEEPPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLD  
DRNSSRYVIRIDQDGLTLPERTLYLAQDEDESEKILAAAYRVFMERVLSLLGADAVEQKAQEILQ  
VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLLDQIFQEDFSEEEVLLA  
TDYMQQVSQLIRSTPHRVLHNYLVWRVVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVC  
LGQANRHFGMALGALFVHEHFAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAARAKLO  
YMMVMVGYPDFLLKPDADVKEYEFVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLLPP  
QALNAYYLPNKNQMVFPAGILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGN  
LLHWWTEASYSRFLRKAECIVRLYDNFTVYNQRVNGKHTLGENIADMGVKLKAYHAYQKWVRE  
HGPEHPLPRLKYTHDQLFFIAFAQNWCIKRRSQSIYQLVLTDKHAPEHYRVLGSVSQFEEFGR  
AFHCPKDSMPNPAHKCSVW

**Important features of the protein:****Transmembrane domain:**

amino acids 64-88

**N-glycosylation sites.**

amino acids 255-259, 322-326, 656-660

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 722-726

**N-myristoylation site.**amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,  
169-175, 170-176, 237-243, 450-456, 604-610, 607-613**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

**Prenyl group binding site.**

amino acids 772-777

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 609-619

**Neutral zinc metallopeptidases, zinc-binding region proteins.**

amino acids 609-619

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**FIGURE 121**

CGGACTGCCCCGACCGCGCGATGGAGTCGACCGGCAGCGTCGGGGAGGCCCCGGGCGGACCCC  
GGGTGCTGGTGGTGGGCGGCGGCATCGCGGGGCTGGGCGGCGCAGAGGCTCTGCGGCCACT  
CCGCCTTCCCGCACCTGCGGGTCCTGGAGGCCACGGCCCGCGCCGGGGGCCGCATCCGCTCGG  
AGCGCTGCTTCGGTGGCGTGGTGGAGGTGGGCGCGCACTGGATCCATGGGCCCTCCCGGGGTA  
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCAGGAGA  
ACCAGCTGGTGGAGACCGGGGGTCACGTGGGCCTGCCCTCCGTGAGCTACGCCAGCTCCGGGG  
CCAGCGTGAGCCTCCAGCTGGTGGCGGAGATGGCGACTCTGTTCTACGGCCTGATAGACCAGA  
CCCGGGAGTTCCTGCACGCTGCAGAGACCCCGGTGCCAGCGTCGGGGAGTACCTCAAGAAGG  
AGATTGGCCAGCACGTGGCCGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCCG  
TCCTGAACTCCTTCTTCAACCTGGAATGCTGTGTGAGCGGCACCCACAGCATGGACCTGGTGG  
CCCTGGCACCCCTTTGGGGAGTATACCGTGCTGCCGGGGCTGGACTGCACCTTTTCTAAGGGCT  
ATCAAGGACTCACAACTGCATGATGGCCGCCCTGCCGGAGGACACTGTAGTTTTTGAGAAGC  
CTGTGAAGACCATCCACTGGAACGGGTCTTCCAGGAGGCAGCCTTTCCCGGGGAGACCTTTC  
CAGTGTGCGGTAGAGTGTGAGGATGGAGACCGGTTCCCGGCGCACCATGTCATCGTCACCGTGC  
CCTTAGGTTTTCTTAGGGAACATTTGGACACCTTCTTTGACCCTCCCCTGCCGGCTGAGAAGG  
CAGAAGCAATCAGGAAGATAGGCTTTGGGACCAACAACAAAATCTTCCTGGAGTTTGAGGAGC  
CCTTCTGGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGGAGGACACGTCGCCCCCTGGAGG  
ATGCTGCCCCCTGAGCTACAGGACGCCTGGTTCGGGAAGCTCATTTGGCTTTGTGGTCTGCCTG  
CCTTTGCGTCTGTCCACGTTCTCTGTGGGTTCATTGCCGGAAGTCTGAGTCTGAGTTCATGGAGA  
CTCTGTGCGGATGAAGAAGTACTTCTGTGTCTCACCCAAGTGTCCGGAGAGTGACAGGAAACC  
CACGGCTCCCCGCGCCCAAGAGCGTCTGCGGTCTCGCTGGCACAGCGCCCCGTACACTAGGG  
GGTCTACAGCTACGTGGCCGTGGGCGAGTACTGGGGGCGACCTGGACCTGCTGGCTCAGCCCC  
TCCCTGCAGACGGCGCCGGCGCCAGCTCCAGATCCTGTTTGCGGGGGAAGCCACACATCGCA  
CGTTTTACTCCACGACGCACGGGGCTCTGCTGTGCGGGATGGAGGGAGGCCGACCGCCTCCTCA  
GTCTGTGGGCCCCGCGAGGTGCAGCAGCCCAGGCCGAGGCTCTAGCTGGGCCCAGCCTACTCTG  
TTCCACCCGTGTCGGGGGTAGGCTGGGACCGTCATTTCTTCTGACAGATTTAGTCTGGCTTG  
AAATTTGGGGATGTTAATGAGGGTCTCTGGTTTTTGGTAACCAGGGCCACCTTCTCAGTTCT  
TGTGTCTGTTATTGGAGTCTGGCCAGGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA  
TGCTGGACACATAAAGCAAGTTACAGCCACAAAAAAAAAAAAA

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**FIGURE 122**

MESTGSVGEAPGGPRVLVVGGGIAGLGAAQRLCGHSAPPHLRVLEATARAGGRIRSERCFGGV  
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQENQLVETGGHVGLPSVSYASSGASVSLQL  
VAEMATLFYGLIDQTREFLHAAETPVPSVGEYLLKKEIGQHVAGWTEDEETRKLLAVLNSFFN  
LECCVSGTHSMDLVALAPFGEYTVLPGLDCTFSKGYQGLTNCMMAALPEDTVVFEPVKTIHW  
NGSFQEAAPGETFPVSVECEDGDRFPAHHVIVTVPLGFLREHLDTFFDPPLPAEKAEAIRKI  
GFGTNNKIFLEFEEPFWEPCQLIQLVWEDTSPLEDAAPELQDAWFRKLIGFVVLPAFASVHV  
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA  
VGSTGGDLDLLAQPLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV  
QQPRPRL

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 364-385

**N-glycosylation site.**

amino acids 253-257

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 408-412

**N-myristoylation sites.**amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,  
216-222, 227-233, 443-449, 484-490**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497

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**FIGURE 123**

CGGACGCGTGGGGGAAGATGGATAAATAATTCTGTACACAGTGGCCCTGGCCTCTGGAGCTCAGCTGCCAGTCCAC  
GTCTAGGGAATCTTAGCATCTGGGACCAAGACACTTTACAGCAATCATCACCTTTGTCAGAGGAGGTGAGCTCAC  
CAGGACTCATCTGCCATTTTCAGACCTTTTGTCTGTACCTGCCAGGTGGCCCCACTGCTGACGAGAGATGGTGGGA  
TCTCTCAGTCTCCCCGACTCCTTGAAGCCAGTATCGCTGACCAGCAGTCTTGTCTTCTCATGCACCTCCTCCT  
CCTTCAGCCTGGGGAGCCGAGCTCAGAGGTCAAGGTGCTAGGCCCTGAGTATCCCATCCTGGCCCTCGTCGGGGA  
GGAGGTGGAGTTCCCGTGCCACCTATGGCCACAGCTGGATGCCAGCAAATGGAGATCCGCTGGTTCCGGAGTCA  
GACCTTCAATGTGGTACACCTGTACCAGGAGCAGGAGCTCCCTGGCAGGCAGATGCCGGCGTTCCGGAACAG  
GACCAAGTTGGTCAAGGACGACATCGCCTATGGCAGCGTGGTCCCTGCAGCTTCACAGCATCATCCCCCTTGACAA  
GGGCACATATGGTGCCGCTTCCACTCCGACAACCTTCTTGCCGAAGCTCTCTGGGAACTGGAGGTAGCAGGGCT  
GGGCTCAGACCCTCACCTCTCCCTTGAGGGCTTCAAGGAAGGAGGCATTAGCTGAGGCTCAGATCCAGTGGCTG  
GTACCCCAAGCCTAAGGTTTCACTGGAGAGACCACAGGGACAGTGCCTGCCTCCAGAGTTTGAAGCCATCGTCTG  
GGATGCCAGGACCTGTTTCACTCTGGAAACATCTGTGGTCTCCGAGCGGGAGCCCTCAGCAATGTGTCCGTCTC  
CATCCAGAATCTCCTCTTGAGCCAGAAGAAAGAGTTGGTGGTCCAGATAGCAGACGTGTTCTGATCCCGGAGCCTC  
TGCGTGGAAGAGCGGTTCTGTCGCGACCTGCCGCTGCTGTTGGTCTCGCGCGCTGGCGCTGGGCGTCCCTCCG  
GAAGCAGCGGAGAAGCCGAGAAAAGCTGAGGAAGCAGGCGGAGAAGAGACAAGAGAACTCACTGCAGAGCTGGA  
AAAGCTTCAGACAGAGCTTACTGGAGACGGGCTGAAGGCCAGGCTGAGTGGAGAGCAGCCAAAAATATGCAGT  
GGATGTGACGCTGGACCCGGCCTCGGCGCACCCAGCCTGGAGGTGTCGGAGGATGGCAAGAGCGTGTCTTCCCG  
CGGGGCGCCGCGCAGGCCCGGCGCTGGCCACCCGACGCGTTCTCGGAGCAGACGTGCGCGCTGAGCCTGGAGCG  
GTTCTCCGCGCGCCGCGCACTACTGGGAGGTGCACGTGGGCGCGCGCAGCCGCTGGTCTTGGGCGCTGCCTGGC  
CGCGGTGCCGCGCGCGGGGCTGCGCGCCTGAGCCTGCGGCGCGCTACTGGGTGCTGGGGCTGTGGAACGGCTG  
CGAGTACTTCGTCTGGCCCCGACCGCGTCGCGCTCACCTGCGCGTGCCCCCGGCGCGCTGGGCGTCTTCTCT  
GGACTACGAGGCCGGAGAGCTGTCTTCTTCAACGTGTCCGACGCTCCACATCTTACCTTCCAGCACCTT  
CTCGGGCGCGCTCTGTGCGTACTTCAGGCCCAGGGCCACGACGGCGGCGAACATCCGGATCCCTGACCATCTG  
CCCGCTGCCGCTTAGAGGGACGGGCGTCCCCGAGAGAAAGACAGTACACCTGGCTACAGCCCTATGAGCCCGC  
GGACCCGCGCTGGACTGGTGGTGAAGGCGCCCTCGTGCCGCGGGACTGGCCCCGGGGGGCCCCCTGGATCCAG  
GCCAGCGCTTTGCTCTCTGCTCCGTCTGAAGGGAGCAGGTGCACAGCCAAAATGTAGCGAGGGGGACAAAGA  
GAGGGACCTTTGCTACGTAGATGTGTATGTGTAGTGCGATTTTCTTCAAGGAAAGGAGACAAAGTCCAAAGCTCG  
TTTGTGGATTGTGGGACTGAGCGAAGGAGTACAAATATATCCACGTGCTCAGAGCTGGGGTGCTCACGGTGGGC  
GGTGGGCAAGAAGCCAGCATGGAAGAAAGAAAGGAGAAAACCTTTGGTGAAGTGCCTTAGAGGGATCAGTTAATTTG  
TATAGTTTTATATTTTTGTATATGTTTGTAGCTCTAAAAGGTGCGAGATGCAATAACACTTCGTAAGCAACGA  
GTTTACCTAAGTAAGGCTCAGATCCTAGTTTTAAAAACCTTTCCCATTAATAAGTTGGAGGAACAGCTGCT  
TCTGAGCCGGGGCAAAAATTTCAAGGTGAGCCTGGAGCATTGTGTGTGGTGAAGTAAAAATAAAGGCTCAAAACGT  
GACGGCAACCCGGCAAAAGGTAGGGAGCCAGGCCGAAGGGGCTCACTGACCAATTGTGGGACAATTTGAACAT  
CAGGATGAATAATGACAGGAGAGATTATAACACACTGAATAAAAACATAATCCATGAGTTCATGCTGATACTCAA  
ATTTCTTTTTAAAAAGGAGAAACAGGAAGGTTCTTTTGGAGGTGAAATCTAATTATTGGTGAGAGTCTTGGAGA  
ACAGGCTGTTTCCAGTCTCAAAGCAGTAACCTTATACACTACTTATAAGTTTGAAAGGGGAAAGGTTACCTTTAC  
AATGGAGACATCTACCAGATCATCCAAGTGATTAATTTAACATCATCAATGATGGGACCAAGGACATTATTAGT  
TTGACAACTGGGGAAAGAAGTGTCTTACCCCTACCCCAAGACATTCTCTGTGCGCCAGGCTGGAGTGCA  
GCCTCAACCTCCTGGGCCAAGTGATCCTCCACCTCAGCACACAACACCATGCCCAATTTTAAGTGGCTTATAG  
AGACGGGGGTCTCACTTTGTTACCCAGGCTGGTCTCAAACCTCTGCGCTCAAGCAATCCTCCCACCTGGGCTCC  
CAAAATGCTGGGTGTACAGGCATGAGCCGCTGTGCCTGGCTTCATTTTTCAGAGTGAGACATTTGACTGTGGCTA  
TGTAAGGAGAACATTCTTGTCTTAGCAACATACTGAAGTTTTTAGATATTAAATTACCACAGTGTCTGCCACTGA  
ATTTCCAGTGACTAAGTGGAAAAATATAAAACATATGAATATAAAGAAAGAAAGAGACAAGTCAAATGTAGTAAA  
ATGACAACACTTGGTGACTCTAGGTGACTGGTCGACAGATGTTTATTGACTATCAATGTGGCTTTGCTGTGGGT  
TTGAAATTTTGAACTAAGAGTTGGGTGGCGGGGAGAAGGATACACCAAAAACTAAGTGATTATCTTTGGATG  
GGAAATGTTTGGTAATTGCATTCTTAAATGTCTTCTTTGTATTTTTTAATGTTCAATAATGTATATGTATCAG  
TTCTGTAATAAAGGGGAAACACTTTTCA



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**FIGURE 124**

MVDLSVSPDSLKPVS LTSSLVFLMHLLLLQPGEPSSEVKVLGPEYPILALVGEEVEFPCHLWP  
QLDAQQMEIRWFRSQT FNVVHLYQEQQELPGRQMPAFRNRTKL VKDDIAYGSVVLQLHSIIPS  
DKGTYGCRFHSDNFSGEALWELEVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH  
QGQCLPPEFEAIVWDAQDLFSLETSVVVRAGALS NVSVSIQNLLLSQKKELVVQIADVFPGA  
SAWKSAFVATLPLLLVLAALALGVLRKQRRSREKLRKQAEKRQEKLTAELEKLQTELDWRRAE  
GQAEWRAAQKYAVDVTLDPASAHPSLEVSEDGKSVSSRGAPPGPAPGHPQRFSEQTCALSLE  
FSAGRHYWEVHVGRRSRWFLGACLAAPRAGPARLS PAAGYWVLGLWNGCEYFVLAPHRVALT  
LRVPPRRLLGVFLDYEAGELSFNVS DGS HIFTFHDTFSGALCAYFRPRAHDGGEHPDPLTICP  
LPVRGTGVPEENDSDTWLQPYEPADPALDWW

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 247-272

**N-glycosylation sites.**

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

**Tyrosine kinase phosphorylation site.**

amino acids 105-114

**N-myristoylation sites.**

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

**Amidation site.**

amino acids 390-394

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**FIGURE 125**

TATAGTCCCAGCTACTCATGGGGCTGATGCAGGTTGAGGCAGGAGGTTTCATGAGCCCAGGAGGTTGGAGCTGTAA  
TGAGCTAGGATTCTGCCTCTGCACTCCTAGCTGGATGACAGAGCAAGACCCTGTCTCAAAAAAGAAAAA  
AAAAAGAATGCATGAACCAGACATGACAGTTCCTGGCCTCAAAGATCTTCCAAAGGAAATGATTTTTTTTTAAACC  
ACCAATGCTGCAGAAAAAGCAACATATTTAAGTTATCCAATAACACCTATCCAATAATTGTAAATCATTATCAT  
GACATGGTAGAGTTGTTTATATTTCTTTTCTTTTAGGTGAAACACCATTCAAAGTCGTAGTCAAATCTCTTTCA  
CCTAAAGAGTTGGTCCGGATACATGTCCCTAAACCTTTGGACAGGAATGATGGAACATTTTGTATGAGATATAGG  
ATGTATGAAACTGTCGATGAAGGCCTGAAGATAGAGTCTTTATGGTGATGAACATGTGGCTCAGTCTCCCTAT  
ATTTTGAAGGACCAGTGTACCATGAGTACTGTGAGTGTCCGGAAGATCCTCAGGCCTGGCAGAAAGACTCTTTCT  
TGTCCAACCAAGGAACCACAGATTGCAAAAGATTTTGCTTCTTTCCAGCATCAATCTCCAGCAAATGCTAAAA  
GAAGTCCCCAAAGGTTTGGGGATGAGAGAGGTGCCATTGTTTATTACAGGATTCTCAATAACCATGTTTACCGG  
AGATCTTTAGGGAATAACACAGACTTCAAGATGTTCTCTGATGAGATTTGTTTATCATTGACAAGAAAGTCCCT  
CTCCAGATTTAGAATTTTTATGTTAATCTTGGAGATTGGCCCTTGGAGCATCGAAAAGTCAATGGAACCCCTAGC  
CCCATACCTATCATTTTATGGTGTGGCTCTCTGGATTCAAGAGATGTTGTCTTCCAACGTATGACATCACCCAC  
TCCATGCTTGAAGCCATGCGGGGTGTACAAATGATCTCCTCTCTATTAGGGAAATACAGGGCCTTCTGGATC  
AATAAACAGAGAGAGCTTTCTTCAAGGTAGAGACAGCCGAGAGGAGAGGCTCCAGTTGGTACAGCTGTCCAAA  
GAAAATCCTCAGCTACTAGATGCAGGAATTACAGGATATTTCTTTTCCAAGAGAAAGAAAAGGAGCTTGGAAAA  
GCCAAGTTGATGGGTTTCTTTGATTTCTTTAAGTACAAGTATCAAGTAAATGTGGATGGGACCGTGGCTGCTTAC  
AGATATCCATATCTCATGCTGGGCGACAGTCTGGTTTAAAGCAGGACTCGCCATATTATGAACATTTCTACATG  
GCACTAGAACCCTTGAAGCATTATGTTCCAATTAAGAAATCTGAGTGATTTATTAGAGAAAGTTAAATGGGCT  
AAGGAAAATGATGAAGAAGCCAAGAAGATTGCAAAAGAAGGACAGTTGATGGCTAGGGACCTACTACAGCCACAC  
AGGCTTTTACTGCTACTATTACCAAGTACTGCAGAAATATGCCGAGCGCCAGTCCAGCAAACCCGAAGTACGTGAT  
GGAATGGAACCTGTTCTCAGCCAGAAGATAGCACAGCCATCTGCCAGTGCCACAGGAAAAAGCCTTCAAGAGAA  
GAACTTTGAGTCTAGCCCAGAATCACACTCCTGTGTATCCCGGTACACTTTAAGGAAAGATTGAATCTAAGCTGT  
GAAGGACAGTATAGAAGACTGCACCAAGTGGACTAGTTCTCCCGTGGCTTTATATATGTAGATGGATATAGCAG  
TACTGGTTGAGTATCCCTCATCTGAAATGCTTAGGACCAGGAGTGTTTCAGGCTTCAGATTTTTTAAGATTTGGG  
AATATTTGTCATGTACATAATGAGGTATCTTGGGGATGAGATCCAAGTCTAAACACAAAATTCATTTATATTTAT  
ATATACCTTGTTCACATACCTGAAGGTAATTTTATATAATATTTTAAATAATTTGTGCATGAACACAAAGTTTGT  
ATACATTGAAGTGTGAGAAAGCAAAGGTGTCACTATCTTAGCGACCCAAGTGGTGGTGTGAGCACTCAAAAAGTT  
TTGGATTTTGGGGTATTTTCAAGATTTTAGATTTTGTATGAGGAATGTTCAACCTGTATTTGAACAAGCATTACCA  
AATATCATTTGAATATTAATATCTTTTGGCTAAAACTGCTATTATCAGCATCATAGTTTCTCTAAAAAGAAAACT  
TGGGGATCATAGCCGATAGAGAGACTTGCTAAAAATATAAATCAGCCTCTGCAAACTGTTTACATATTTATGGT  
TTACATATTTTATTGGTTTATTTCTATCCCTGTTCACTTTTCTCTTCCACTTCCAATTATGAAGAGAAAATAT  
TTGTTTCAAGGTTGTCCCCCGCCCCCGTCACTGCATAATTTCTCTCTTACAAGCTGCTTTTGGCTTTCATTAA  
TAACAGCTTCTTTTGAAGGTCTGATAAGGATATTTAAGGAAGAAGAGAATGACTCTGTTATTAAAGGTGGCAT  
GGAGACTGTGGAGGGAATATTTTAAAGCACTACTCATATCCTTTAAACTAAATTTTGCCAAAGCCCGAGACAA  
CATTAAAGGAGAAATTTGACCTTAAGTTAGTAATTTCAAATCTATCTGAGTTGTATACCCATCAAGAGCAATACAG  
TTATTAACATAGATGAAGGTATGCTATAGGCATCATTATTATCTATATTGAATAGGTGAAAGATAACTGTAG  
TCAGGTGAAAGGCATTATCATTTTAAAGCTGAAAAGGGGATCCTTGAAAACACTGAAAACCTCTACAACAATCT  
TCAGGAAGCCTGCTATCTTGGGATTCATAATAATAGGCCAAGAACAAAGGCAAGCATCCATTCTCTACTCCACC  
ACTTTTCTATTTTCAAGTGGGTGCTGCTACGATGAAGACTTTGGAAATTTCTTTCTCTTTTAGGACAGGGTCA  
GGATTTAGGACTCATAGCCTGAAAGCTCATTTACATACTCCTTGTAAACCATCAGTCCAAGGTTTCAAGTTCAATAAG  
TGCATGTTCTAAACAAGAGCTATCCTCATTTCAAATTTTAAATATGTACTCTGGCCGGTTCAGTGGCTCACG  
CCTGTAATCCCAGCACTTTGGCAGGCCGAGATGGGCGGATCTTTGAGGTGAGGAGTTTGAAGCAGCCTGGCCA  
ACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCATTTGCCTGTAATCCCAGCT  
ACTCGGGAGGCTGAGGCAGGAGAACTCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTACACCACTG  
CACTCCAGCCTGGGTGACAGAGTGAGACTCCATCTCAAAACTGAAAATAAAAATAAAAATATGTATTCTCTTAA  
CTGAAATATTTACTTAATCTGGAACAATGTAACATTTTAAAGTGGTTACATCTATTCTTGTGTAAGAACAA  
TAAACAGAATTTTTTGAAGTAAAGCAATTTTCAAGACAGTCTAATCAATGCCAAGTATCCAAGGCAAACTC  
TAATACCATCCATTGTGCAAAACCACAAGCAGCAAGTATTAATAAGAGCAAGCTGTCTGAGCCCATACCTA  
ATGAATTTGTGCTTTAAATATTGTACATTGTGTTGAGGCTGTCAAACCTGGGATTATGGCAAGAAAGGTTGGC  
TAACCTCATACCTTTCTGCCTCAAATTCAGGTGCTAAAGGCTAATGGCATTTTAAACATCTTCAATTTTAA  
TTTATATTGCTCTGCCAAACAGGCCTAATAGTTAAAGCAAGTTGAGACAAACCAGGCAGATTCAAGTGTGTGGA  
ACAGGAAGGATGTGCTTTAAAAAAGGTGGAATCCCTCAAAATTTCTATAGGAGACAGCAGCCTTAATCTACA  
TAATTTCTCATCTCGCAATTCAAGCCGAGCCTTTAAGAGGTTAGTGTTAATGGCTTTCTGGTTTGAACAAAA  
ATGCATCTATGTGGTTGAAAGTTTGGGAGGAGATTACCAATATCTGAGGAGAAGATGGAGTGAAGGGAATCTT  
ACTTTTGTCTTTTATACCTTTCTATAATATTTAGATTTTCTTTTACTGTAAAGTATGGATCAAAATGCAAAATAAG  
AAAAATGCCAACCTTAGAAAAGACAATAAATGCACAAAAGATATAAACAGGAACAGCAAAATATTTATTTTTTC  
CATTTTGTCTTTTTTAAATCTATGTTTGAACCTTTATATCTTGGGACTTATGTATATATATACCTTTTAAATAAA  
ATAAATTTTCTAAATAAAAGTTG

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**FIGURE 126**

MVELFIFLFLLLGETPFKVVVKSLSPKELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL  
YGDEHVAQSPYILKGPVYHEYCECPEDPQAWQKTLSCPTKEPQIAKDFASFPSINLQQMLKEV  
PKRFGDERGAIVHYTILNNHVYRRSLGKYTDFKMFSDDEILLSLTRKVLLPDLEFYVNLGDWPL  
EHRKVNGTSPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLLSIQGNTGPSWINKT  
ERAFFRGRDSREERLQLVQLSKENPQLLDAGITGYFFFQEKELGKAKLMGFFDFFKYKYQV  
NVDGTVAAYRYPYLMGLGDSLVLKQDSPYYEHFYMALEPWKHYVPIKRNLSDLLEKVKWAKEND  
EEAKKIAKEGQLMARDLLQPHRLYCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC  
HRKKPSREEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 250-254, 363-367

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 444-448

**N-myristoylation site.**

amino acids 208-214, 319-325, 388-394

**Endoplasmic reticulum targeting sequence.**

amino acids 448-453

**Mitochondrial energy transfer proteins signature.**

amino acids 25-34

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**FIGURE 127**

AGCCGTCGGAGGGAGCCGGAGCGCTTCTCCCGAGTTGGTGATAGATTGGTGGTCATCCAACAT  
GCAGAAATGAATGAGCAGTGAAAAGCAGCAGAGCCGATGGGTCATGAGGATGTAAGTGCCTTT  
GAAGGCTTCCACACCCCTCTACTCCAGGAATCATGAATAAACTGGAGGATAAGCAGGACCAGAT  
GATACCATGAAGAGAAGTTTACAGGCCCTCTATTGCCAACTGTTAAGTTTCCTGCTGATCTTG  
GCACTGACCGAAGCGCTGGCATTGTCATCCAGGAACCATCTCCAGGGAATCTCTTCAGGTC  
CTCCCTTCAGGCACTCCCCCGGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACT  
TCTGTGGTGATGCTGACCCCCAATCCCGATGGACCCCCCTCACAGGCTGCAGCTCCCATGGCA  
ACACTGACACCCCGTGAGAGGGGACCCCTCCTACGCACACCATCTCCACCATCGCTGCGACA  
GTAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCCCCGCTCCAGCAGCCATGGCAACC  
ACATCCTCCAAGCCAGAGGGCGCCCTCGAGGGCAGGCTGCCCCCACCATCCTGCTGACAAAG  
CCACCGGGGGCCACCAGCCGCCCCACCACAGCGCCCCCCCCGCACTACCACACGCAGGCCCCC  
AGGCCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTCATCACGCCCTGTCCCGCCTGCACCT  
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAAATCCAAGCTCCACACCTCTGGGG  
CAGAAGCGGCCCTGGGGAAAATCTTTCAGATCTACAAGGGCAACTTCACAGGGTCTGTGGAA  
CCAGAGCCCTCTACCTCACCCCCAGGACCCCACTCTGGGGCTACTCCTCTTCACCACAGCCC  
CAGACAGTGGCTGCGACCACAGTGCCCGAGCAATACCTCATGGGCACCCACCACACCTCCCTG  
GGGCTGCAAAGGACAAGCCAGGCCTTCGCAGAGCAGCCAGGGGGGTGGTTCTACCTTCACC  
AGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTGAGTCCACAAGCTGCC  
CCAGTGCCCTTCTCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCT  
TGGCTTACTGTTACCCCTGGCACCAGCAGACCTCTGTCTACCAGCTCTGGGGTCTTCACGGCT  
GCCACGGGGCCACCCAGCTGCCTTCGATACCAGTGTCTCAGCCCCCTTCCAGGGGATTCTT  
CAGGGAGCATCCACAACCCCAAGCTCCAACCCATCCCTCCAGGGTCTCAGAAAGCACTATT  
TCTGGAGCCAAGGAGGAGACTGTGGCCACCCTCACCATGACCGACCGGGTGCCAGTCCTCTC  
TCCACAGTGGTATCCACAGCCACAGGCAATTTCTCAACCGCCTGGTCCCCGCCGGGACCTGG  
AAGCCTGGGACAGCAGGGAACATCTCCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCC  
ACCATCTGCCTGAGCAAGATGGATATCGCCTGGGTGATCCTGGCCATCAGCGTGCCCATCTCC  
TCCTGCTCTGTCTGCTGACGGTGTGCTGCATGAAGAGGAAGAAGAAGACCGCCAACCCGGAG  
AACAACCTGAGCTACTGGAACAACACCATCACCATGGACTACTTCAACAGGCATGCTGTGGAG  
CTGCCCAGGGAGATCCAGTCCCTTGAAACCTCTGAGGACCAGCTCTCAGAGCCCCGCTCCCCA  
GCCAATGGCGACTATAGAGACACTGGGATGGTCCTTGTTAACCCCTTCTGTCAAGAAACACTG  
TTTGTGGGAAACGATCAAGTATCTGAGATCTAACTACAGCAGGCATCACTTTGCCATTCCGTA  
TTTTTCGTCTCTAAATTATAAATATACAAATATATATATTATAAATATAACCTTGTGTAACCC  
TGACTTAATGAGAAACATTTTCAGCTTTTTTTCCTATGAATTGTCAACATCTTTTTTACAAGT  
GTGGTTTAAAAAAAAAAAAAATTTACAGAATGATCTGTGGCTTTATAAAATAAAGGTATTTCT  
AAGCAAAAAAAAAAAAAAAAAA

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**FIGURE 128**

MKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESLQVLPSGTPPGTMVTAPHSSTRHTSV  
VMLTPNPDGPPSQAAAPMATLTPRAEGHPPTHISTIAATVTAPYSESSLSTGPAPAAAMATTS  
SKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRPPGSSRKAGNSSRPVFPAPGG  
HSRSKEGQRGRNPSSTPLGQKRPLGKIFQIYKGNFTGSVEPEPSTLTPTPLWGYSSSPQPQT  
VAATTVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDATAASGAPVSPQAAPV  
PSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQG  
ASTTPQAPTHPSRVSESTISGAKEETVATLTMTDRVPSPLSTVVSTATGNFLNRLVPAGTWKP  
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAI SVPISSCSVLLTVCCMKRKKKTANPENN  
LSYWNNTITMDYFNRHAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFCQETLFV  
GNDQVSEI

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 469-487

**N-glycosylation sites.**

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 495-499

**N-myristoylation sites.**amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,  
288-294, 296-302, 351-357, 374-380, 427-433, 442-448**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

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**FIGURE 129**

AGGCGAGGCGCGGCGCCGCTGCACACACGCACACGGAGCTATGGGGTGCCATGTTGCCACCAG  
CTGCCACGTGGCCTGGCTTTTGGTGCTGATCTCTGGATGCTGGGGCCAGGTGAACCGGCTGCC  
CTTCTTACCAACCACTTCTTTGATACATACCTGCTGATCAGCGAGGACACGCCTGTGGGTTT  
TTCTGTGACCCAGTTGCTGGCCCAAGACATGGACAATGACCCCTGGTGTTTGGCGTGTCTGG  
GGAGGAGGCCTCTCGCTTCTTTGCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGCC  
ACTGGACAGAGAGACCAAGTCAGAGTTCACCGTGGAGTTCTCTGTCAGCGACCACCAGGGGGT  
GATCACACGGAAGGTGAACATCCAGGTCCGGGATGTGAATGACAACGCGCCACATTTACAA  
TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACCAGTGGGGACGCCCATCTTCATCGTGAA  
TGCCACAGACCCGACTTGGGGGCAGGGGGCAGCGTCTCTACTCCTTCCAGCCCCCTCCCA  
ATTCTTCGCCATTGACAGCGCCCCGCGGTATCGTCACAGTGATCCGGGAGCTGGACTACGAGAC  
CACACAGGCCTACCAGCTCACGGTCAACGCCACAGATCAAGACAAGACCAGGCCTCTGTCCAC  
CCTGGCCAACTTGGCCATCATCATCAGATGTCCAGGACATGGACCCCATCTTCATCAACCT  
GCCTTACAGCACCAACATCTACGAGCATTCTCCTCCGGGCACGACGGTGCGCATCATCACC  
CATAGACCAGGATAAAGGACGTCCCCGGGGCATTTGGCTACACCATCGTTTCAGGGAATACCA  
CAGCATCTTTGCCCTGGACTACATCAGCGGAGTGCTGACCTTGAATGGCCTGCTGGACCGGGA  
GAACCCCTGTACAGCCATGGCTTCATCCTGACTGTGAAGGGCACGGAGCTGAACGATGACCG  
CACCCCATCTGACGCTACAGTCACCACGACCTTCAATATCCTGGTTATTGACATCAATGACAA  
TGCCCCGGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTGGGCTT  
TGCCCTTCCACTCTTCATCCAGGTGGTGGACAAGGATGAGAATTTGGGCCTGAACAGCATGTT  
TGAGGTGTACTTGGTGGGGAACAACCTCCACCACTTCATCATCTCCCCGACCTCCGTCCAGGG  
GAAGGCGGACATTCGTATTCCGGTGGGCTCCCACTGGACTACGAGACCGTGGACCGCTACGA  
CTTTGATCTCTTTGCCAATGAGAGTGTGCCTGACCATGTGGGCTATGCCAAGGTGAAGATCAC  
TCTCATCAATGAAAATGACAACCGGCCCATCTTCAGCCAGCCACTGTACAACATCAGCCTGTA  
CGAGAACGTACCGTGGGGACCTCTGTGCTGACAGTCCCTGGTGAGTCCCCGCTTCACTGCAGG  
GCCACTGAGCTCTCCAGGGCCGACTGTGGTGAAGCACCCAGAGGGATTTTGTCCAAGGGACCT  
CAGCAATCAGGGAAGGAGGCACCCCCAAATCCCTGAGCTGTGTTTGGTGTATTAAATAAA  
GTTTTTGGACTCTTCAGGAAGGGGCTCCCTTGACCTAGGTTGCAATATGGAAAAGGAGCCAAC  
CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTTCTGCCTTTCCCTGAGAGAGACTCAG  
TGAGGGTGGGCTGGGAGCCCTGGAAGCCCCCTCAAATGGGTGGGAAGGTGCCAGCCATCCTTG  
AGAAGGGCAACCCTCTCCATGTGAGCACAGGCACCAGAGAGGGGCAGGCGCCTGGAGGGTACC  
GGGGCACCCCACTGCCCCATGGCTGGACTTGCCCTTTGACAAGGGGCCCTCCAGTGTCATT  
TGTATCTGTCAGTACTCTTGTTGCAAGGGACAGAAACCCTTAAGTAGTTCAAGCAAAAAAGG  
ATTGGCTCATGTAACCAAAAGTATAAGTGATTTAGGCCGGGCTCGGTGGCTCACGCCTGTC  
ATCCAACACCTTGAGAAAGCCGAGGTGGGCGGATCACTTGAGGTGCGGAGTTTGAGACCAGCC  
TGCCCAACATGGCAAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGGTGTGGTGGCAC  
ACGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGG  
AGGTTGCAGTGAGCCGAGATTGTGTCACTGCCCTCCAGCCTGGGCGACAGAGCCAGATTCTGT  
CTC

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**FIGURE 130**

MGCHVATSCHVAWLLVLISGCWGVNRLPFFTNHFFDTYLLISEDTPVGSSVTQLLAQDMDND  
PLVFGVSGEEASRFFAVEPDTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN  
DNAPT FHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSFQPPSQFFAIDSARGIVTV  
IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQDMDPIFINLPYSTNIYEHSPPG  
TTVRIITAIDQDKGRPRGIGYTIVSGNTNSIFALDYISGVLTNLGLLDRENPLYSHGFILTVK  
GTELNDDRTPSDATVTTTFNILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVVDKDE  
NLGLNSMFEVYLVGNNSHHFIISPTSVQKGADIRIRVAIPLDYETVDRYDFDLFANESVPDHY  
GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLVSPRFTAGPLSSPGPTTVVRHP  
EGFCPRDLSNQGRRHPQIPELCLLVY

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 355-374

**N-glycosylation sites.**amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,  
472-476**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

**Amidation site.**

amino acids 515-519

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**Leucine zipper pattern.**

amino acids 298-320

**PTS HPR component serine phosphorylation site signature.**

amino acids 377-393

**Cadherins extracellular repeated domain signature.**

amino acids 120-131, 336-347

**Cadherins extracellular**

amino acids 120-144, 336-360

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**FIGURE 131**

GTGGGCCGCCCCCTGCTGCTGCCGTCCATGCTGATGTTTGCGGTGATCGTGGCCTCCAGCGGGC  
TGCTGCTCATGATCGAGCGGGGCATCCTGGCCGAGATGAAGCCCCTGCCCTGCACCCGCCCCG  
GCCGCGAGGGCACAGCCTGGCGCGGGAAAGCCCCAAGCCTGGGGGCCTGTCCCTCAGGGCTG  
GGGACGCGGACTTGCAAGTGCGGCAGGACGTCCGGAACAGGACCCTGCGGGCGGTGTGCGGAC  
AGCCAGGCATGCCCCGGGACCCCTGGGACTTGCCGGTGGGGCAGCGGCGCACCCCTGCTGCGCC  
ACATCCTCGTAAGTGACCGTTACCGCTTCCTCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA  
ACTGGAAGCGGGTGATGAAGGTGCTGGCAGGCGTCCTGGACAGCGTGGACGTCCGCCTCAAGA  
TGGACCACCGCAGTGACCTGGTGTTCCTGGCCGACCTGCGGCCTGAGGAGATTCGCTACCGCC  
TGCAGCACTACTTTAAGTTCTGTGTGCGGGAGCCCTTGGAACGCCTCCTCTCTGCCTACC  
GCAACAAGTTTGGCGAGATCCGAGAGTACCAGCAACGCTATGGGGCTGAGATAGTGAGGCGGT  
ACAGGGCTGGAGCGGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCCCGAGTTCCTGAGAT  
ACCTGGTGGATGAGGACCCTGAGCGCATGAATGAGCATTGGATGCCCCGTGTACCACCTGTGCC  
AGCCTTGTGCCGTGCACTATGACTTTGTGGGCTCCTATGAGAGGCTGGAGGCTGATGCAAATC  
AGGTGCTGGAGTGGGTACGGGCACCACCTCACGTCCGATTTCCAGCTCGCCAGGCCTGGTACC  
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGCAGTGCCCCCGGGCCCTGCTGCAGG  
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCCTCTTTGCCTACCCACTGCCTAATGTCACCA  
AGGAGGCGTGTCAGCAGTGAACCATGGGTGTGGGGCCAGCAGCTGGTGGGGACTGGTTTCAACG  
CCAGCTTTCTGTGCTTCTGCCTGTCATTCCGAGAAACTCTGGCTCTGGGGCTTGGGGCTTCTC  
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAGTTCCTTGTCCAGGGTGGGCACCCACAGTGA  
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCTCATTGGGGGGATCTCTTGGGGGGCA  
GACACCAGTTTGCCAATGAAGCAACACATCTGATCTAAAGACTGGCTCCAGACCCCGGGCTGC  
CAGGATTATGCAGTCCACTTGGTCTACCTTAATTTAACCTGTGGCCAAACTCAGAGATGGTAC  
CAGCCAGGGGCAAGCATGACCAGAGCCAGGGACCCTGTGGCTCTGATCCCCCATTTATCCACC  
CCATGTGCCTCAGGACTAGAGTGAGCAATCATACTTATAAATGACTTTTGTGCCTTTCTGCT  
CCAGTCTCAAAATTTCTACACCTGCCAGTTCTTTACATTTTCCAAGGAAAGGAAAACGGAA  
GCAGGGTTCTTGCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCTCTGTGCC  
CAGCCTCTTCCTTGAGTTCTCGGAACCTCCTCCCTAATTCTCCCTTCCTTCCCCACAAGGCCT  
TTGAGGTTGTGACTGTGGCTGGTATATCTGGCTGCCATTTTCTGATGCATTTATTTAAAT  
TGTACTTTTGTAGATAACCCTTGTAAGGGCTTTGTTTTCTAATAGCTGACTTTTAAATAAG  
CAGTTTTATATAT



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**FIGURE 132**

MLMFAVIVASSGLLLMIERGILAE MKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ  
DVRNRTLRAVCGQPGMPRDPWDLVPGQRR TLLRHILVSDRYRFLYCYVPKVACSNWKRVMKVL  
AGVLDSDVRLKMDHRSDLVFLADLRPEEIRYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE  
YQORYGAEIVRRYRAGAGPSPAGDDVTFPEFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF  
VGSYERLEADANQVLEWVRAPPHVRF PARQAWYRPASPESLHYHLCSAPRALLQDVL PKYILD  
FSLFAYPLPNVTKEACQQ

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 67-71, 325-329

**Tyrosine kinase phosphorylation sites.**

amino acids 152-159, 183-183

**N-myristoylation sites.**

amino acids 89-95, 128-134

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**FIGURE 133**

CGGCAGTTCTGGCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGGGTCGTAGTGCTGTTTCTG  
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTCTCCATG  
GCCTGGGCACCAAGTTCCCGGTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCAGAGGCC  
AATTCGTCGCGGCGGCGGTGGAGATCGCAGGTCGCTCAGGCTTGCAGATGGGTCAAGGGTTGT  
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCA  
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTTCTAACACCAATCATCGTAAACAAGTCC  
AAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA  
TTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGTCTACCTGAATGCAACTG  
ACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACTTCTCTGGCAAGGGT  
TGTGCAAATCCACTTGGGGTCACTGTTCCATATACAATAAGAACCCACCTTTAGGATTTTCTT  
TTAGAAAATTGTATATGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCCAGATGAGG  
GAGTGAACTACTTTATGTCCAAGGGTATCCTGGATGATTGCGCAAAGGAAATAGCAAAGTTTA  
TCTTCTGTACAAGAACTAAATTGGAAAAAAGTGAATCTATCTTGATGAAAGGAGAGATG  
TCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAAATGCACTGAGAG  
AATTTTTTCGTCATATCCATGCCCTGAAGAGCGTGGAGAGTATCTTGAACTCTTATAACAA  
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTG  
ATGCTGTCTATGTACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATG  
TGAAGAATAAAATGTCAAAAAGGGAATTTATTGAAATACCCGTCGCGCTGCTCAAAATATTA  
GTGAAGATTTTGTAGGGCATCTTTATGACAATATCTACCTTATTGGCCATGTGGCTGCATAAA  
AAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCCAAGGACTTAGCAGAT  
ATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC  
CTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAATAAATAATTTTGCAGA  
ATTTTTCCTAATTTTGTGTTTATCACGTTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTT  
AACGAATGATAAACTGACATTATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGA  
AAAACCTTTATCCATTTCCATTCTTTATACAAATACCATGTAATGTGTACATATTTAACTAAAG  
AGATTTATAGTCATAATTATTTATTGTAAAGATTTTAACTAAAGTTTTCTTTCTCTC

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## **FIGURE 134**

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMDASNISNTNHRKQVQGGIDIYHLLKARKSK  
EQEGFINLEMLPPELSFTILSYLNATDLCLASCVQDLANDELLWQGLCKSTWGHCSIYNKNP  
PLGFSFRKLYMQLDEGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTR TLNWKKLRIYL  
DERRDVLDDLVT LHNFRNQFLPNALREFFRHIHAPEERGEYLETLITKFSHRFCACNPDLMRE  
LGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNISEDFVGHLYDNIYLG  
HVAA

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 253-272

#### **N-glycosylation sites.**

amino acids 37-41, 87-91, 298-302

#### **N-myristoylation site.**

amino acids 110-116



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**FIGURE 136**

MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF  
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAKGM  
SETFETLHNLVHKGVKVVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL  
TEFLCANHVLKGKDTSCLAEQWSGKKGDTAALGGKSKKKSSRAKAAGGRSSSSKQRKELGGL  
EGDPSPEEDEGIQKASPLTHSPPEL

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**N-glycosylation site.**

amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 227-231, 228-232

**Tyrosine kinase phosphorylation site.**

amino acids 142-150

**N-myristoylation sites.**amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,  
250-256, 263-269**Amidation sites.**

amino acids 212-216, 222-226

**ATP/GTP-binding site motif A (P-loop).**

amino acids 62-70

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**FIGURE 137**

CACGCCTCCCGCTGCCAGCCCGGCACCGGGATCTTAATCAGTCACTATGAAAACCTCATTAGCT  
CCACAGCAATGAGTCCTCCACTGCTGAAGCTTGGCGCTGTGCTTAGTACCATGGCAATGATCT  
CAAACCTGGATGTCCCAAACCTCTCCCATCCTTGGTGGGACTGAACACCACGAGGCTGTGCGACTC  
CGGATACCTTAACCTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC  
CTGATGGGCGGTGCATTTGCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGGATGCCA  
AAAGCAGGCAACTTCGCCAACTACTGGAAAAGGTTTCAAGAACATGTCCAGTCTATTGAAGTCT  
TAAACTTGAGAACTCAGAGAGATTTCATATGTTTTAAAAATGGAAACCCAAATGAAAGGGC  
TGAAGGCAAAATTTCCGCAGATTGAAGATGATCGAAAGACACTTATGACCAAGCATTTTCAGG  
AGTTGAAAGAGAAAATGGACGAGCTCCTGCCTTTGATCCCCGTGCTGGAACAGTACAAAACAG  
ATGCTAAGTTAATCACCCAGTTCAAGGAGGAAATAAGGAATCTGTCTGCTGTCTCACTGGTA  
TTCAGGAGGAAATTGGTGCCTATGACTACGAGGAACACACCAAAGAGTGCTGAGCTTGGAAA  
CAAGACTTCGTGACTGCATGAAAAAGCTAACATGTGGCAAACCTGATGAAAATCACAGGCCAG  
TTACAGTCAAGACATCTGGAACCCGATTTGGTGGCTTGGATGACAGACCCTTTAGCATCTGAGA  
AAAACAACAGAGTCTGGTACATGGACAGTTATACTAACAATAAAATTGTTTCGTGAATACAAAT  
CAATTGCAGACTTTGTGCTAGTGGGGCTGAATCAAGGACATACAACCTTCCTTTCAAGTGGGCAG  
GAACTAACCATGTTGTCTACAATGGCTCACTCTATTTTAACAAGTATCAGAGTAATATCATCA  
TCAAATACAGCTTTGATATGGGGAGAGTGCTTGCCCAACGAAGCCTGGAGTATGCTGGTTTTTC  
ATAATGTTTACCCCTACACATGGGGTGGATTCTCTGACATCGACCTAATGGCTGATGAAATCG  
GGCTGTGGGCTGTGTATGCAACTAACCAGAAATGCAGGCAATATTGTATCAGCCAACTTAACC  
AAGATACCTTGGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGGGGAAT  
CTTTCATGATCTGTGGGACACTGTATGTACCAACTCCCACTTAAGTGGAGCCAAGGTGTATT  
ATTCCTATTCCACCAAAACCTCCACATATGAGTACACAGACATTCCCTTCCATAACCAATACT  
TTCACATATCCATGCTTGACTACAATGCAAGAGATCGAGCTCTCTATGCCTGGAACAATGGCC  
ACCAGGTGCTGTTCAATGTACCCCTTTTCCATATCATCAAGACAGAGGATGACACATAGGCAA  
ATGTGACATGTTTTTCAATTGATTTAAACAGTGTGATTTGTGATAAACTCTATAAGACCCCTTCC  
GTTTTTTTCTTCACTATTATTTTTTTCATCATTTCTCCAAAGCAAAGCATTTTTTATTGTAAAGTT  
GGTGTTCAAAAACATAGCTGAGCTTGTCTAAGTTACCATGTTGGAACACATCTTAAGTTCT  
AAATTTACAAGGCCTATCATGTCCTTGTATGAAAAGCACTAAAAAAAAAAAAAGAGTTAAGT  
GGCTAAAGTCATAGTTTGGCAAGAGATTAATGATCTGCCTTATATTAGAGTCAGAGACTAATG  
GTGGCTTAAATGCACGAATGTCTTTTTTTTTTAAACTGTCAATTTTTTACTGTCTTTTGCTCCA  
TCTCAGGAAATATTTTGGTAGGAATTAGGAGAACAAAAGCACTTTTATCCCATTTATTTCTT  
TAAAAAATGTAAGGATTTTCAATTTATATTGAAAAATAATATTAATCATTTTGTGTTAACACAA  
TTCTCTGATGCGGTGCTGTACAGTCATTTTTTAAATCTCTTGCTAACATTTTATTGGCAGTATG  
TATTTCTACCATTTGTAACCACCATTGTGCTATTGTATCTCTTCACTTCTGTGAAAGTAATATT  
TTTTATAAANACACTGNAATTTTAAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAA

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**FIGURE 138**

MSPPLLKLGAVLSTMAMISNWMSQTLPSLVGLNTRLSTPDTLTQISPKEGWQVYSSAQDPDG  
RCICTVVAPEQNLCSDAKSRQLRQLLEKVQNMSQSIEVLNLRRTQRDFQYVLKMETQMKGKLA  
KFRQIEDDRKTLMTKHFQELKEKMDLLEPLIPVLEQYKTDAKLITQFKEEIRNLSAVLTGIQE  
EIGAYDYEELHQRVLSLETRLRDCMKKLTGKLMKITGPVTVKTSGRFGAWMTDPLASEKNN  
RVWYMSYTNKIVREYKSIADFEVSGAESRTYNLPFKWAGTNHVYNGSLYFNKYQSNIIKY  
SFDMGRVLAQRSLEYAGFHNVPYPTWGGFSDIDLMADEIGLWAVYATNQNAGNIVISQLNQDT  
LEVMSWSTGYPKRSAGESFMICGTLYVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI  
SMLDYNARDRALYAWNNGHQVLFNVTLFHIIKTEDDT

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 215-219

**Tyrosine kinase phosphorylation site.**

amino acids 106-114

**N-myristoylation sites.**

amino acids 9-15, 31-37, 235-241, 239-245

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**FIGURE 139**

GAAGCAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGCTGAGCAAAGGCCTTCACCAATGGCCG  
AGTCCCCCGGCTGCTGCTCCGTCTGGGCCCCGCTGCCTCCACTGCCTGTATAGCTGCCACTGGA  
GGAAATGCCCCAGAGAGAGGATGCAAACCAGCAAGTGCGACTGTATCTGGTTTGGCCTGCTCT  
TCCTCACCTTCCTCCTTTCCCTGAGCTGGCTGTACATCGGGCTCGTCCTTCTCAATGACCTGC  
ACAACCTCAATGAATTCCTCTCCGCCGCTGGGGACACTGGATGGACTGGTCCCTGGCATTCC  
TGCTGGTCATCTCTCTACTGGTCACATATGCATCCTTGCTATTGGTCCTGGCCCTGCTCCTGC  
GGCTTTGTAGACAGCCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCTCCTCATTATGC  
TGCTTGTTGGCGGCTGGCCTTGTTGGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC  
GTGTGTCACTGCAGGCCACAGCCCCATTCCTTCATATTGGAGCAGCCGCTGGAATTGCCCTCC  
TGGCCTGGCCTGTGGCTGATACCTTCTACCGTATCCACCGAAGAGGTCCCAAGATTCTGCTAC  
TGCTCCTATTTTTTGGAGTTGTCCTGGTCATCTACTTGGCCCCCCTATGCATCTCCTCACCT  
GCATCATGGAACCCAGAGACTTACCACCCAAGCCTGGGCTGGTGGGACACCGAGGGGCCCCCA  
TGCTGGCTCCCGAGAACACCCTGATGTCTTGCGGAAGACAGCTGAATGCGGAGCTACTGTGT  
TTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCTTCCTCATGCATGATGAGCACCTCA  
GCAGGACCACGAATGTAGCCTCTGTATTCCCAACCCGAATCACAGCCCACAGCAGTGACTTCT  
CCTGGACTGAACTGAAGAGACTCAATGCTGGATCCTGGTTCCTAGAGAGGCGACCCTTCTGGG  
GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAG  
AAGAGCTATTGGAGGAAGCTGCAGCCCTCAACCTTTCATCATGTTGCACTTGCGCCGACCCC  
CACAGAACCACACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA  
GGGTGCCCCAAGCCATGGTCTTTTGGCTACCAGATGAAGATCGGGCTAATGTCCAACGACGGG  
CACCTGGAATGCGCCAGATATATGGACGTGAGGAGGCAACAGAACGGAGAGGCCCCAGTTTC  
TTAACCTCCCCTATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT  
CGGTGAACCTATTTGTAGTGAACAAGCCCTGGCTCTTCTCTCTGCTTTGGTGTGCAGGGGTGG  
ATTGCGTCACCACCAACGACTGCCAGCTGCTGCAGCAGATGCGTTACCCTATCTGGCTTATTA  
CCCCCAAACCTACCTAATCATATGGGTCATTACCAATTGTGTTTCCACCATGCTGCTTTTGT  
GGACCTTCCTCCTCCAAAGGAGATTTGTTAAGAAGAGAGGGAAAACCTGGCTTAGAAACAGCAG  
TGCTGCTGACAAGGATCAACAATTTTCATGATGGAGTGAATGCCCTGCCCTGCTTCCCCACCCA  
AGCCAGTCTACATTGCCCAAACAGCAAGGGTTGGAGAGTGGCTTAAGTGAATGCTTCAGGGG  
TGGTGGGTTGCAAGTGGGGGGAGCTTTGCCAACAGGAGGTTTGAACCATGAGGGCCCTCTGC  
CCAGGTGATGGGCATTCCCTAAGCTGCTATGGAATCTGCTCCCTTTGGGGTTTGGACCTGAGA  
TGTTTGGGAAGAGAGTGAGTAATGAGAAGTTTCTCCTCAAATGAACTAGAACAGAGGAAGTA  
AAAGGGAGATTGCTCGGA



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**FIGURE 140**

MAESPGCCSVWARCLHCLYSCHWRKCPRERMQTSKDCIWFGLLFLTFLLSLSWLYIGLVLLN  
DLHNFNEFLFRRWGHWMDSLAFLLVISLLVTYASLLLVLALLRLCRQPLHLHSLHKVLLLL  
IMLLVAAGLVGLDIQWQQEWHSRLRVSLQATAPFLHIGAAAGIALAWPVADTFYRIHRRGPKI  
LLLLLFFGVVLVIYLAPLCISSPCIMEPRDLPPKPGLVGHRGAPMLAPENTLMSLRKTAECGA  
TVFETDVMVSSDGVFPFLMHDEHLSRTTNVASVFPTRIAHSSDFSWTELKRLNAGSWFLERRP  
FWGAKPLAGPDQKEAESQTPALEELLEEEAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVL  
NARVPQAMVFWLPDEDNANVQRRAPGMRQIYGRQGGNRTERPQFLNLPYQDLPLLDIKALHKD  
NVSVNLFVVKPWLFSLLWCAGVDSVTTNDCQLLQOMRYPIWLITPQTYLIWVITNCVSTML  
LLWTFLLQRRFVKKRGKTGLETAVLLTRINNFME

**Important features of the protein:****Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506.

**N-glycosylation sites.**

amino acids 349-353, 362-366, 415-419, 442-446

**N-myristoylation sites.**

amino acids 163-169, 413-419, 523-529

**Leucine zipper pattern.**

amino acids 93-115, 109-131

**Glutamine amidotransferases class-II active site.**

amino acids 1-13

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FIGURE 141

[illegible]

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**FIGURE 142**

MYLVAGDRGLAGCGHLLVSLGLLLLLLARSSTRALVCLPCDESKCEEPRNCPGSIVQGVCGCC  
 YTCASQRNESC GGTFGIYGTCDRGLRCVIRPPLNGDSLTEYEAGVCEDENWTDQLLGFKPCN  
 ENLIAGCNIINGKCECNTIRTCSNPFEPSPQDMCLSAKRIEEKPDCKARCEVQFSPRCPE  
 DSVLIEGYAPPGECCPLPSRCVCNPAGCLRKVCQPGNLNILVSKASGKPGECCLYECKPVFG  
 VDCRTVECPVQQTACPPDSYETQVRLTADGCCTLPTRCECLSGLCGFPVCEVGSTPRIVSRG  
 DGTGPKCCDVFEVCVNDTKPACVFNNVEYYDGMFRMDNCRFCRCQGGVAICFTAQCGEINCER  
 YYVPEGECCPVCEDPVYPFNNPAGCYANGLILAHGDRWREDDCTFCQCVNGERHCVATVCGQT  
 CTNPVKVPGECCPVCEPTIITVDPPACGELSNCITLTGKDCINGFKRDHNGCRTCQCINTEEL  
 CSERKQGGCTLNCPEGFLTDAQNCEICECRPRPKKCRPIICDKYCPLGLLKNKHGCDICRCKKC  
 PELSCSKICPLGFQQDSHGCLICKREASASAGPPILSGTCLTVDGHHHKNEESWHDGCRECY  
 CLNGREMCALITCPVPACGNPTIHPGQCCPSCADDFVVQKPELSTPSICHAPGGEYFVEGETW  
 NIDSCTQCTCHSGRVLCETEVCPPLLCQNPSRTQDSCCPQCTDQFPRPSLSRNNSVPNYCKND  
 EGDIFLAAESWKPDVCTSCICIDSVISCFSESCPSVSCERPVLKRGQCCPYCIEDTIPKKVVC  
 HFSGKAYADEERWDLDSCTHCYCLQGQTLCTVSCPPLPCVEPINVEGSCCPMCPEMYVPEPT  
 NIPIEKTNHRGEVDLEVLWPTPSENDIVHLPRDMGHLQVDYRDNRHLHPSEDSSLDSIASVVV  
 PIIICLSIIIAFLFINQKKQWIPLLCWYRTPTKPSSLNNQLVSVDCCKKGTRVQVDSSQRMRLRI  
 AEPDARFSGFYSMQKQNLQADNFYQTV

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 940-962

**N-glycosylation sites.**

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 992-996

**N-myristoylation site.**

amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,  
 439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,  
 845-851

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 52-63, 844-855

**Cell attachment sequence.**

amino acids 314-317

**Leucine zipper pattern.**

amino acids 3-25

**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 57-69

**VWFC domain proteins.**

amino acids 448-456, 382-390

**C-terminal cystine knot proteins**

amino acids 60-86

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FIGURE 143

[illegible]

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**FIGURE 144**

MVARVGLLLRALQLLLWGHLDQAQPAERGGQELRKEAEAFLEKYGYLNEQVPKAPTSTRFSDAI  
RAFQWVSQLPVSGVLD RATLRQMTRPRCGVTD TNSYA AWAERISDLFARHRTKMRRKKRFAKQ  
GNKWYKQHLSYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD  
HNDGLGNAFDGPGGALAHAF LPRRGEAHFDQDERWSLSRRRGRNLFVVLAHEIGHTLGLTHSP  
APRALMAPYYKRLGRDALLSWDDVLAVQSLYGKPLGGSVAVQLPGKLFTDFETWDSYSPQGRR  
PETQGPKYCHSSFDAITVDRQQQLYIFKGSHEVAADGNVSEPRPLQERWVGLPPNIEAAAV  
SLNDGDFYFFKGGRCWRFRGPKPVWGLPQLCRAGGLPRHPDAALFFPPLRRLILFKGARYYVL  
ARGGLQVEPYPRSLQDWGGIPEEVSGALPRPDGSIIFFRDDRYWRLDQAKLQATTSGRWATE  
LPWMGCWHANSGSALE

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 164-168, 355-359

**N-myristoylation sites.**amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,  
509-515**Amidation site.**

amino acids 312-316

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 237-247

**Matrixins cysteine switch**

amino acids 231-262, 271-284

**Hemopexin domain protein**

amino acids 66-108, 231-262

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**FIGURE 145**

GCCGGCTAGGGGCCCGGAGCCGCACGCAGCCGCGGGGCTCCGAGAGGGCGCGCACTGGGGCTGGGACTGCGCGGGC  
CCGCCGCTGCGAGCGCCACTGAGCGGTGCGCAACTTCGGAGGCACAGCGCCGAGCCAGGCGAGCGCTCAGAGA  
CCCGGAGCCAGAGGGGCGCGCGGAGCCTCGTTTCGAGAGCCGCGCCAGGCACCCACCGCTCCGAGTGCCAGG  
CGGCCCTCCGCGCAGCGTGGCTTCCGCTGCCCCACGGAAGGCACGGGCTGGCGCTGCCGGGCGCGGGGAGGAC  
GGCGAGGAGGAGGCGCGCGGCGGAGACGGCGCGCGGAGACTGGGGCCAGGAGACAGCCCTGGGGGAGAGGC  
GCCCCAACCAGGCCGCGGGAGC**AT**GGGGGCGCGGAGCGGAGCTCGGGGCGCGCTGCTGCTGGCACTGCTGCTCTG  
CTGGGACCCGAGGCTAGCCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCCTGACTCCTTCCCGTCAGCGCC  
AGCAGAGCCGCTGCCCTACTTCTTGCAGGAGCCACAGGACGCCCTACATTGTGAAGAACAAGCCTGTGGAGCTCCG  
CTGCCGCGCCTTCCCGCCACACAGATCTACTTCAAGTGAACGGCGAGTGGGTGAGCCAGAACGACCACGTCAC  
ACAGGAAGGCCTGGATGAGGCCACCGGCTGCGGGTGCAGGAGGTGCAGATCGAGGTGTGCGGCGAGCAGGTGGA  
GGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGGCTGGAGCTCCGCGAGGACACCACCAAGAGTCGCCG  
AGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCA  
TGAGGTTCTCTGCACTGCGCGCCGCGGAGGGGCTGCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGT  
CATCGACCCACCCAGGACACCAACTTCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCGCGCTGTC  
GGACTGCGCAACTATACCTGCGTGGCCAAAGACATCGTGGCCAAACGCCGAGCACCCTGCCACCGTCATCGT  
CTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAACCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAA  
GCGCACCCGAGCCTGCACCAACCCGCTCCACTCAACGGAGGGGCTTCTGCGAGGGCAGGATTCCAGAAGAC  
CGCCTGCACCACCATCTGCCAGTGCATGGGGCGTGGACGAGTGGAGCAAGTGGTACGCTGCAGCACTGAGTG  
TGCCCACTGGCGTAGCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCGGTGACTGCAGCGGGACGCTGCT  
CGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAACTCTAAGCGACCCCAACAGCCACCTGCT  
GGAGGCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCTGGTGTGGCAATCCTCATGGC  
GGTGGGGTGGTGGTGATCCGCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGAC  
TGGTGGTTTCCACCCGCTCAACTTAAAGACGGCAAGGCCAGCAACCCGAGCTCCTACACCCCTCTGTGCCTCC  
TGACCTGACAGCCAGCGCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCAT  
GACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGG  
GCCAGGCTGGCAGATGGGGCTGACCTGCTGGGGCTTCCGCGCTGGCAGATACCTAGCGATTTCCGCCGGGA  
CACCCACTTCTGCACTGCGCAGCGCCAGCCTCGGTTCCAGCAGCTCTTGGGCTGCCCGAGACCCAGGGAG  
CAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGTGGTGCC  
CAATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTCCCGCT  
TTCAGAAGGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCGCT  
CATCCTCACCATGCCCACTGTGCCGAAGTCAGTGCCGTGACTTCCAGTGGATCTTTCAGCTCAAGACCCAGGCCACCA  
GGGCACTGGGAGGAGGTGGTGACCTGGATGAGGAGACCTGAACACACCTGCTACTGCGAGCTGGAGCCAG  
GGCTGTACATCTCTGCTGGACAGCTGGGCACCTACGTGTTACGGGCGAGTCTATTCCCGCTCAGCAGTCAA  
GCGGCTCCAGCTGCGCGTCTTCCGCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCCTGGA  
GGACAGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAA  
ACCGCTAATGTTCAAGGACAGTTACCAACACTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTTGAGAGG  
CAAGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCAC  
TTTACCCCTGGAGAGGCACAGCTTGGCTCCACAGAGCTCACCTGCAAGATCTGCGTGGGCAAGTGGAGGGGA  
GGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCC  
TGGCAGCACTGTACACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAA  
CAGCTAGATGCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTATGGACCCGTACCT  
GAATTACTTTGCCACCAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGG  
GGACCTCAACAGCCTGGCGAGTGCTTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGG  
GGACTGCT**G**AGCCTCCTGGGACAGCGGGCTGGCAGGGACTGGCAGGAGGCAGGTGCAGGGAGGCCTGGGGCAGCC  
TCCTGATGGGGATGTTTGGCCTCTGCTTCTCCAGTTCACAGCCAGAGTTGCCTCTCCTCTCTTCCCCAA  
CCCCAGACCATGACCAGCCTTAGAAAATCCATGTACTCTGTTGTTAGAGGGCCAGAGTTCTTCTCCACCCCC  
GCTCTCTCTCTTGGCCTGAGATCTCTGTGCAGGAACCAAGATGGGGCTGAAGCCTCTGGAGGAGTTGGTTGG  
GGGCGGGCAGGAGGAGGCCCTCCCTCCACCCCCCACCCTCAGCCCGGCAACTTCTGGGTTCGTTGGTGGTGGT  
TTCCGTTCTCGTTTTCTTCTCCGTTATTGATTTCTCTTTCTCCCTAAGCCCCCTCTGCTTCCACGCCCTTT  
TCCTCTTTGAAGAGTCAAGTACAATTAGACAACTGCTTTCTCTGTCCAAAAGCAAAAAGGCAAGGAAAGAA  
AGAAAGCTTCAGACCGCTAGTAAGGCTCAAAGAAGAAAGAAACACCAAAACCACAAGGGAAAGAAAGAAACCCAG  
TTTCTTAGGAAACGCAACGATTTATTATCCAGATTATTTGGATAAGTCCTTTTTTAAA

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**FIGURE 146**

MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPSDFPSAPAEPLPYFLQEPQDAYIVKNK  
 PVELRCRAFPATQIYFKCNGEWWVSQNDHVTQEGLEATGLRVREVQIEVSRQQVEELFGLEDY  
 WCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGVPVAEVEWLK  
 NEDVIDPTQDTNFLTIDHNLIIIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW  
 AEWSPCSNRCGRGWQKRTRCTNPAPLNGGAFCEGQAFQKTACTTICPVDGAWTEWSKWSACS  
 TECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKTLSDPNSHLLEASGDAALYA  
 GLVVAIFVVVAILMAVGVVVYRRNCRDFDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV  
 PPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLPSLKVKVYSSSTGSGPGLADGADLLG  
 VLPPTYPSPDFARDTHFLHLRSASLGSQQLLGLPRDPGSSVSGTFGCLGGRLSIPGTGVSLLV  
 PNGAIPQGFYEMYLKAEESTLPLSEGTQTVLSPSVTCGPTGLLLCRPVILTMPHCAEVSA  
 RDWIFQLKTAHQHWEVVTLDEETLNTPCYQCLEPRACHILLDQLGTIVFTGESYSYSAVK  
 RLQLAVFAPALCTSLEYSLRVYCLEDTPVALKEVLELERTLGGYLVEEPKPLMEKDSYHNLRL  
 SLHDLPHAHWRSKLLAKYQEIPFYHIWSGSQKALHCTFTLERHSLASTEITCKICVRQVEGEG  
 QIFQLHTTLAETPAGSLDTLCSAPGSTVTTQLGPYAFKIPLSIQKICNSLDAPNSRGNDWRM  
 LAQKLSMDRYLNYFATKASPTGVILDLWEALQDDGDLNSLASALEEMGKSEMLVAVATDGDC

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 374-395

**N-glycosylation sites.**

amino acids 222-225, 347-350

**Glycosaminoglycan attachment site.**

amino acids 492-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 233-236, 234-237

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

**Tyrosine kinase phosphorylation sites..**

amino acids 216-223, 773-780

**N-myristoylation sites.**

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 541-551

**ATP/GTP-binding site motif A (P-loop).**

amino acids 926-933

**Growth factor and cytokines receptors family signature 2.**

amino acids 306-312

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**FIGURE 147**

GAGAGGGACAGAGGCTGGAGAAGGATGTATGGCCTGCCCTGGGCTTGTCTGTTCCCTCCTGAGCCTGAGCCCTT  
ACCTTCCTGACCCCATGAAGCACACACTGGCTCTGCTGGCTCCCTGCTGGGCCTGGGCCTGGGGCTGGCCCTGA  
GTCAGCTGGCTGCAGGGGCCACAGACTGCAAGTTCTTGGCCCGGCAGAGCACCTGACATTACCCACAGAGCCA  
GGGCCCGGTGGCTGGCCCTCGAGTTCTGTGCCCGCAGGACTCCTGGACTCCCTCTATGGCACCGTGCGCCGCTTCC  
TCTCGGTGGTGAGCTCAATCCTTTCCCTTCAGAGTTGGTAAAGGCCCTACTGAATGAGCTGGCCTCCGTGAAGG  
TGAATGAGGTGGTGCGGTACGAGCGGGCTACGTGGTATGCGCTGTGATCGCGGGCTCTACCTGCTGCTGGTGC  
CCACTGCCGGGCTTTGCTTCTGCTGCTGCCGCTGCCACCGGGCGCTGCGGGGACGAGTGAAGACAGAGACAAGG  
CGGTGGCCTGTGAGCGCGCGCCCTCATGGTCTTCTGCTGCTGACCACCCTCTTGTGCTGATTGGTGTGGTCT  
GTGCCTTTGTACCAACCAGCGCACGCATGAACAGATGGGCCCCAGCATCGAGGCCATGCCTGAGACCCTGCTCA  
GCCTCTGGGGCTGGTCTCTGATGTCCCCAAGAGCTGCAGGCCGTGGCACAGCAATTCTCCCTGCCCCAGGAGC  
AAGTCTCAGAGGAGCTGGATGGTGTGGTGTGAGCATTGGGAGCGCGATCCACACTCAGCTCAGGAGCTCCGTGT  
ACCCCTTGTGCGGGCGCTGGGCAGTTTGGGCCAGGTCTGCAGGTCTCCGTGCACCACCTGCAAACCTTGAATG  
CTACAGTGGTAGAGCTGCAGCGGGCAGCAGGACTGGAGCCAGCCATCCGGGAACACCGGGACCGCTCCTTG  
AGCTGCTGCAGGAGGCCAGGTGCCAGGGAGATTGTGCAGGGGCCCTGAGCTGGGCGCCGACCCCTGGAGCTGGGTG  
CTGACTTCAGCCAGGTGCCCTCTGTGGACCATGTCTGCACCAGCTAAAAGGTGTCCCCGAGGCCAACTTCTCCA  
GCATGGTCCAGGAGGAGAACAGCACCTTCAACGCCCTTCCAGCCCTGGCTGCCATGCAGACATCCAGCGTGGTGC  
AAGAGCTGAAGAAGGCAGTGGCCCAGCAGCCGGAAGGGGTGAGGACACTGGCTGAAGGGTTCCCGGGCTTGGAGG  
CAGTTCCCGCTGGGCCAGGCACTGCAGGAGGTGGAGGAGAGCAGCCGCCCCCTACCTGCAGGAGGTGCAGAGAT  
ACGAGACCTACAGGTGGATCGTGGGCTGCGTGTGCTCCGTGGTCTATTCTGTTGCTCTGCAACCTGCTGG  
GCCTCAATCTGGGCATCTGGGGCTGTCTGCCAGGACGACCCAGCCACCCAGAAGCCAAGGGCGAGGCTGGAG  
CCCGCTTCTCATGGCAGGTGTGGGCCTCAGCTTCTCTTGTGTCACCCCTCATCTCCTGGTGTTCGCCACCT  
TCCTGGTGGGTGGCAACGTGCAGACGCTGGTGTGCCGGAGCTGGGAGAACGGCGAGCTCTTGAGTTTGACAGACA  
CCCCAGGGAACCTGCCCCCTCCATGAACCTGTGCAACTTCTTGGCCTGAGGAAGAACATCAGCATCCACCAAG  
CCTATCAGCAGTGCAAGGAAGGGGCAGCGCTCTGGACAGTCTGCAGCTCAACGACTCCTACGACCTGGAGGAGC  
ACCTGGATATCAACCAGTATACCAACAAGCTACGGCAGGAGTTGCAGAGCCTGAAAGTAGACACACAGAGCCTGG  
ACCTGCTGAGCTCAGCCGCCCGCCGGGACCTGGAGGCCCTGCAGAGCAGTGGGCTTCAGCGCATCCACTACCCCG  
ACTTCCCTCCTCAGATCCAGAGGCCCGTGGTGAAGACCAGCATGGAGCAGCTGGCCAGGAGCTGCAAGGACTGG  
CCCAGGCCCAAGACAATTCTGTGCTGGGGCAGCGCTGCAGGAGGAGGCCAAGGACTCAGAAACCTTCACAGG  
AGAAGGTCGTCCCCCAGCAGAGCCTTGTGGCAAAGCTCAACCTCAGCGTCAGGGCCCTGGAGTCTCTGCCCCGA  
ATCTCCAGCTGGAGACCTCAGATGTCTAGCCAATGTACCTACCTGAAAGGAGAGCTGCCTGCCTGGGCAGCCA  
GGATCCTGAGGAATGTGAGTGAGTGTTCCTGGCCCGGAGATGGGCTACTTCTCCAGTACGTGGCCTGGGTGA  
GAGAGGAGTGACTCAGCGCATTGCCACCTGCCAGCCCTCTCCGGAGCCCTGGACAACAGCCGTGTGATCCTGT  
GTGACATGATGGCTGACCCCTGGAATGCCTTCTGGTTCTGCCTGGCATGGTGCACCTTCTTCTGATCCCCAGCA  
TCATCTTTGCCGTCAAGACCTCCAAATACTTCCGTCTATCCGGAAACGCCTCAGCTCCACCAGCTCTGAGGAGA  
CTCAGCTCTTCCACATCCCCCGGGTTACCTCCCTGAAGCTGTAGGGCCTTGTGGGGTGAGGTGACCTGAGGCTG  
CCTGTCTCCCTTTGATTTAGCCTGGGCCACAGGACTTCGGTAGCTCTTGCCCCAGAGCCAGGCTGGCATCCA  
GGCCTGGACTGTCCCAGTTCCGGCTTACCTGGCCCCACCTTGCTGCTCCTTTCCACCCCTTTCTGTCTACGAC  
CCCCATCATTACGCTCAGAATCACATGGGACTTCTGTGAGCTGCAGAGCCAGCAAGTCCCTACAGGTGTCAAC  
CGTTACCCCATGCTGGTGGCATCCTCACAGGAAGAGCCTGTTCTCCACCTGCTGGAGCCTGGACCCTGGGGTGG  
GACAGAGCCCTCGTCCAACCCCACTCCCCCTCCCGTGTGCTTCCCCCTGCCAAGCCTCCCCCTGCCAAGCCTCC  
CCCTGCCCTCTCTGAGCCCTCGCCCCCACACCGTCTCATCTGGCCTCCCCCTGGCCCCACTTCCCTCTT  
ATGCCCTTCTTGGCCCTTTGCTTCTCCCTTAGTCCCTCTTACCATATCTCCACTGCTACCTTGTGGCCCCA  
GAGACCACCTGCCCAACCAAACTCAGGTAACGCCACTAATCAGGCAGGGGCCACCATGGCCTAGGTCTGGG  
CTGGCTGCAGGCCCTGCCTCATGGCCTCTGAGCCCTCCACTGCCCCAGGGCCTTGGGCCCTCTGCAGATCTCATC  
CAGGATTTATTGTTGTCCAGTGGGGTGAGGGAGGCCTGTCTGAAGGCCGAGCCTCCCTGCCTGCACCCAAGTTAG  
AAATGGGGGTACCAGCACTTAGCTTCTCTGAGTGTGGCTCCCAAGGAAGGGACCTGGGACCTGGGCCACAGT  
GGGGCTTGGCCTTACCTTTTCAAGGAAGCATCTTCCACAGCCCCACCCAACCTTTCTTAGGATGATCTGGT  
GGCCAGAACAGGATTTTGCACGGCCCCCTTTATCCTGCGCATGTGGCCTAGGGTCATCCCCAGCCCATCCCTGTG  
TCAGCCCTGAGTGTGGACACTGCGTTCCAGAAATGAGGAAGAGGAGAGAGAAGAGATGGACAGACCTCAGATCC  
ATTAAAGTGTCTCACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 148**

MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL  
DSLYGTVRRFLSVVQLNPFPSSELVKALLNELASVKVNEVVRYEAGYVVCVAVIAGLYLLLV  
PTAGLCFCCCRCHRRCCGRVKTEHKALACERAALMVFLLLTLLLLIGVVCAVFTNQTH  
EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAQQFSLPQEQVSEELDGVGVSIGSAIHTQ  
LRSSVYPLLAAGVSLGQVLQVSVHHLQTLNATVVELQAGQDLEPAIREHRDRLELLQE  
ARCQGDCAALSWARTLELGADFSQVPSVDHVLHQLKGVPEANFSSMVQEENSTFNALPA  
LAAMQTSSVVQELKKAVAQQPEGVRTLAEGFPGLEAASRWAQALQVEESSRPYLQEVQR  
YETRWIVGCVLCSVVLFFVLCNLLGLNLGIWGLSARDDPSHPEAKGEAGARTLMAGVGL  
SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLLGLRKN  
ISIHQAYQQCKEGAALWTVLQLNDSYDLEEHLQDINQYTNKLRQELQSLKVDTSQSLDLLSS  
AARRDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE  
EAQGLRNHLHQEKVVPQQSLVAKLNLSVRALESSAPNLQLETSVDLANVTYLGELPAWAA  
RILRVNSECFLAREMGYFSQYVAWVREEVTQRIATCQPLSGALDNSRVILCDMMADPWNA  
FWFCLAWCTFFLIPSIIFAVKTSKYFRPIRKRLSSTSSEETQLFHIPRVTSCLK

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

**N-glycosylation sites:**amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,  
684-688, 707-711, 725-729**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 811-815

**Tyrosine kinase phosphorylation site.**

amino acids 95-103

**N-myristoylation sites.**amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,  
228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,  
477-483, 500-506, 536-542, 644-650, 761-767**Phospholipase A2 histidine active site.**

amino acids 129-137

**4Fe-4S ferredoxins, iron-sulfur binding region signature.**

amino acids 126-138

**Mitochondrial energy transfer proteins signature.**

amino acids 80-89

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**FIGURE 149**

CACAGCTCCCTTCCCAGGACGTGAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCA  
GCCTGCTCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTG  
CCAAGGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA  
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC  
TTTGGGTGGTGCCTGGGGCACTCCCACAGGTGTAGCACTCCCAAAGCAAGACTCCAGACAGCG  
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCCTTTCAGCCTTCAC  
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGGCTGCAAGGACCCTGGGAAAGTTCCAG  
AACTCCACGTCCTTGTCTCAATTGTGCCATCAACTTTCAGAGCTATCATGAGCCAACCTCACC  
CCACAGGGCCTCAGTCGCCACCATGTGGGCCTCTCCAGTGCAAACCACCGAGCATTCACCAT  
GACCGGTCACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAGGGTGGCAAGCACC  
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTTCAGGTCCATTGAGCCTCCTGGCA  
TTTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTCCTAGCCTCCTGACATGAGTCTGC  
TGGAAGAGCATCCAAACAAACAAGTAATAAATAAATAAATAAACTCA

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**FIGURE 150**

MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRRLCCHRVSPNSTNLKGHHVRLCKPC  
KLEPEPRLWVVP GALPQV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 48-52

**Amidation sites.**

amino acids 23-27, 33-37

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**FIGURE 151**

CACCGGAGGGCACGCAGCTGACGGAGCTGCGCTGCGTTTCGCCTCGTTTGCCTCGCGCCCTCCA  
CTGGAGCTGTTTCGCGCCTCCCGGCTCCCACCGCAGCCACCCGGCAGAGGAGTCGCTACCAGC  
GCCAGTGCGCTCTGTCACTCCGCAAACCTCTTGCCGCCCCGGGCTGGGCACCAAATAC  
CAGGCTACCA**ATGGT**CTACAAGACTCTCTTCGCTCTTTGCATCTTAACTGCAGGATGGAGGGTA  
CAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCACCGACC  
ACCATCTGGACTAGCTCTCCACAAAACACTGATGCAGACACTGCCTCCCCATCCAACGGCACT  
CACAACAACCTCGGTGCTCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAAGAACATT  
TCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCAGGTTTGAATTGGGAAGGCACAAACACA  
GACCCCTCACCTTCTGGGTTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACCACGTTGGAG  
GAACACAGCTCGGGCACTCCTGAAGCAGGCTGGCAGCTACACTGTCGAGTCCGCTGCTGAG  
CCTCCACACTCATCTCCCCTCAAGCTCCAGCCTCATCACCTCATCCCTATCAACCTCACCA  
CCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACCAGACCCCAACCC  
ACTGGAGCTCCAACCTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGACCACACCCCACT  
TCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAACCTGTGTAGGCAAA  
GTGATGTGTGAGCTCATAGACATGGAGACCACCACCTTTCCAGGGTGATCATGCAGGAA  
GTAGAACATGCATTAAAGTTCAGGCAGCATCGCCGCCATTACCGTGACAGTCATTGCCGTGGTG  
CTGCTGGTGTTTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCTCTCTATGGAAGACTTTTG  
GACGACCATGACTACGGGTCTGGGGAAACTACAACAACCTCTGTACGATGACTCT**TAACA**A  
TGGAATATGGCCTGGGATGAGGATTAAGTGTCTTTATTTATAAGTGCTTATCCAGTAGAATT  
AATAAGTACCTGATGCGCATTTGAACGACAATCTTAAGCCCTGTTTTGTTGGTATGGTTGTTTT  
TGTTTTCTCCCTCTCCTCTGGCTGCTACAACCTTCCCTTTCTGGTACAAGAAGAACCATTCT  
TTAAAGGTGAGTGGAGGCTGATTTGCAGCTGAAGTGGGCCAGCCTTGACCAGCCAGGCCAGA  
CCACCATGGTGAAGGCTTCTTTCCCCACTGCAGGACCCACTTTGAGAAGGATCGAGGAGGAGG  
ATTTGGGTTGTTTTGTTAGGGGTTACTTTCAGGGGAACATTTTCAATTTGTGTTATTTCTTAAAC  
TTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGAAGGAAATGAGCTCTACGAGGATTT  
CACCTTGCATGGGAGAGAGCAGGGTTTTCTCAGATTCCTTTTTTAATCTCTATTTATCTGGTTG  
TTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGCTGGAAAGCAGCTTCTTAGCTGCCTAAT  
TAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGGGGCCAGCAGGTCACGGGGCAGAATCTCT  
CAGGTTGCTGTGGGATCTCAGTGTGCCCCCTACCTGTTCTCCCCCTCCAGGCCACCTGTCTCTGT  
AAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCACAAGTGATCAGCAGAGTT  
GCATTTCCAAAGAAAAAGGCTATGAGATGAGCTGAGTTATAGAGAGAAAGGGAGAGGCATGTA  
CGGTGTGGGGAAGTGGAAGAGAAGCTGGCGGGGGAGAAGGAGGCTAACCTGCACTGAGTACTT  
CATTAGGACAAGTGAGAATCAGCTATTGATAATGGCCAGAGATATCCACAGCTTGGAGGAGCC  
CAGAGACTGTTTGCTTTATACCCACACAGCAACTGGTCCACTGCTTTACTGTCTGTTGGATAA  
TGGCTGTAAATGTTTAAAAAC

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## **FIGURE 152**

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNN  
SVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEEHS  
SGTPEAGVAATLSQSAAPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQPTGA  
PTAPESPTEESSSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELIDMETTTTTFPRVIMQEVEH  
ALSSGSIAAITVTVIAVVLLVFGVAAYLKIRHSSYGRLDDHDYGSWGNYNPNPLYDDS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 258-278

#### **N-glycosylation sites.**

amino acids 58-61, 62-65, 80-83, 176-179

#### **Casein kinase II phosphorylation sites.**

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-144, 164-167, 191-194, 195-198, 200-203

#### **Tyrosine kinase phosphorylation site.**

amino acids 289-296

#### **N-myristoylation sites.**

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

FIGURE 153

[illegible]

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**FIGURE 154**

MLVHCVGLLLTGALLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV  
LGTTLGSAVLVACVDYFLEGLALGSLGQRLQTLPALPSLC

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 38-55, 60-78

**N-myristoylation sites.**

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 67-78

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**FIGURE 155**

TGCAATTAAAGGAGTCGGGTCTCTAACTGTTGATCTGTTTTTTTCCCTTCTGAGCAATGGGAGC  
TTACCATCTTTATCCTGAGACTGGCCATTTACATCCTGACATTTCCCTTGTACCTGCTGAACT  
TTCTGGGCTTGTGGAGCTGGATATGCAAAAATGGTTCCTTACTTCTTGGTGAGGTTCACTG  
TGATATACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTCTTCAGTAACCTGCAGGAGTTTG  
CGGGCCCCCTCCGGGAAACTCTCCCTGCTGGAAGTGGGCTGTGGCACGGGGGCCAACTTCAAGT  
TCTACCCACCTGGGTGCAGGGTGACCTGTATTGACCCCAACCCCAACTTTGAGAAGTTTTTGA  
TCAAGAGCATTGCAGAGAACCGACACCTGCAGTTTGAGCGCTTTGTGGTAGCTGCCGGGGAGA  
ACATGCACCAGGTGGCTGATGGCTCTGTGGATGTGGTGGTCTGCACCCTGGTGCTGTGCTCTG  
TGAAGAACCAGGAGCGGATTCTCCGCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGGCTTTCT  
ATTTTCATGGAGCATGTGGCAGCTGAGTGTTGACTTGAATTACTTCTGGCAACAAGTCTGG  
ATCCTGCCTGGCACCTTCTGTTTGATGGGTGCAACCTGACCAGAGAGAGCTGGAAGGCCCTGG  
AGCGGGCCAGCTTCTCTAAGCTGAAGCTGCAGCACATCCAGGCCCCACTGTCTTGGGAGTTGG  
TGCGCCCTCATATCTATGGATATGCTGTGAAATTAGTGTGAGCTGGCAGTTAAGAGCTGAATGG  
CTCAAAGAATTTAAAGCTTCAGTTTTACATTTAAATGCTAAGTGGGAGAAGAGAAACCTTTT  
TTTTGGGGGGCGGTTTTTTTGGTTTGTGTTGGTTTTTTTTTTTTTTTTTGGCAGGAGAATCTC  
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTGTACTCTAGCCTGGGTG  
ACAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAGTAGAGACAGGGAGAC  
GGGGTCTCACTGTGTTGCCTAGGCCGGTCTTGAACCTCTGGGCTCAAGTGATTCTCCACCTT  
GACCTCCTAAATTGTTGGGATTACAGGTGTGAGACAGTGCACCTGGCCGAAATAGCTCAAGTT  
TCTGAAAAACAAATCTGAATCTATTTGTTATTCTTAGCGTCACTGGTCTGGCTTTTCAGAATTA  
ACATACAAGGTGCCACACCTAGTTCTGCCCAGCTTTATGTCTTTTATTCCAGTATTCCACCA  
AAGTTTGTTTTCTGCATTCCAGTTCTCAAGTCTTAAGATAAAGATTGTACTTGACAGTTTAG  
TATATCCATAAACTATTTGAGGTGGTTAAGGTTCTTGGGTTCATTTTCTTAATACTTTGCT  
GAATATTGTAGATTGTAGGCAATGAAAAAGTCTACTAAATTAGGAAAACCTTGAATAATTAGG  
TATCCTAGGTAAGAGCCCCATAACATCAAGCAATCTGTGAGTCTGTAAAGAAATAAATATTTT  
TTGGATTATTCTTATCTAATTCCACCCCTGTTGGAAGATGATTTCTTTGTTCTTTGCAACTAT  
GGAAGCTGTGAAAATCATCACAAGTGCCTCTGAAAGCGAGTGTTAGGTTGGTTAGAGGGTTTA  
ATATTTTCTGCAATGGTTTGTAGGAATTTTAATAAATGTAGTATATTTTCTGAGATGATTTTG  
TAAAAGTACTATTTTAAATATCAAATCAACCAATAAATTCACATTTGTGTTAGGAACAAA



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## **FIGURE 156**

MELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRFTVIYNEQMASKKRELFSLNQ  
EFAGPSGKLSLLEVCGGTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAA  
GENMHQVADGSVDVVVCTLVLCVKNQERILREVCRLRPGGAFYFMEHVAAECSTWNYFWQQ  
VLDPAWHLLFDGCNLTRESWKALERASFSLKLQHIQAPLSWELVRPHIYGAVK

**Signal peptide:**

amino acids 1-29

**N-glycosylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 78-84, 80-86, 91-97, 201-207

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**FIGURE 157**

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT  
GCCACGACCGGGCCTCTCCCTGGCGTTTGGTCACTCTGCTTCATTCTCCACCGCGCCTATGG  
TCCCTCTTGGAGCCAGCGTGGCGGGCCTGGCGGCTCCCGGGTGGTGAGAGAGCGGTCCGGGAA  
CGATGAAGGCCTCGCAGTGCTGCTGCTGTCTCAGCCACCTCTTGGCTTCCGTCCTCCTCCTGC  
TGTTGCTGCCTGAACTAAGCGGGCCCCCTGGCAGTCCTGCTGCAGGCAGCCGAGGCCGCGCCAG  
GTCTTGGGCCTCCTGACCCTAGACCACGGACATTACCGCCGCTGCCACCGGGCCCTACCCCTG  
CCCAGCAGCCGGGCCGTGGTCTGGCTGAAGCTGCGGGGCCGCGGGGCTCCGAGGGAGGCAATG  
GCAGCAACCCTGTGGCCGGGCTTGAGACGGACGATCACGGAGGGAAGGCCGGGGAAGGCTCGG  
TGGGTGGCGGCCTTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA  
CCGTGTTGATGGTGGTGAGCGGCGCGGTGCTGGTGTACTTCGTGGTCAGGACGGTCAGGATGA  
GAAGAAGAAACCGAAAGACTAGGAGATATGGAGTTTTGGACACTAACATAGAAAATATGGAAT  
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTTGATGCCAATCATCCTC  
GAAGATTAAAGATGTGCCTTTTGATGAAAGAACTTTATCTTTCTACAATGAAGAGTGGAATTC  
TATGTTTAAGGAATAAGAAGCCACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTT  
TAACAACCTTTAATTTGCTGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTAT  
AGAAGTACTCTATTAATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTG  
TTTGAAAATTACTATAAAACGGTGTTTTCTGGTCGGTTTTTGTTCCTGCTTACCATATGATT  
GTAAATTGTTTTATGTATTAATCAGTTAATGCTAATTATTTTTGCTGATGTCATATGTTAAAG  
AGCTATAAATTCCAACAACCAACTGGTGTGTAATAAATAATTTAAATTTTCCTTTACTGAAAGG  
TATTTCCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAT  
ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCTCTTAAAAA  
AAAAA

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**FIGURE 158**

MKASQCCCCLSHLLASVLLLLLLPELSGPLAVLLQAEEAAPGLGPPDPRPRTLPPPLPGPTPA  
QQPGRGLAEAAGPRGSEGGNGSNPVAGLETDDHGKGAGEGSVGGGLAVSPNPGDKPMTQRALT  
VLMVVS GAVLVYFVVRTVVRMRRNRKTRRYGVLD TN IENMELTPLEQDDEDDNTLFDANHPRR

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 124-140

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,  
157-160

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**FIGURE 159**

GCTGCAGGCGGCGACGGCTACACC**ATG**GGCCGGCTGCTGCGGGCCGCCCGGCTGCCGCCGCTG  
CTTTCGCCGCTGCTGCTTCTGCTGGTTGGGGGAGCGTTCCTGGGTGCCTGTGTGGCTGGGTCT  
GATGAGCCTGGCCCAGAGGGCCTCACCTCCACCTCCCTGCTAGACCTCCTGCTGCCCACTGGC  
TTGGAGCCACTGGACTCAGAGGAGCCTAGTGAGACCATGGGCCTGGGAGCTGGGCTGGGAGCC  
TCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC  
TTCTGGGAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTAT  
GTTTTTCTGACTTAAGTGAAGGAGGTTCCATTGAAGACACTAGCCAGGCTCAAGAGCTG  
CCAAACCTCCCCCTCTCCCTTGCCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCTCCC  
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA  
GAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCCAAGCCTCAG  
GTCCGTGACTTTTCTCTCACCAGCAGCAGCCAGACCCAGGGGCCACCAAAAGCAGGCATGAA  
GACTCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCAGCTTGCTG  
CTGCCCTCAGTCACCCCAACTACAGTGACTCCGGGGGACCAGGACTCCACCAGCCAAGAGGCA  
GAGGCCACAGTGCTGCCAGCTGCAGGGCTTGGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGC  
GAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAGCAGGAGGTGCCGGCCTTGCCCT  
TCATTCCCTCAAACCACAGCTCCCACTGGGGCCGAGCACCCAGATGAAGATCCCTTCTGCTCT  
AGAACCTCAGCCTCTTCCCCACTGGCCCTGGAGACATGGAAGTACACCTTCTCTGTCTACC  
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGG  
ATACCCTGGGATTTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTAC  
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAG  
CTCCTGGCCCTGGTGGAAGAGGTGCTGCCCCGCCATGGCAGTGGCCACCATGGGGCCTGGCAC  
ATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACACTGGTGGGCGAGCAG  
GGGTGGTGCCCACTCAAGATGTCCTTTCCATGCTGGGTGACATCCGAGGAGCCTGGAGGAG  
ATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGCGGGCCAGCCAGGTGCGCAGC  
GACTACGGCACGCTCTTCGTGGTGCTGGTGGTCATTGGGGCCATCTGCATCATCATCATTGCG  
CTTGGCCTGCTCTACAACTGCTGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTGCGACGGC  
GAGGAGCTGCGCTTCGTGGAGAACGGCTGCCACGACAACCCACGCTGGACGTGGCCAGCGAC  
AGCCAGTCGGAGATGCAGGAGAAGCACCCAGCCTGAACGGCGGCGGGGCCCTCAACGGCCCCG  
GGGAGCTGGGGGGCGCTCATGGGGGGCAAGCGGGACCCCGAGGACTCGGACGTGTTTCGAGGAG  
GACACGCACCTG**TGA**GCGCAGCCGAGGCGCAGGCCGAGTGGGCCGCCAGGACCAAGCGAGGTG  
GACCCCGAAACGGACGGCCCGGAGCCCGCACCAGCCCCGCGCCTACCCGGGCGCCCCCGCGG  
CCTGGCCCTCGGCGCGGGCTCCTTCCCGCTTCCCCGACTTCACACGGCGGCTTCGGACCAAC  
TCCCTCACTCCCGCCCGAGGGGCAGGCCTCAAAGCCCGCCTTGCCCCGCTTTCCCGCCCCTG  
AACCCCGGCCCCGCGGGCGGGCGGCTTCTGCGCCCCGGGACTCAATTAAACCCGCCC  
GGAGACCACGCCGGGCCAGCAAAA

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**FIGURE 160**

MGRLLRAARLPPLLSPLLLLLVGGAFILGACVAGSDEPGPEGLTSTSLLDLLLPTGLEPLDSEE  
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPTADYVFPDLTEK  
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMPPREEEEEEEEEEREKEEVEKQEEEEEEEL  
LPVNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSSLLPSVTPTT  
VTPGDQDSTSQEA EATVLP AAGLGVEFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTAP  
SGAHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQLLEGQA AEAQSRIPWDSTQV  
ICKDWSNLAGKNYIILNMTENIDCEVFRQHRGPQLLALVEEVLPRHSGHGHGAWHISLSKPSE  
KEQHLLMTLVGEQGVVPTQDVL SMLGDIRRSL EEEIGIQNYSTTSSCQARASQVRSDYGTLFVV  
LVVIGAICIIIIALGLLYNCWQRRLPKLKHVSHGEELRFVENGCHDNPTLDVASDSQSEMQEK  
HPSLNGGGALNGPGSWGALMGGKRDPEDSDVFEEETHL

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 499-521

**N-glycosylation sites.**

amino acids 106-110, 193-197, 395-399, 480-484

**Glycosaminoglycan attachment site.**

amino acids 77-81

**N-myristoylation sites.**amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,  
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590**Amidation site.**

amino acids 588-592

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**FIGURE 161**

CCAGGGCGGAGCGCAGCTGCGCCGGGCTTGGGCGCCTGGGGCCGCCGCTCCCCACCGTCGTTT  
TCCCCACCGAGGCCGAGGCGTCCCGGAGTCATGGCCGGCCTGAACTGCGGGGTCTCTATCGCA  
CTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGCCGCGCGGGGCAGAAGCTTTTGAGATT  
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCCGACTCTGCTGGCA  
AAACCCCTGTTACATCGTCATTTCTAAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAA  
AGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAGAATCACTTTGTCATAGAGATCCAGAAA  
AATATTGACTGTATGTCAGGCCCATGTCCTTTTGGGGAGGTTTCAGCTTCAGCCCTCGACATCG  
TTGTTGCCCTACCCTCAACAGAACTTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTA  
GAGCTGCAGTTTTTCCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCCAGACGGA  
GTCACTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGC  
AATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGG  
TTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGC  
ATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAA  
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTTCGTTTCCTGCACACCTGCGGGCCAGC  
GTCTCCTTCCTCAACTTCAACCTCTCCAACCTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC  
ATCCCGGGCTCCACCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATG  
GCGGGGAACCTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCCAAAGTCCAGGGATCCTC  
CGGCTGCAGTTCCAAGTTTTTGGTCCAACATCCACAAAATGAAAGCAGTGAGTGAGCCCCACTT  
TCCTTTTTCTTCCTCCTCCAGCACCTTCGTTGTTTCCTGGGTAGTCTGCCTGGGTGAGGCTCC  
CTTCCTGTTTCTCATCTGTGGCTTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTTCAGG  
AAGTGGGTTGCTAGGCAGTTAGACAGGCTTGTTGGTGAACACCCGGTATGTAGTTCCATTTCA  
GCACAATAAAAAGAAATCTTGCATTCAAGATGCTAAATTGTTTTTAACGAAAA

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**FIGURE 162**

MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPDLLAKPCYIVISKR  
HITMSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLPLTLNRTFI  
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRI GTFCSNGTVSRIKMQ  
EGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTW  
QFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQG  
CDQDAQSPGILRLQFQVLVQHPQNESSE

**Signal peptide:**

amino acids 1-29

**N-glycosylation sites.**amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,  
310-314, 339-343**Tyrosine kinase phosphorylation site.**

amino acids 276-284

**N-myristoylation sites.**

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309

**FIGURE 163**

CAACCACACACACACACCTGGGGAATTGCTGGCCTGACTTCTGACCCCTGACTCCTCATACCCCTTCCTC  
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCAGACCACTGGCCCTTCC  
CCCGCCCTGTGGTGACTTCATAAAGGTTACTAGCTTCTCCCCTGGCCTTGAGACCCACACGAT  
GGCCCTGCTGGCTCTGGCCAGTGCCGTCCCCTCTGCCCTGCTGGCCCTGGCTGTCTTCAGGGT  
GCCCCCTGGGCCTGTCTCCTCTGCTTCACAACCTACTCTGAGCGCCTCCGCATCTGCCAGAT  
GTTTGTGGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCTTCACGGCCGCCTTCCA  
GGGCCTCTCTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTTGGGGAAG  
GTGCAGAGGGAGGGCAGGAGAGGCCCAGAGGGTCAGGCTGAGGGACAGACAGAGAGAAACAGT  
CAGAGGAGAAAGGCTCAAAGACCATGAGAACAACAGAGACTTAGGGACAGAGAGACACAGACA  
GGGAAGACAGCAGGGCAAAGACTCAGAGAGGGGAGGATGGAGAGTCAGAGAGGGGAAGATGG  
AGACTCAGAGAGAGGGGAGGATGGAGACTCAGAGAGAGAGGAAGATGGAGACTCAGAGGGAAA  
GATGGAGACTCAGGAGTATGGAGAGTCAGAGAGGGGAGGATGGACACTCAGGGGAGGATGGAG  
AGTCAGGAGGATGGAGACTCATAGAAAGGGGAGGATGGAGAGTCAGGAGAGGTTGGAGACTGG  
AGAGGGAATAGAGACCCAGAAAGGGGAGGATGGAGACTCAGAGGGTGGAAGATGGAGACTCAA  
AGAGGATGGAAACCCAGAGAGAGGAGGACAGAGATGAGGCAGAGACTAGGGGAAGCAGGATAG  
CGACTGGTCGGGGGCAGAGACTCAGGGAGGATAGAGACTCACAGAGAGGTGAGGATAGAGACT  
TGGGAGGGACTCAGGAAGCATAGCGACTGTGGGGCAAAGAGTCAGAGAGGGGAGGATACAGAC  
TTGGGAGGGCAGAGACTCAGAAACAGAATGTTTCGCATTAGGGACATGGTGTTGCGGGGAGCTG  
CCTCCCCCAGCCCCTGCTCCCTCCCTCACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA  
CACCTTCACCCAGATGACCCATGCCCTGCAGGAGCTGGCTGCTGCCAGGGATCCTTTGAGGT  
TGCTTCCCTGATGCTGCAGAGAAAATGAAGAAGGTCATTACACAGCTTAAAGAAGCCAGGC  
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTCGCGCGGCGTTTCTCTGCAGCGGGTGCTACTC  
TAGGGTCTGCGACCTCCCGCTGGACTGCCAGTTCAGGATGTGACAGTGAAGTTCGGGGCGACCA  
GGCTATGTTTTCTTGATCGTAACTTCCAGCTGCCAAAGGAGGAGATCACCTATTCTTGAA  
GTTTCGAGGAGGAGGTCTCCGACTCAGGACTTGTCTATTTCGAGATATGCCGCGGGCCGA  
AGGATACCTGGCGCGGATCCGCGCGGCTCAGCTCACGCACCGCGGGACGTTCTCTGCGTGAT  
CAAGCAAGACCAGCGCCCCCTGGCCCGGCTCTACTTCTTTCTTAACGTCCTCGGGGCCCTCGC  
ATCAGCGAGTGCGACAGTGTGGCGTGGTGAGTTCTGGGGACTCCGGAGCCCCAGCATCTAGC  
TCCCCGCTGTCTCAGATCCCACCGAGAAGTCTGGGTTCCCAGCAACCTCCAACCCAGGAGGAT  
GTTCTTTTCGATGGTACTGCAGTGGCAACTAACAAAGGTATCTTTCTCTCTTCCCTATCCTATT  
TCCATCTTGAAAATAAAGAATATATTTCAACTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA



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## **FIGURE 164**

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRSPLKEECEEAFTAAF  
QGLSDTEISEETIHTSSVSWGRCRGRAGEAQRVRLRDRQRETVRGERLKDHENNRDLGTERHR  
QGKTAGQRLREGRMESQRGEDGDSEGEDGDSEEREEDGDSEGKMETQEYGESERGGWTLRGGW  
RVRRMETHRKGRMESQERLETGEGIETQKGEDGDSEGGRWRLKEDGNPERGGQR

**Signal peptide:**

amino acids 1-26

**N-myristoylation site.**

amino acids 65-71

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**FIGURE 165**

[illegible]

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## **FIGURE 166**

MELSDVTLIEGVGNEVMVAGVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH  
VDHLVAGQGNPEPTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR  
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFPGQES  
QMKLIYQGRLLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVGS  
LMVPVFVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLVFGMYGR

**Signal peptide:**

amino acids 1-36

**Transmembrane domains:**

amino acids 246-267, 275-301

**N-glycosylation sites.**

amino acids 162-166, 211-215

**N-myristoylation sites.**

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

**Cell attachment sequence.**

amino acids 97-100

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**FIGURE 167**

GGCGGCTGTGTGTCGCGCGGAGCCGAAGCGCGCAGGCCCGTCCCGGTGGCCGGGGAGCGGGCGGGTGGGGCGCCA  
TGTGGTTCATGTACCTGCTGAGCTGGCTGTGCTCTTTCATCCAGGTGGCCTTCATCACGCTGGCTGTGCGGCTG  
GACTCTATTACCTGGCAGAACTGATAGAAGAATACACAGTGGCCACCAGCAGGATCATAAAAATACATGATCTGGT  
TCTCCACCGCTGACTGATTGGCCTCTACGTCTTTGAGCGCTTCCCCACCAGCATGATTGGAGTGGGCTATTCA  
CCAACCTCGTCTACTTTGGCCTCCTCCAGACCTTCCCTTCATCATGCTGACCTCGCCTAACTTCATCTGTCTG  
GTGGACTAGTGGTGGTGAATCATTACCTAGCATTTAGTTTTTTGCAGAAGAATATTATCCCTTCTCAGAGGTCC  
TGGCCTATTTCACTTTCTGCTGTGGATAATTCGGTTTTCGGTTTTTGTGTCACTTTGGCCGGGGAGAACGTCC  
TGCCCTCTACCATGCAGCCAGGAGATGATGTCGTCTCCAATTATTTACCAAAGGCAAGCGGGGCAACGCTTAG  
GGATCCTGGTTGTCTTCTCCTTCATCAAAGAGGCCATTCTACCCAGTCGTCAGAAGATATACTGACCCCCATGCA  
GGCAGGATGTGGGGGGCAAGATCAGGAGAGTCAGGCCCTGGGCTCTATGCCAGGTGGGGACCAGAAGTCGGGA  
AGGCACCTACCACCTGCCCTGGCTTTCTTCCCTCAACTCTGGAGCCCCATCCCCACCCTCCTTGGGGGGCTCAG  
CTTGGCTCAGATCTGATGCTTCAAGAGGCTGTAACTCAGAGGGCACCAGGAGGGTGGCAGAGCCTGCTTAGCC  
AGGAGGCCGAGGTCCCTCAGTCCCTCCCTGTCCCTTCCAAGGTGGGTGAGGAGGTTCTGGCCCCGCTGGGGCAGG  
CAGGGCAGGGTCTGTGAAGCTTAAGAGCAGATGGTGACAAGTTCTCTGGGCAGGTGGCCATGGGGAGGGGCCATG  
GCTTGGCATGTCCAACAGAAATAGTTTTTGTCTGTTGAACGCTGATTTCTGTCCAAGTGCAGATTTCCGTTTGAAT  
AAAGCTTCGCTTCTAGGTGGCACTGTTTGCCTTAATACCCTGACAGTTTCATCTTCTTCTCTCTGTAACCTTC  
TGCTCTGGACTGGACTCACTTTTCTGCTCCAGGACTCCTTTTCTGGGTTTGGGTCTTGCCCTTCCAAGGGACT  
GTTCTTGTGGCCCTTAATGGGAAGGGGGCAGGGGTGAGGAGCTGAGCCTGCTCAAGGAGTGGGAAGTGGGGCTAT  
AGGCAGCCTCTCTGATGCACTCTCTTCCATCTCTTCCCAAGGCTCCGTGACTGTCAAAGTGGGAGTAGGAGAG  
GGGACAATTTAGGACTGGGCTAGATTTTCAAGAAGCATCTACAATATCCTATTATAAATCTTCTCTGGGAAA  
AGGAGTGGTTTCTGGCTGAATACTATCTTAGGCTCAAGGAGAAACAAAATAAAAATTAGCTTCCAGGCAGCCTGT  
TTTTAAAGAAATGGGACTAATGGGAGAAGCTGTTTGTCACTTAAGAGCATCCAAGCCCTGGCCCTCTGTGCAC  
TCTTGGCTCCTGGGGAGATATATCTGCCTTCTAAGAAGGCAGGCCAGGTCTTGGGCACAGACCTGCATTGTTGA  
CCTTGCATCCAACATATAGTGCCTTGCAAGTGCTCAACAGTACATATTGGAATGAAGTCCCTATGAGAGCCATTT  
CTGGCCATGTTCTATACCTCAAAGTGAGGCTGGCAGGTACAGAGATGAAGTACACATGTGATACATTTAAGCC  
ACTGGAAAAACCCCTGTGCTTGAAAATATTTCTCTATATCATGCCTGGAGTTCCATCATAGCCCTTCATTTCT  
TGGCTTTAGCATTTACCTTCTCTTAAGAATACCAGCTTTCCCTTTCCCTGAGAGGAAGAGCACATGTTGGTCTC  
CTCTTAGTGTGAACGAGATTGCCAGGCCCTTTTCTCCTATGCACACCAGGATAGACAAGGCAGGGGATACTGGCA  
GCCTGCATCATCCTCCCATTTGGGCTGACAGCTGGCCCTACTTTCTCCTCTGCTGCTTGGTCCCTCACCTTGAT  
GATGTGGCTTCGCCCCCTCCACTCTACTGCCAGTGTTCTCCAGGGGTGCTAAATCCAGCAGACCCCTTTCTCTG  
TCTTACTAGATCTGGGCAGCATTTGACATGGCTGATCACCCCTTGCTTCTTGGATGGCACTTCCCTGGCACCTCT  
GTGGCTAGTTGTCTACCTCCCTGGCTGTTCCCTTTCAGGCTTCCGTGCAGGCTTCTCCACTTGGCCATGCACAGT  
AGGGTCTTTAGGGTTCTGCTGTGGGCTCCCTAGGGAAGCCCATCCATCTGGATGGTTCAGGATGGTGAGGAA  
TTTAGAGTTGACCTCCAGCCCCAACATCCTTCTGATCACTGAACCACAGTTTTGCTGCCCTTAGGTGCACAG  
ACAATTCAGGTCCATGGCCAGATGGTACTTGTCTTCTGCAAACCTGCCCTTCTGGGTACTTCCCTTGACC  
CCGAGATCACTCAGGAGCCAGACAGGAACTTATTCTATTCCTGTTTTCTTCTGCCCACCACATCCAATCTC  
TCAAAACGGTCAGGTCTACCTTAACATCTCTTGATTGAGCCACTCCCACTGTCATCAGTTTACCTGGATTAT  
CGTGACAGCCTCCTACTGCTTCTCTATCATGTGGCCAGAGCTATCTTCTAAAATGCATTGCATAGTTGATCAAG  
TCACTCTCTGGCCTAAAACCTTCCCTTGCTCCCTGCTGCCCTCAGGATAAAGTCTGGACCCCTCAGCATGGCTTG  
TGAGACTCATGGTGTCTTGTCCCTGCTCACCTCTCTGGTCTCATCACTTGCTTCTTGCATTCTGGGTCCCAGC  
CTCCTGTATCCAGAGATGCAGTGGCTCTCCATTGCCACTCTGATTCCTCCTTTCTTTTGGTCACAGAGAAAGGT  
ACTTTCTCTGTCAAATCTCAACTTAGACTTGACTTCTCCAAGGAGCTTGGCTATACTCTCTCTCCCGACCCC  
CACCTTGGCATACTACAGATCACTCTGGGCTCACTTGCTGCCTAATGGTCATCTCCCCAGTAGACTGTAAGC  
TCCTTGAGGGCAAGGATTGTGTTGAATTTTTGTATTAAAGTGCCTGGCTTGGTGCCTGGCACCTAGAAAGCAC  
TCAATAAATGTTGTTTAAATGAA

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## **FIGURE 168**

MWFMYLLSWLSLFIQVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIGLYVFE  
RFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCGLVVVNHYLAFQFFAEYYPFSEVL  
AYFTFCLWIIPEAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGKRGKRLGILVVFSFIKEAIL  
PSRQKIY

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 126-146

**Casein kinase II phosphorylation site.**

amino acids 145-148

**N-myristoylation sites.**

amino acids 73-78, 82-87

**Amidation sites.**

amino acids 168-171, 171-174

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 91-101

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**FIGURE 169**

CAAAGCCCTACCCTCACCATTACCAGGTCCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG  
TTAGAAGGTGCAGAGCGTGGAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG  
TCCCTGGGCGCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCGCGTGAATACA  
**CATGG**CTCTGTTACGAAAAATTAATCAGGTGCTGCTGTTCCCTTCTGATCGTGACCCCTCTGTGT  
GATTCTGTATAAGAAAGTTCATAAGGGGACTGTGCCCAAGAATGACGCAGATGATGAATCCGA  
GACTCCTGAAGAACTGGAAGAAGAGATTCCCTGTGGTGATTTGTGCTGCAGCAGGGAGGATGGG  
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTTCTATGT  
AGTGGGACTCCGGAATACTCTGACTCGAATACGAAAATGGATTGAACATTCCAAACTGAGAGA  
AATAAACTTTAAATCGTGGAATTCAACCCGATGGTCCTCAAAGGGAAGATCAGACCAGACTC  
ATCGAGGCCCTGAATTGCTCCAGCCTCTGAACTTTGTTTCGATTTTATCTCCCTCTACTTATCCA  
CCAACACGAGAAAGTCATCTATTTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT  
GTATGACACCACCTTGGCCCTGGGCCACGCGGCGGCTTTCTCAGATGACTGCGATTTGCCCTC  
TGCTCAGGACATAAACAGACTCGTGGGACTTCAGAACACATATATGGGCTATCTGGACTACCG  
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCCAGCACCTGCTCTTTCAATCCTGGTGTGAT  
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAAGCAATTGGAGAAATGGATGCA  
AAAGAATGTGGAGGAAAACCTCTATAGCAGCTCCCTGGGAGGAGGGGTGGCCACCTCCCCAAT  
GCTGATTGTGTTTCATGGGAAATATTCCACAATTAACCCCTGTGGCACATAAGGCACCTGGG  
CTGGAATCCAGATGCCAGATATTTCGGAGCATTTTCTGCAGGAAGCTAAATTACTCCACTGGAA  
TGGAAGACATAAACCTTGGGACTTCCCTAGTGTTTACAACGACTTATGGGAAAGCTGGTTTGT  
TCCTGACCCTGCAGGGATATTTAAACTCAATCACCATAGCT**TGAT**ATAACTCTACCCTTAAAT  
ATTCCCTGTATAGAAATGTGGAATTGTCCCTTTGTAGCCAACCTATAACATTGTTCTTTATGAA  
TATTACCTTTGATACATATGATCCACAATATAAAAACCAAAACTACTGTGTGCAAATTATAC  
CTTGACCATATAGGCATTGATTAACCTTCTTTAAGTACATGTGATAACTATGGAAATCAAGAT  
TATGTGACTGAAAAACATAAAGGAAGAGACCCATCTAGATAACAGCAATCAACCTGCTTAATT  
CTGAATGACAATTATATCCACAAATTTTAAACTTCTACATGTATTTTTCACATGAAGATCT  
CCTTAACAGGTTGCCAACCTTTTCTTTTATAAACTATTACATTTAAATATGGACGTCTGAA  
AAATAAAATATTCATCATTTTTTAAAA

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## **FIGURE 170**

MALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESETPEELEEIPVVICAAAGRMG  
ATMAAINSIIYSNTDANILFYVVGRLNTLTRIRKWIEHSLREINFKIVEFNPMLKGGKIRPDS  
SRPELLQPLNFVRFYLPLLIHQHEKVIYLDLDDVIVQGDIQELYDTTLALGHAAAFSDDCDLPS  
AQDINRLVGLQNTYMGYLDYRKKAIKDLGISPSTCSFNPVIVANMTEWKHQIRITKQLEKWMQ  
KNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFLQEAKLLHWN  
GRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 234-238

**Tyrosine kinase phosphorylation site.**

amino acids 253-261

**N-myristoylation sites.**

amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,  
266-272

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**FIGURE 171**

GCCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAGATGGAGCCCCAGCTGGGGCCTGAGGCTGCC  
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGGTCTCAGCCCTGAGCTGTTCTTTCTCC  
TTGCCAGCTTCTTCCCTTTCTTCTCTGGTGCCCCAAGTCAGAACCAGCTACAATTTTGGAAGG  
ACTTTCCTCGGTCTTGATAAATGCAATGCCTGCATCGGGACATCTATTTGCAAGAAGTTCTTT  
AAAGAAGAAATAAGATCTGACAACCTGGCTGGCTTCCCACCTTGGACTGCCTCCCGATTCTTCTG  
CTTTCTTATCCTGCAAATTACTCAGATGATTCCAAAATCTGGCGCCCTGTGGAGATCTTTAGA  
CTGGTCAGCAAATATCAAAACGAGATCTCAGACAGGAGAATCTGTGCCTCTGCATCAGCCCCA  
AAGACCTGCAGCATTGAGCGTGTCTGCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC  
AAGCGCCTCACGCCGGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAATAAAGTTCCTG  
TGTATGCTGAGATTAACACCAGTGAAAAAGCCTGGCATGGAGCCCAGCACTGAGAACTTCCAGA  
AAGTGTTAGCCTTCTCCCAACTGTGTTATACCAACCACATTTTCAAATAGTAATCATTAAGA  
GGCTTCTGCATCAA



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**FIGURE 172**

MEPQLGPEAAALRPGWLALLLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRTFLGLDKCNAC  
IGTSICKKFFKKEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD  
RRICASASAPKTCSEIRVLRKTERFQKWLQAKRLTPDLVQDCHQGQRELKFLCMLR

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 100-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 158-161

**N-myristoylation sites.**

amino acids 56-61, 65-70

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 18-28

**Prenyl group binding site (CAAX box).**

amino acids 179-182

**Leucine zipper pattern.**

amino acids 5-26

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**FIGURE 173**

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCACCTGGGCTGGCTC  
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCGTCGCTTAAGGCCACTCC  
TATTCTACGGCTGACCCCTGGTGGTCACGTGGATCTGTTGCCACGCAAGTCTGGGTCTTCG  
GCGATTGACCGGGGTCTTGCTGTTCCGGGAGCCTCTCCTAAGCTGCCTGTTCCGCGGAGAGTT  
TGGAGGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCGCAGCACGCTGGAGTCCCG  
CTTAGGTACCACTTAGCGTCAGGGGAGCTGGGTCAGGCGGTCCGCCGGACACCCCGTGTGTGG  
CAGGCGGCGAAGCGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC  
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGGCCACGGCGGCGGC  
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATGAAAGGCTGGGGTTGGCTGGCCC  
TGCTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG  
CATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCAGGTGGACCCCAAGAAGACCA  
TTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG  
CCCGCTCAGAGGCCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG  
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG  
AATCCAGTGAAGTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCCTCAAGT  
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTCCCGAGAGG  
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA  
TATCGCATGATGAGCTATGAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG  
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTAAAAATA  
TGAAACCAAAAGT

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**FIGURE 174**

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGsFRINPDGS  
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGRNGESSELDLQGIRID  
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCdHALHISHDEL

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 12-18, 16-22, 29-35

**Endoplasmic reticulum targeting sequence.**

amino acids 179-184

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**FIGURE 175**

CGCAGCGCGGCAGTCCTGATGGCCCCGGCATGGGTTACCGCTGCTGCCCCCTGCTGTGCTCCTG  
GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAAGTGCAGGGTGGG  
AGATTCTGATGGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGCG  
ACAGTGAAACCCCTTTGCCATCGACATATTTCTGTACCAACAAAGATTTTCAGGGATTTTGTC  
AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT  
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA  
GTGGAAGGCAATTTTGGAGGCAGCCTGCAGGTCTGGCTCTGGCATCCGAGAGAGACTGGAG  
CACCCAGTGTTACACGTGAGCTGGAATGACGCCCGTGCCTACTGTGCTTGGCGGGGAAAACGA  
CTGCCCACGGAGGAAGAGTGGGAGTTTGCCGCCCGAGGGGGCTTGAAGGGTCAAGTTTACCCA  
TGGGGGAAGTGGTTCCAGCCAAACCGCACCAACCTGTGGCAGGGAAAGTTCCCCAAGGGAGAC  
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCCGCCAGAACAACCTAC  
GGGCTCTATGACCTCCTGGGGAACGTGTGGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG  
CAGGACATGCGCGTCCTCCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC  
CGGGCCCCGGGTCACCACCAGGATGGGCAACACTCCAGATTCAGCCTCAGACAACCTCGGTTTC  
CGCTGTGCTGCAGACGCAGGCCGGCCGCCAGGGGAGCTGTAAGCAGCCGGGTGGTGACAAGGA  
GAAAAGCCTTCTAGGGTCACTGTCATTCCTGGCCATGTTGCAAACAGCGCAATTCCAAGCTC  
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC  
CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGCCCAATGTGTGTT  
GACGATGGCTGGGGGCCAGGTGTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA  
CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTAAGCATTTTAAAATCTATTC  
TCTCCCCCTTCTCCCTGGATGATTGAGGAAGCTGACATTGTTTCTCAAGGCAGAATTTTCC  
TGGTTCTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG  
GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAACAGGCAGACATGTAAGTATTGCA  
AAGCACAGTTCAGTCCTAAAAGGGTCTGGGAGAACCAGATGATGTACTAGGTGAAGCATTGCA  
TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT  
TTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGGGTCTTTCTCTGTTGCCAGGCTAGAGTGAAGT  
GTGATCACGGCTCACTCTAGCCTTGAATTCCTGGGCCCCAAGCAATTCTCCACCTCAGCCTCC  
TGAGTAGCTGGGACTACAAGTGTGCACCACCATGCCTGGCTAATTTTTTGAATTTTTGTAGTG  
ATGGGATCTCGCTCTGTTGCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCCACC  
TCGACCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCCCTTCTCCATA  
TGCTCCAAAACATGTCCCTGGAGAGTAGCCTGCTCCACACTGTCACTGGATGTCATGGGG  
CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA

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## **FIGURE 176**

MARHGLPLLPLLSLLVGAWLKLGNQGATSMVQLQGGREFLMGTNSPDSRDGEGPVREATVKPFA  
IDIFPVTNKDFRDFVREKKYRTEAEMFGWSFVFEDFVSDEL RNKATQPMKSVLWWLPVEKAFW  
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ  
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFFPAQN NYGLYDLLGNVWEWTASPYQAAEQDMRVL  
RGASWIDTADGSANHRARVTTRMGNTPD SASDNLGFRCAADAGRPPGEL

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 191-195

**N-myristoylation sites.**

amino acids 23-29, 25-31, 175-181

**Amidation site.**

amino acids 159-163

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**FIGURE 177**

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCCTGCTGGGCCACAGGCGAGCGCTTTAT  
TTCTGGAGCTGAGGGCTAAACTTTTTGACTTTTCTTCTCCTCAACATCTGAATCATGCCAT  
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCGTGGTGGCTCAGCTCCTTAACCTTTGGGGCGC  
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTTCGCTTCCCGGACAGGAGGCAAGAGCATT  
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT  
TTTTGTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTTGGATGGCT  
CAGAGGACTGGGTGTACTACAGAATTTCTCACGAGGAGAAGGACCTGTTTTTTAACTTGACGG  
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG  
TTAAGATGATGGCTTCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTTCTACAGCAGGGCA  
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTCCAACCTACCAC  
ATGGAGACTTTTTTCAATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC  
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA  
TTGTGACTCACATGTCCTCCTGGGTGAAGAATCTGTTTTGTTCTTTTGGTAGTTTTATTAAA  
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA  
TGACATTCAAATCTCTTCTGTATTCTCTTGCCAGAAAGTGACATTCTTTTGTGTTGTATAAA  
CCCTTTCATTGTC

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**FIGURE 178**

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRFPDRRQEHFIKGLPEYHVVGPPVRVDAS  
GHFLSYGLHYPIITSSRRKRDLDGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL  
SHVKMMASAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDDFFIEPVKKHPLVEGGY  
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 11-15, 105-109, 125-129

**N-myristoylation site.**

amino acids 149-155

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**FIGURE 179**

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTCCTTTTCT  
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGATATGTTGTGGATTACAGTTTTCTCT  
GCCTTGCCTACGACTGTTTCTGGTTGTTACCTGTTATCTTTTATTATTACTCCACAAAGAAAT  
ACTTGGATGTTCTGCTGTTTGTCTGAGCTCTGCACTGGGAGACAAATTAAGTCCGTAAGTCTAGG  
CCTTTCGAGTATTCTTAAGAATTTTCTGAAAGTACAGTTTTTCTGTATCTGACTGGGAATAA  
TATATCTTATATAAATGAAAGTGAATTAACAGGACTTCATTCTCTTGTAGCATTGTATTGGA  
TAATTCTAACATTCTGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTCT  
ATTTCTAAATAATAATTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT  
TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTCCGAGAGGAGTATTTAATGATCT  
AGTTTCAGTTCAGTACTTAAATCTACAAAGGAATCGCCTCACTGTCCTTGGGAGTGGTACCTT  
TGTTGGTATGGTTGCTCTTCGGATACTTGATTATCAACAATAACATTTGAGGATATCAGA  
ATCAGGCTTTCAACATCTTGAAAACCTTGCTTGTGTTGTATTTAGGAAGTAATAATTTAACAAA  
AGTACCATCAAATGCCTTTGAAGTACTTAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC  
TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCCTGAA  
AAATTCAAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGGAATTAATAATCTTAAACATTT  
GATCTTAAGTCATAATGATTTAGAGAATTTAAATCTGACACATTCAGTTTGTAAAGAATTT  
AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT  
GGGAGCATCTTTGAAGATCCTTAATCTGTCAATTAATAATCTTACAGCCTTGCATCCAAGGGT  
CCTTAAGCCGTTGTCTTCATTGATTCATCTTCAGGCAAATCTAATCCTTGGGAATGTAAGT  
CAAATTTTGGGCCCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA  
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAACATTACAAATTGTGTACATC  
TTCAATAAATGTATCCAGAGCTTGGGCTGTTGTAAATCTCCTCATATTCATCACAAGACTAC  
TGCGCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC  
TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA  
TGCCCTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAATACAACTTACTACTTC  
TGTTACCTTGAATTTGGAAAAAACAGTGCTCTACCGAATGATGCTGCTTCAATGTCAGGGAA  
AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGCTAGC  
TTTTTTCATCTTAGCTTGTGTTTTAATCATTTTTTTGATCTACAAAGTTGTTTCAGTTTAAACA  
AAAATAAGGCATCAGAAAATCAAGGGAAAATAGACTTGAATACTACAGCTTTTATCAGTC  
AGCAAGGTATAATGTAAGTGCCTCAATTTGTAACACTTCCCCAAATCTCTAGAAAGTCCTGG  
CTTGGAGCAGATTGCACTTATAAACAATTTGTTCCCTGAAAATGAGGCACAGGTCATTCTTTT  
TGAACATTCTGCTTTATAACTCAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT  
GATTTAACTGAAACCTCCTTATATAATTATATACTTTAGTTGGAAATATAATGAATTATATG  
AGGTTAGCATTATTAAATATGTTTTTTNTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 180**

MCGLQFSLPCLRLFLVVTCYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPESTV  
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG  
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSQYLNLRNRLTVLGSGTFVGMVALRILDLSN  
NNILRISESGFQHLENLACLYLGSNNLTQVPSNAFEVLKSLRRLSLSHNPIEAIQPFQKGLA  
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLKLNLIYKLDNRNIISI  
DNDTFENMGASLKILNLSFNNTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA  
ITLNIYQNPSPMRGRALRYINITNCVTSSINVSRAWAVVKSPIHHKTTALMMAWHKVTNG  
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTNLNLEKNSALPN  
DAASMSGKTSLECTQEVEKLNEAFDILLAFFILACVLIIFLIYKVVQFKQKLKASENSRENRL  
EYYSFYQSARYNVTASICNTSPNSLESPPGLEQIRLHKQIVPENEAQVILFEHSAL

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 530-547

**N-glycosylation sites.**amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,  
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

**N-myristoylation sites.**

amino acids 3-9, 69-75, 126-132, 174-180

**ATP/GTP-binding site motif A (P-loop).**

amino acids 506-514

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**FIGURE 181**

GGCCTGGCGCGGCGCTCCGGTAAGGCGTGTGTGCGGCAGGGCGGGGACAGAACCGTCCTCTCG  
GGCTCTGGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG  
GCATTGCTCCCCCTGGCACAGTTGGCCTCTTTCCAGAAGCCCGTTTTGTTTGTTTTACGTCT  
AAATTCGCGTCGGTTCTTATTTCTCTCCCTGGCAAGGTCTGAAGACGGGTAGGAGAATAACCT  
GTGTCAGCGTGTTATGATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT  
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAACCCC  
TCCTAAGATCCCTTATAAGGCCATCGCACTTGCCACTGTGCTGTTTTTGATTGGCGCCTTTCT  
CATTATTATAGGCTCCCTCCTGCTGTCAGGCTACATCAGCAAAGGGGGGCGAGACCGGGCCGT  
TCCAGTGCTGATCATTGGCATTCTGGTGTTCCTACCCGGATTTTACCACCTGCGCATCGCTTA  
CTATGCATCCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTTGATGACTAGCA  
CCCACCCCATAGCTGAGGAGGAGTCACAGTGGAAGTGTCCAGCTTTAAGATATCTAGCAGAA  
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTTGCAGATGTTTAAGAAAATAATGGCCAGATT  
TTTTGGGTCTTCCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT  
TTTCATCCCTGGGCCCTGACAAGTTTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA  
TTCTGTAATGGAAAAGTGTTCCTGCCACCACCCTCTGTAGAGCTGAGCATTCTTTTAAATA  
GTCTTCATTGCCAATTTGTTCTTGTAGCAAATGGAACAATGTGGTATGGCTAATTTCTTATTA  
TTAAGTAGTTTATTTTAAAAATATCTGAGTATATTATCCTGTACACTTATCCCTACCTTCATG  
TTCCAGTGGAAGACCTTAGTAAAATCAAAGATCAGTGAGTTCATCTGTAATATTTTTTTTACT  
TGCTTTCTTACTGACAGCAACCAGGAATTTTTTTATCCTGCAGAGCAAGTTTTCAAATGTAA  
ATACTTCCTCTGTTTAACAGTCCTTGGACCATTCTGATCCAGTTCACCAGTAGGTTGGACAGC  
ATATAATTTGCATCATTTTGTCCCTTGTAATCAAGATGTTCTGCAGATTATTCCTTTAACGG  
CCGGACTTTTGGCTGTTTCCTAATGAAACATGTAGTGGTTATTATTTAGAGTTTATAGCCGTA  
TTGCTAGCACCTTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT  
AGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTAGCTTGCAAAAAGTGACTTATATTCCA  
AAGAAATTAAAATGTTGAAATCCAAATCCTAGAAATAAAATGAGTTNNTTCCAAAAA  
AAA

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**FIGURE 182**

MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLIIG  
SLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

**Transmembrane domains:**

amino acids 45-66, 79-95

**N-myristoylation sites.**

amino acids 11-17, 75-81

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**FIGURE 183**

CTAAAAAATACAAAAATTAGCTGGGCGTGGTGTCTGTACCTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGA  
GAATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATTAAGTCACTGCACTCCAGCCTGGGTGACAGA  
GCAAGACTCTGTATCAAAATAAATAAATAAAGTACAACCTCTGGATGGGCATGGTGGCTTATGTCTGTAATCCCAG  
CACTTTGGGAACCTTGAGGCGGGTAGATTGCTTGAGTCCGGGAGTTTGAGACCAGTCTGGGTAATATGGTAACCCCT  
GTCTACCAAAAAATACAGGTATTAGCCAGTCTCATAACTCGGTCTCAAAATAAATAAATACATACATACATAGATG  
AAAATTTAAAAAATAAAGTCCAACCTCAGCGGTTTTTCAGCATATTTACAGAGTTGTACAATCTTCACCACTATCTA  
ATTTCAGAACATTTTCATCACCCCCAAAAGAAACCTAACCCATTGACTATCTCTCCATTTCTCCCTCTCCCTAG  
CCTCTGGCAACCACTAATCTCTTTTGTCTCTATAGATTTGCCTATTTTGGACAGTTCATATACAAGGAATCAT  
ACCACATGTAGCCTTTTGTGTCCGGCTTCTTTGATTAAATAGAATGTTTTCAAGGCTCATCTATGCTGTAGCCTGT  
ATCAGCACTTCATTCTTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTTTCCACTAGCTGAT  
GGACATTTGGGTTGTTTCCACCTTCTGGCTATTATAAATATTGCTGCTATAAATATTCACTTACAAGTTTTTGTG  
TGGACATATGTTTTATTTCTTCTGGTATATCCTTCGGAGTGGAACCTGCTGGATCAGGTGGTAACCTTAGGTCTA  
ACCTGGCAGTTAAACAGAATCCTATGCATGCTGTAGTCCATGAGTTGAAATAAACACTTGACCCATAGTAAGTGC  
CAGATCATCTTCATTTACAGCAACCCAGTAATTTACAGATGAGGAAATGAAGGCTCCCAGAGGTGAACCTGGCTT  
TTCCCATTTGAGCAGTTCCAAGTCAGACAGTTAAAAAGTGGCAGGACCTGGAAGAGAAGCTAGTTCTTTACCCCT  
GGCATTTCAGGGCTGCCTCCTGGGCTACGGGGCTGGCATTAGAAATAGAGCTAAGGCTGCTGCCAAGGCAGGTGC  
CCAGTCTGCCTCCTCTGTGTCTTATTCCACTTTCTCTGCAGCCCTCCAGGGGACCCCTCTCTCAGCCACCCTC  
TCTCTGGTGAATGTCACAGTGTGCGGAAGATCAAAGATACGGTGCAGAAACTGGCTTCGGACCATAAAGGACATT  
CACAGCAGTGTATCCCGAGTGGGCAAAGCCATTGACAGGAACCTCGACTCTGAGATCTGTGGTGTGTGTGTCAGAT  
GCGGTGTGGGACGCGCGGAACAGCAGCAGCAGATCCTGCAGATGGCCATCGTGGAACACCTGTATCAGCAGGGC  
ATGCTCAGCGTGGCCGAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGACTTGGATTTCAAGCAGCCTTTCCTA  
GAGTTGAATCGAATCCTGGAAGCCCTGCACGAACAAGACCTGGTCCCTGCGTTGGAATGGGCCGTCTCCACAGG  
CAGCGCCTGCTGGAACCTCAACAGCTCCCTGGAGTTCAAGCTGCACCGACTGCACCTCATCCGCTCTTGGCAGGA  
GGCCCCGCGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACCTCCAGCCCTTTGCTCGGCTGCACCAGCGGGAG  
ATCCAGGTGATGATGGGCAGCCTGGTGTACCTGCGCTGGGCTTGGAGAAGTCACCCCTACTGCCACCTGCTGGAC  
AGCAGCCACTGGGCAGAGATCTGTGAGACCTTTACCCGGGACGCTGTTCCCTGCTGGGGCTTTCTGTGGAGTCC  
CCCCTTAGCGTCAGCTTTGCCCTGGCTGTGTGGCGCTGCCTGTGTTGATGAACATCAAGGCTGTGATTGAGCAG  
CGCAGTGCACCTGGGGTCTGGAATCACAAGGACGAGTTACCGATTGAGATTGAAGTAGGCATGAAGTGTGGTAC  
GCTCATCTGTGGCCATGTTATCTCCCGAGATGCACTCAATAAGCTCATTAAATGGAGGAAACACTCCGTGTTGCT  
TGCCCCATCCTCCGCCAGCAGACGTGAGATTCCAACCCCTCCCATCAAGCTGAAGTGTCCCTACTGTCCCATTGGAG  
CAGAACCCGGCAGATGGGAAACGCATCATATTTGATTTCCTACCTGGAAGGAATTTTGTGAAAGGGGTTTTAC  
CTGTGAGCCTTGGTCTGTCTCGGTAGGGTGGTCAACTTCAGTGGACTGTGGTTGGTTTCAGAGCGCTGGCTGAG  
GAGTTCCACTGAGGGGAGCACTGGAGCAGCCCTTTGGCAGAGGCTGAGGAGGGAGATGGACCAGCCACGCTGG  
CACCTGGCTCCATGGCATAAGGAAAGGGAGATGCTGGCCTCTGTGCTCCTGCTGTCTTTTCTGTTTCTGTTTGC  
GTTTGACTTAGTAGCAACCGACAGAGTGGCAAGGGATTTGGTCTTCAGCAGTAGACATCCTTCCACCCCTGCCCT  
CAGCCAAGTCTCTTGCTGCCATGCCAATGCTATGTCCACCCTTGCCCTCGGCCAAGAGTGTCCAGCGGTGGCC  
CACCTCTTCTCCCACTACAGCTCAACAGTATGTACCATCTCCACTGTAAATAGTCCAGTTAGAACGGAATG  
CCGTTGTTTTATACTTTGAACAAATGTATTTACTGCCCTTCTCAAAA

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**FIGURE 184**

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFSEICGVVSDAVWDAREQQQQILQMAIV  
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRILEALHEQDLGPALEWAVSHRQRLLEL  
NSSLEFKLHRLHFIRLLAGGPAKQLEALSYARHFQPFARLHQREIQVMMGSLVYLRLGLEKSP  
YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVLNMNIKAVIEQRQCTGVW  
NKHDELPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLCGHVISRDALNKLINGGKLKCP  
YCPMEQNPADGKRIIF

**Transmembrane domain:**

amino acids 222-241

**N-glycosylation site.**

amino acids 129-133

**Tyrosine kinase phosphorylation site.**

amino acids 151-159, 184-193

**Amidation site.**

amino acids 327-331

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 222-233

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**FIGURE 185**

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTAAT  
CTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC  
TTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA  
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTGAC  
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT  
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC  
CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAG  
AACGAACCAAATTAAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA  
GATTTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC  
TGTCACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCCTCTGAT  
TGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT  
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG  
CAGGTCATACCATGACCGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG  
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT  
GGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGT  
CAACTGGAGGTCCTGCACATGCAATTTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACA  
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA  
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATTAAGAGAATGT  
GCACATCCTTACATTAAGCCTGAGAGAA

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**FIGURE 186**

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKNGYVQSPRF  
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDISETSTIIRGRWCG  
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY  
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV  
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGNGCGGTVNWRSCNCSG  
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 262-266

**Tyrosine kinase phosphorylation site.**

amino acids 256-265

**N-myristoylation sites.**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1.**

amino acids 1-56

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**FIGURE 187**

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG  
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG  
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT  
TGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTGACAGCTCC  
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA  
AAAAATCGTGATTAACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAG  
CAGAACATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCC  
TCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA  
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT  
GTCCAGCTTCGACCAGGATTCTAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAACTGATGCCAACA  
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCTGAGTGTCTGTGAGAA



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**FIGURE 188**

MPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRIHVGKEKHPANLILYGNEDKRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPPDKTVIEWEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP  
QLQDLDPQAQEHDTSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

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**FIGURE 189**

**ATG**TGCTGCTGGCCGCTGCTCCTGCTGTGGGGGCTGCTCCCCGGGACGGCGGGCGGGGGGCTCG  
GGCCGAACCTATCCGCACCGGACCCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC  
CAGCGGGGCAGCCAGATCGCCTTCCGCCTCCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC  
TTCTCGCCACCGGGGCCATGGCGTCCGCCGACATCGTCGTGGGCGGGGTGGCCACGGGGCGG  
CCCTACCTCCAGGATTATTTACAAATGCAAATAGAGAGTTGAAAAAGATGCTCAGCAAGAT  
TACCATCTAGAATATGCCATGGAAAATAGCACACACAATAATTGAATTTACCAGAGAGCTG  
CATACATGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCCCTAC  
CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGACCAAGAGT  
TTGCGGTTATTGAATCCTGAGAAAAGTAGTGTGCTATCTACAGCCTTACCATACTTTGATCTG  
GTAAATCAGGACGTCCCCATCCCAACAAAGATACAACATATTGGTGCCAAATGTTTAAGATT  
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG  
AGTCTGGTGCACCACATCCTGCTCTATCAGTGCAGCAACAACCTTTAACGACAGCGTTCTGGAG  
TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCCCTCACCTGTGAAACTGTGATT  
TTTGCCTGGGCTATTGGTGGAGAGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC  
ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACCTTATGAGGAA  
GGCTTAATAGATAATTCTGGACTGAGGTTATTTTACACAATGGATATAAGGAAATATGATGCT  
GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG  
TTCCAGTCTGAGGGTCACTGCACTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA  
AGTGGAATTCATGTGTTTGTCTTCTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG  
CGTCATTTTCGAAAAGGGAAGGAAATGAAATTACTTGCCTATGATGATGATTTTGACTTCAAT  
TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAACAATCTTACCAGGAGATAACCTAATTACT  
GAGTGTGCTACACACGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT  
GAAATGTGTCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT  
CCAGACATTATGGAACAACCTCAGTTCATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC  
TGGCCTTTCATTATCAAAGTCCCAAGCAATATAAAAACCTTTCTTTCATGGATGCTATGAAT  
AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCCTCAGCCTGCCAGTG  
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTCGATTCAAGGAATGACAGCATTACCT  
CCAGATATAGAAAGACCCCTATAAAGCAGAACCTTTGGTGTGTGGCACGTCTTCTTCTCTTCC  
CTGCACAGAGATTTCTCCATCAACTTGCTTGTGTTGCCTTCTGCTACTCAGCTGCACGCTGAGC  
ACCAAGAGCTTGTGATCAAAATTCTGTTGGACTTGACAATGTTTCTATGATCTGAACCTGTC  
ATTTGAAGTACAGGTTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGGAGACTTTTCTTC  
CCCATTTTCCCTCCCTCCTTTTTCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT  
CTCTTTCTTAGAAATACCTGATGTTATATATACATGGTCAATAAAAATAAACTGGCCTGACTT  
AAGATAACCATTTTAAAAAATTGGGCTGTCATGTGGGAATAAAAGAATTCTTTCTTCTCTAA  
AAAAAAA

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**FIGURE 190**

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLLDSEGKYWLGWSQRGSQIAFRLQVRTAGYVGFG  
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIIEFTREL  
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTKSLRLLNPEKTSVLSTALPYFDL  
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE  
SGHECYHPNMPPDAFLTCTETVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEE  
GLIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEALEAEKP  
SGIHVFAVLLHAHLAARGIRLRHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT  
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASI PDIMEQLQFIGVKEIYRPVTT  
WPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVLVSLPVNVRCSTDNAEWSIQGMTALP  
PDIERPYKAEPLVCGTSSSSSLHRDFSINLLVCLLLLSCTLSTKSL

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 56-73, 378-393, 583-602

**N-glycosylation sites.**

amino acids 114-118, 247-251, 476-480, 517-521

**N-myristoylation sites.**amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,  
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

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**FIGURE 191**

GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTGTTCTTTATAACAT  
TTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGG  
CATATCTCAACCAAGTTCTACTCTCTTGAATAGAAAGGAATCATCTTGTTCAAAGCAAGAATA  
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGGAA  
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC  
AGTATGGCTACACCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA  
CTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA  
AAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA  
GGACTCGAGTCCATGGTCGGTGTCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG  
CCTTTCCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAACCTGGACCA  
AGGATGGAGCAGGATTCAACTTGTTTCTTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGC  
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA  
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG  
TACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCTGACTTGACTTTTGACG  
CTATCACAACCTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT  
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTCTGGCCATCTCTGCCAGCTGATC  
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGA  
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG  
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAACCTACTTCTTTG  
TGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA  
GAGTGGTAAAACACTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGAT  
TCTTCTTTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC  
GAATCATGAGAACTAATACTTGGTTTCAATGCAAAGAACCAAGAACTCCTCATTGTTTTG  
ATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT  
TGTTTATTTTTTGGTATTGTTCAATTGCTGAAAAACACTTCTATTTATCAATTAAATTCATAGAC  
CTAAAATAAACCTCAACAGGTCTTTTAATATAAATTCTGCTTCAAATAGAATAAAACCATTC  
TTTAACAAC

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**FIGURE 192**

MKRLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLIEGNHLVQSKNRS LI DDKI  
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVDPVGQYGYTLPGWRKYNLT YRI INYTPDMARAA  
VDEAIQEGLEVWSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGLGHAFPPGPGL  
GGDTHFDEDENWTKDGAGFNLFVAAHEFGHALGLSHSNDQTALMF PNYVSLDPRKYPLSQDD  
INGIQSIYGGLPKVPAKPKEPTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEF  
ELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA  
AVCDKTRKTYFFVGIWCWRFDEMTQTMKGFPQRVVKHFPGISIRVDAAEQYKGFFFFSRGS  
KQFEYNIKTKNITRIMRTNTWFQCKEPKNSSF GFDINKEKAHSGGIKILYHKSLSLFIFGIVH  
LLKNTSIYQ

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

**N-myristoylation site.**

amino acids 71-77, 205-211, 223-229

**Hemopexin domain signature.**

amino acids 171-202, 207-238, 318-334

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 213-223

**Matrixins cysteine switch.**

amino acids 89-97, 207-238

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**FIGURE 193**

CACAATCAGGTCCCATTCTATAGATGGGGAAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA  
AGGCTGGTATACCTGCACCCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGGCTGTCA  
TCCAGTCTCCTCCCTGCCCCTGCTGGTGCACTTCCTGCCTCTGCTGGTGCACTTTCTGCCCCCT  
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCCT  
GCTGGTGCACTTTCTGCCCCCGCTGATGCACTTCCTGCCTCTGCTGGTGCACTTCCTGGCTCT  
GCTGGCACACTTCCTGCCTCTGCTGGTGCACTTCCTGGCTCTGCTGGCGCACTTCCTGCCCC  
TGCTGGTGTATTTCTGCCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACTTCCTGCCTC  
TGCTGGCGCACTTCTTGCCTCTCCAGGCCCTACCTTAGCCTCTCCCTCTTATATATGGAAGTCT  
TCCCAGTTCACTGACACTGGTAACAGGGACTCTGCTCTTGGTGTGCTGTCTGCCCTGGGGAT  
GGGCATCTGTGTCTTCCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA  
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCCTACACCCACCAGGATTTTCCAATAAAGAGA  
TGTTACCA

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**FIGURE 194**

MVLGNGGCHPVSSLPLLVFHFLPLLVFHFLPLLVYLLPLLGRFLPRLVYLLPLLVFHFLPPLMHFL  
PLLVFHFLALLAHFLPLLVFHFLALLAHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

**Signal peptide:**

amino acids 1-39

**N-myristoylation sites.**

amino acids 4-10, 109-115, 116-122

**Leucine zipper pattern.**

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,  
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,  
65-87, 66-88

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FIGURE 195

[illegible]



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**FIGURE 196**

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN  
AKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLLVYCTDLPPTSIIITFHNEARST  
LLRTIRSVLNRTPTHLIREIILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADI  
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWS  
LHFQWEQLSPEQKARRLDPTPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFR  
VWMCGGSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYYAARPFAL  
ERPFNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQET  
PNLKLSPCAKVKGEDAKSQVWAFTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK  
TGSHEHIAHLCLDMDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

**Transmembrane domain:**

amino acids 475-493

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-6

**Tyrosine kinase phosphorylation sites.**

amino acids 68-75, 401-409

**N-myristoylation sites.**

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

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**FIGURE 197**

GCAGCTCACCTTCGCGAGCCGCGATGGGGGAAGACGACGCCGCGCTTCGGGCTGGCAGCAGGGGGCTCTCCGACC  
CGTGGGCAGACTCAGTGGGAGTGGGACCCCGCACACGGAGCGCCACATCGCCGTACACAAGCGGCTTGTGCTGG  
CCTTCGCTGTGTCCCTCGTGGCATTGCTCGCGGTCACAATGCTCGCTGTGCTGCTCAGCCTGCGCTTCGACGAGT  
GCGGGGCGAGTGCCACGCCAGGCGCCGACGCTGGCCCTCAGGCTTTCGGAGCGCGGCGGCAACGGGAGCCTCC  
CTGGATCGGCCCGGCGCAACCACCGCAGGCGGGGACTCCTGGCAGCCGAGCGGGTGGGGTGGCCAGTCCGG  
GGACCACGTCGGCCCGAGCCGCTCGGAGGAGGAGCGGGAGCCGTGGGAGCCGTGGACGCAGCTGCGCCTGTGCG  
GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCGCCTTCATGGAGAACTTCACCTTCTCCGGGGAGGTCA  
ACGTGGAGATCGCGTGGCGGAACGCCACCCGCTACGTAGTGTGCACGCTTCCCGAGTGGCGGTGGAGAAAGTGC  
AGCTGGCCGAGGACCGGGCTTCGGGGCTGTCCCTGTAGCCGCTTTTTCTCTACCCGCAAACCCAGGTCTTAG  
TGGTGGTGCTGAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACAACGCGCTCATCGAGA  
ATGAGCTCCTGGGCTTCTCCGAGCTCCTATGTGCTCCACGGGGAGAGAAGATTCTTGGTGTACTCAGTTTT  
CGCCTACACATGCCAGAAAGGCATTTCTTGTGTTGATGAGCCAATCTACAAGGCTACTTTCAAATCAGCATCA  
AGCATCAAGCAACCTATTTATCTTTATCTAATATGCCAGTGGAAACTTCCGTGTTTGGGAAGATGGATGGGTTA  
CGGATCACTTTTACAGACCCCTCTCATGTCCACATATTATTAGCCTGGGCAATTTGCAACTTCACATACAGAG  
AACTACCACCAAGAGTGGGGTGTAGTACGATTATATGCAAGACCTGATGCTATCAGAAGAGGATCCGGGGACT  
ATGCTCTCCATATAACAAAGAGATTAAAGAAATTTATGAAGACTACTTTAAAGTGGCCTATTCTTGGCAAAAC  
TAGATCTTTTAGCTGTGCTAAGCATCCGTATGCTGCTATGGAGAAGTGGGACTAAGTATTTTGTGGAACAAA  
GAATACTGCTGGATCCAGTGTTCATCTATTTCTTATTGCTGGATGTCACCATGGTCATTGTTTCATGAGATAT  
GTCACCACTGGTTTGGTGACCTTGTGACGCTGTGTGGTGGGAAGACGTGTGGCTGAAGGAAGGGTTTGCTCACT  
ACTTTGAATTTGTTGGTACAGACTACCTCTATCCTGGCTGGAACATGGAAAAGCAGAGGTTTCTGACCGATGTTT  
TGCATGAAGTGTGCTGCTGGACGGTTTGGCCAGTCCCATCCAGTATCACAGGAAGTGTGACGGCAACAGATA  
TTGACAGGGTGTGTTGACTGGATCGCATATAAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTTTATGGGCC  
ATTCACTTTTCCAGAGGGGTTTGCAGATTATTTAACCATTCATAAGTATGGTAATGCAGCCAGAAATGATCTCT  
GGAATACATTATCGGAGGCTTTAAAAAGAAATGGGAATATGTAATATACAAGAAGTAATGGATCAGTGGACAC  
TCCAGATGGGTTATCCTGTTATCACCATCTTGGGAACACAACAGCAGAAAATAGAATAATAATACCCAACAGC  
ATTTTATCTATGATATCAGTGTCTAAAACCTAAAGCACTTAAACTTCAGAATAACAGTTACCTGTGGCAGATTCAT  
TAACTATTGTGGTAGGAAATAGAAGCCATGTGTCTTCAGAAGCAATTATTTGGGTGTCTAACAAATCAGAGCAC  
ACAGAATAACTTATTTGGACAAAGGAAGCTGGCTGTGGGGAACATCAATCAAAGTGGCTATTTTAGAGTCACT  
ATGACCTAAGGAAGTGGAGATTATTAATTGATCAATTAATCCGGAATCATGAGGTTCTTCTGTGAGTAACCGAG  
CGGGCTTGATCGATGATGCTTCAGCCTAGCCAGGGCTGGCTATTGCTCAGAAATATTCTCTGGAGATTATCA  
GATACCTGTCTGAGGAGAAGGATTTCTTCTTGGCATGTGTGCCAGCCGAGCTCTTTATCCTCTAGATAAAATAC  
TGGACCGCATGGAAGAACTACAACATTTTCAATGAATATATTTTAAAGCAAGTTGCAACAACATATATCAAGCTTG  
GGTGGCCGAAAAATAATTTTAAATGGATCTCTTGTTCAGCATCCTACCAACATGAAGAACTACGTAGAGAAGTTA  
TAATGCTGGCCTGCAGTTTGGCAACAAGCACTGTCAACACAGGCATCAACACTTATTTAGATTGGATTTCGA  
GCAACAGGAACAGAAATACCATAAAGCTCAAGAGCTCAAGAACTTCATGAAAACTATGATGGGGTAGCTGCTGCTCTT  
TCTGGGAATTCATATGGATGAAATTCATTCCACCACAGCAGTTTCTGAGAAGAAAATATTATTGGAAGCCTTAA  
CTTGCACTGATGACAGGAATTTATTAACAGGCTTCTAAATCTGTCACTGAATTCTGAGGTGGTGTGCTGATCAAG  
ATGCAATTGATGTCATAATCCATGTAGCTCGAAATCCACATGGTCGAGACCTTGCCTGGAAGTTTTTCAGGGATA  
AATGGAAGATATTAATACCAGGTATGGAGAAGCATGTTTATGTATTCCAACTCATCAGTGGTGTACAGAAAT  
TTCTTAATACTGAAGGTGAACCTCAAGAGCTCAAGAACTTCATGAAAACTATGATGGGGTAGCTGCTGCTCTT  
TCTCACGAGCTGTGGAAGCTGTGGAAGCAATGTGCGCTGGAAGTGTCTTACCAAGACGAGCTTTTCCAATGGT  
TAGGAAAAGCTCTAAGACACTAATATATGTATCTTATAAACAACAATTCAACTCAGAAGTTTATGAGAAGACAC  
GCTTTTTGTGGAATGAGGAAAATGTACTACCTAGAAAATGGCCAGATTTTCAGTGTTAACGTGTGGGAGGAATTT  
TTTTTTTTTAGTTTTATTTTTTGGTTTTGGGGGATATTTTTTATTTGTTTCATTCTGTTCTGTTCTCTAC  
TGGGTGTTCTCTCTAAAGAACTCTTGCAAGTGAAACTAGCCATGATTGCTTCAGCTGTACATTCCTTGCTGTA  
CAGGACCAATATGATAGTGTGATGCTGTTGATGTTACAGTCAATTTGGAAGAAACATATTGAGAATATCTGTGCAT  
GGATATATTGCTGCTGTGTTCCAGCATGCTTATTTCAAACGTCAGTGTGTGTGAATATGTGTTACACC  
TAGGATGGGCATTATGCAAAAGCACAAAGATTATATATGACAATCAGTATTGCAATGAAAGAAAACTAAAAACA  
GAAATGATATTCTCAATTTTGGGCAATGTGAGAGGTAATAAGCCCTTGACATGATGAACATCACTTATTTTCAGC  
ACTTGGATTGTCTGGCAATGATTACTGTGTGCTAATCACTTTTCTTTGAGTTAAAGCTGTGTATACATTTTAA  
AGGCATATAGATAGTGTATGCATATGTATATGTACATAGGGAAGCCCCATATGTATATAGTATGTTGTACATGC  
ACATGTACAAAGAATGTCTCAGATCAAGAAAAATTTATCTCTTTTATAAACTTAAGGACAGTTGCAAAAGGCT  
TCAAGGAATTTATCTCAACATTATTCTTTCTATGTCTAATAAATTTCTCAACTGTTATGAATTTTTCATCTAC  
TTCTTGAACAGTGGTCTATTCTGCTACATGAAGATGAATACAACAAAATTTTGTATAAACTCCCAAAAAA  
AAAAA

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**FIGURE 198**

MGEDDAALRAGSRGLSDPWADSVGVRPRTERHIAVHKRLVLAFAVSLVALLAVTMLAVLLSL  
RFDECGASATPGADGGPSGFPERGGNGSLPGSARRNHAGGDSWQPEAGGVASPGTTSAQPPS  
EEEREPEWPWTQLRLSGHLKPLHYNMLTAFMENFTFSGEVNVEIACRNATRYVVLHASRVAV  
EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKI IYNALIENELLGFFRSS  
YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG  
WVTDHFSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPD AIRRGSGDYALHITKRLIE  
FYEDYFKVPYSLPKDLLAVPKHPYAAMENWGLSIFVEQRILLDPSVSSISYLLDVTMIVIHE  
ICHQWFGDLVTPVWVEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLTDVLHEVMLLDGLAS  
SHPVSQEVQLQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLTIHKYGNAARNDL  
WNTLSEALKRNGKYVNIQEVMDQWTLQMGYPVITILGNTTAENRI IITQQHFIYDISAKTKAL  
KLQNNSYLWQIPLTIVVGNRSHVSSEAI IWVSNKSEHHRITYLDKGSWLLGNINQTYGFRVNY  
DLRNWRLIDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPLIIRYLSEEKDFLPWHA  
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGLVQASYQHEELRREVIM  
LACSGNKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSLLEDVWEFIWMKFHSTTAV  
SEKKILLEALTCSDDRNLLNRLNLSLNSEVVLDQDAIDVIIHVARNPHGRDLAWKFFRDKWK  
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAAASFRAVETVEANVRWKM  
LYQDELFWLGKALRH

**Transmembrane domain:**

amino acids 44-63

**N-glycosylation sites.**amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,  
634-638, 649-653, 663-667, 684-688, 800-804, 906-910**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

**Tyrosine kinase phosphorylation site.**

amino acids 520-528

**N-myristoylation sites.**amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,  
825-831, 987-993**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 437-447

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**FIGURE 199**

CGGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCGTCCGCCAGGGGGCTCCGGAAGCTGCCCC  
GGCCCGCGGCTCCTCCCTCGCTCCCGCTTCCCTTTCTCGCTCACCGCCGCCCTCCTTCCCCAGCTCCTCGCC  
GTCCGCGCGCCCCACAGCCAGCGGCTCCGCGCCCCCTGCAGCCACGATGCCCGCGGCCCGGCCCGCGCGG  
ACTCCGCGGGATCTCGCTGTTCTCGCTCTGCTCCTGGGAGCCCCGGCGGCAGCGCTGGAGCGAGATGCTCTTCC  
CGAGGGAGATGCTAGCCCTTTGGGTCTTACCTCCTGCCCTCAGGAGCCCCGGAGAGAGGCAGTCTGGCAAAGA  
GCACCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCTCAGTCCGCGGAAGTGTGGGCGAGCTGGTGTCT  
GGATGGGACCGCACCTCTGCACATCACGACATCCCGAGCCCTGTACCCTGCTTCCAGAGGAGGCCCCGCCCAA  
GCACGCTTGGCCCCAAGAAGAACTGCCTTCGCTCAAGCAGGTGAATCTGCCAGGAAGCAGCTGAGGCCCAA  
GGCCACCTCCGCAGCCACTGTCCAAAGGGCAGGGTCCAGCCAGCGTCCAGGGCCTAGATCTCTCTCTCTC  
CACGGAGAAGCCTGGCCACCGGGGGACCGGACCCCATCGTGGCCTCCGAGGAGGCATCAGAAGTGCCCTTTG  
GCTGGATCGAAAGGAGAGTGGGTCCCTACAACACCCGACCCCTGCAATCTCCCCCTTCACTTCGAGCCCTA  
TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGAGCCTGGGCTGACATGGCCAGGAGGCCCCCCAGGA  
GGACACCAGCCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGA  
GACCACTACCTCCACCATTATCACCACCACGGTCACTACCACCGAGCAAGCACCAGCTCTCTGCAGTGTGAGCTT  
CTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAACAACCTTCTGGAGTGCACATA  
CAACGTGACAGTCTACACTGGCTATGGGTGGAGTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGT  
CTCCATCCGCGGGGTGGACGGCCCTACCCTGACCGTCTGGCCAACCAGACACTCCTGGTGGAGGGGCAGGTAAT  
CCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGGCCTTGGGACCTTCCAGCTTCA  
CTACCAGGCCCTCATGCTGAGCTGCAACTTTCCCCCGCGCCTGACTTGGGGATGTCAGGCTGATGGACCTGCA  
TCCAGGTGGGTGGCCACTTTCAGTCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAA  
TGCTTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGTCTTGTGGAGGGGAGTGCACAATGCCAC  
CATCGGCCCGCTCCTCTCCCCAAGTTACCCTGAAAACACAAATGGGAGCCCAATTCTGCATCTGGACGATTGAAGC  
TCCAGAGGGCCAGAAGCTGCACCTGCACCTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTCACAG  
CGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGGGGCCTGCTGAG  
CGAGGCAACACCATCCGCATCGAGTTACGTCGACCCAGGCCCCGGGCGGCTCCACCTTCAACATCCGATTGGA  
AGCGTTTGAAGAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAA  
CATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCCGCCATCATCGAATGCCAT  
CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGACAGCCATGTGTGGTGGGAGCTCTCTGCTGT  
GGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGT  
GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGA  
TGGCGACGAGGTGATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCCAC  
GCCAGACTTAACCATCCAGTTCATTCCGACCCCTGCTGGCCTCATCTTTGGAAAGGGCCAGGGATTTATCATGAA  
CTACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCA  
CACGGAGTTGGTGGGGGAGCCAGAATCACCTACCAGTGTGACCCCGGCTATGACATCGTGGGGAGTGACACCT  
CACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCCCATTTTGTGAGAAAATTATGTACTGCACCGACCCCGG  
AGAGGTGGATCACTCGACCCGCTTAATTTCCGATCCTGTGCTGCTGGTGGGGACCACTCCAATACACCTGCAA  
CCCCGGTTTTGTGCTTGAAGGAGTTCTTCTGACCTGCTACAGCCGTGAAACAGGGACTCCCATCTGGACGTC  
TCGCTGCCCCACTGCGTTTCGGAGGAGTCCCTGGCATGTGACAAACCCAGGGCTGCCTGAAAATGGATACCAAT  
CCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGA  
AGTGACCATCCGCTGCATCCTGGGACAGCATCCCACTGGAACGGGCCCCCTGCCGTGTGTAAAGTTAATCAAGA  
CAGTTTTGAACATGCTTTAGAAGCAGAAGCGGCAGCAGAGACGTCGCTGGAAGGGGGGAACATGGCCCTGGCTAT  
CTTCATCCCGGTCTCATCATCTCTTACTGCTGGGAGGAGCCTACATTTACATCACAAGATGTCGCTACTATTC  
CAACCTCCGCTGCCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTGGAAACCGAGTTTGACAACCCCAT  
TTACGAGACAGGGGAAACCAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTGAGAAGGGGACTTGTGAA  
CTCAACCACAATCTCCTCGAGACATTCTCAGAGACCATGTGGCACTTGATTGAAACCCCAAGATGTCGACTGT  
CTTTTGTTTAGACTCTTTATCAAAGGTTTACTGTTTTCTTCCCTGTATTTATTATTTAAAGTGAAAAAAA  
AAAAA

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**FIGURE 200**

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE  
ERVVTAPPSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKKLPSLKQVN  
SARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPIVASEEASEVPLWLDRK  
ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPGEPPGDMAQEAPQEDTSPMALMDKGENELTG  
SASEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNPFLECTYNVTYV  
TGYGVELQVKS VNLS DGELLSIRGVDGPTLTVLANQTLLEGGVQVIRSPTNTISVYFRTEQDDG  
LGT FQLHYQAFMLSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGA KMLTCINASKPHW  
SSQEPICSA PCGGAVHNATIGRVLSPSY PENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD  
RMTVHSGQT NKSALLYDSLQTESVPFEGLLSEGN TIRIEFTSDQARA ASTFNIRFEAFEKGHC  
YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGP AII ECINVRDPYWNDEPLCRAMCGG  
ELSAVAGVVLSPNWPEPYVEGEDCIWKI HVGEEKRIFLDIQFLNLSNSDILTIYDGDEVMPHI  
LGQYLGNSGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK  
TTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLSSWSDPPFCEKIMYCTDPGEVDHSTRLI  
SDPVLLVGTTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPLPENG  
YQILYKRLYLPGESLTFMCYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA  
AAETSLEGGNMALAI FIPVLIISLLLGGAYIYITRCRYYSNLRLPLMYSHPY SQITVETEFDN  
PIYETGETREYEVSI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 893-915

**N-glycosylation sites.**amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,  
514-518, 576-580, 618-622, 674-678, 742-746**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

**N-myristoylation sites.**amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,  
629-635, 695-701, 723-729, 766-772, 877-883, 953-959**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

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**FIGURE 201**

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGGAAGTCGGGGTCTCCTTCGCCTTCT  
GTCTTTCTGCGTCTACTAGCAGGTTTGTGCAGGGGAACTCAGTGGAGAGGAAGATATATAT  
CCCCTTAAATAAAACAGCTCCCTGTGTTGCGCTGCTCAACGCCACTCATCAGATTGGCTGCCA  
GTCTTCAATTAGTGGAGACACAGGGGTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG  
GGTATTGACTGATGGCCCCAACCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTACCAG  
GGATTTAATGGAGAAGCTGAAAGGGAGAACCAGCCGAATTGCTGGTCTTGCAGTGTCCTTGAC  
CAAGCCCAGTCCCTGCCTCAGGCTTCTCTCCTAGTGTACAGTGCCCAAATGATGGGTTTGGTGT  
TTACTCCAATTCCCTATGGGCCAGAGTTTGCTCACTGCAGAGAAATACAGTGGAAATTCGCTGGG  
CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCATCTTTCTTCTTGAAGATGAAAATGAAAC  
CAAAGTCATCAAGCAGTGCTATCAAGATCACAACTGAGTCAGAATGGCTCAGCACCAACCTT  
CCCCTATGTGCCATGCAGCTCTTTTACACATGCATGCTGTCATCAGCACTGCCACCTGCAT  
GCGGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCTGTC  
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACAACCTGGGACATTAAAGCCTGACGA  
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTCTTTTCTGGAATGTGGCCCCAGG  
GGCTGAAAGCGCAGTGGCTTCTTTGTACCCAGCTGGCTGCTGCTGAAGCTTTGCAAAGGC  
ACCTGATGTGACCACCCTGCCCCGCAATGTCATGTTGTCTTCTTTCAAGGGGAACTTTTGA  
CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA  
GAATGTTGACTCATTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT  
GCACACAGATCCTGTTTCTCAGAAAATGAGTCTGTACGGAACCAGGTGGAGGATCTCCTGGC  
CACATTGGAGAAGAGTGGTGTGCTGGTGTCCCTGCTGTCATCCTCAGGAGGCCAAATCAGTCCCA  
GCCTCTCCCACCATCTTCCCTGCAGCGATTTCTTCGAGCTCGAAACATCTCTGGCGTTGTTCT  
GGCTGACCACTCTGGTGCCTTCCATAACAAATATTACCAGAGTATTTACGACACTGCTGAGAA  
CATTAAATGTGAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACCTTTGTAACAGACAC  
TGCCAAGGCCCTGGCAGATGTGGCCACGGTGTGGGACGTGCTCTGTATGAGCTTGCAGGAGG  
AACCAACTTCAGCGACACAGTTCAGGCTGATCCCCAAACGGTTACCCGCCTGCTCTATGGGTT  
CCTGATTAAAGCCAACAACCTCATGGTTCAGTCTATCCTCAGGCAGGACCTAAGGTCCCTACTT  
GGGTGACGGGCTTCAACATTACATCGCTGTCTCCAGCCCCACCAACACCACTTATGTTGT  
ACAGTATGCCTTGGCAAATTGACTGGCAGAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA  
TCCAAGTAAAGTCCCAAGTGAAGAAAGAGTATGATGAGTACTCATGGGTCCAGGGCCCTTT  
GCATTCTAATGAGACGGACCGACTCCCCCGGTGTGTGCGTTCTACTGCACGATTAGCCAGGGC  
CTTGTCTCCTGCCTTTGAACTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG  
CCGTGGAAAGATATCCGTGCCCCGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCAC  
CCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCAA  
AGCTGATGTCTTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTGTCATACTGAGGAGGACCCCA  
GCTTTTCTTGCCAGNTCAGCAGTTCAGTTCCTAGAGCATCTGTCCCACTGGGACACAACCACT  
AATTTGTCACTGGAACCTCCCTGGGCCTGTCTCAGATTGGGATTAAACATAAAAGAGTGGAAC  
ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCCTCCCTTCCCTCCGCTCCCTTTCCCATCA  
CCCCTTCCCCATTTCTCTTCTCTCTACTCATGCCAGATTTTGGGATTACAAATAGAAGCT  
TCTTGCTCCTGTTTAACTCCCTAGTTACCCACCCTAATTTGCCCTTCAGGACCCTTCTACTTT  
TTCTTCCCTGCCCTGTACCTCTCTCTGCTCCTACCCCCACCCCTGTACCCAGCCACCTTCT  
GACTGGGAAGGACATAAAAGGTTTAAATGTCAGGGTCAAACCTACATTGAGCCCCTGAGGACAGG  
GGCATCTCTGGGCTGAGCCTACTGTCTCCTTCCCACTGTCTTTCTCCAGGCCCTCAGATGGC  
ACATTAGGGTGGGCGTGTGCGGGTGGGTATCCACCTCCAGCCACAGTGCTCAGTTGTACT  
TTTTATTAAGCTGTAATATCTATTTTGTGTTTTGCTTTTTCTTTTCTTTTGTAAATAT  
ATATATAATGAGTTTCATTAAAATAGATTATCCC

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**FIGURE 202**

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGN SVERKIYIPLNKTAPCVRLLNATHQIGCQ  
SSISGDTGVIHVVEKEEDLQWVLTGDPNPPYMVLLSKHFTRDLMKLGRTSRIAGLAVSLT  
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLEDENET  
KVIKQCYQDHNLSQNGSAPTFFPLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS  
DYNVWSMLKPINTTGTLPDDR VVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA  
PDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM  
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPVILRRPNQSQPLPPSSLQRFLRARNISGVVL  
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLN FVTDTAKALADVATVLGRALYELAGG  
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYV  
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVGPLHSNETDRLPRCVRSTARLARA  
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK  
ADVLFIAPREPGAVSY

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 671-692

**N-glycosylation sites.**

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,  
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,  
573-577, 580-584, 612-616

**Glycosaminoglycan attachment site.**

amino acids 404-408

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 232-236

**N-myristoylation site.**

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,  
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

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**FIGURE 203**

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCTGCCAGGGGAGCCGGGTTTT  
GAGCTCAGGCGCCTCTAGCGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA  
CTGAATAGCAAACCTGAGGCTGAGTAGGGAACAGACCATGAGGTCAGTGCAGATCTTCCTCTCC  
CAATGCCGTTTGTCTCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGCGGAAGATGTA  
ATTTTTCACCCTGAAGGGGAGTTTGAATCGTATGAAGTCACCATTCCCTGAGAAGCTGAGCTTC  
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCGTGTCTACCTACTGCAGTTAAAAGGCAAGAAG  
CACGTCCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCCGACATCTGCGCGTTTTCTCCTTC  
ACAGAACATGGGGAACTGCTGGAGGATCATCCTTACATAACCAAGGACTGCAACTACATGGGC  
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTTAAAGCACATGCATGGGGGGTCTCCGAGGT  
GTATTTAACATTGATGCCAAACATTACCAAATTAGCCCCCTCAAGGCCTCTCCAGTTTGTAA  
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTTGGGAATCAGGTTTGTGGCTTAAGTGATGAT  
GAAATAGAATGGCAGATGGCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCCTGGATCC  
TATAAACACCCAAAGTACTTGGGAATTGATCCTACTCTTTGATCAAAGTAGGTATAGGTTTGTG  
AACAACAATCTTCTCAAGTCATACATGATGCCATTCTTTTGAATGGGATTATGGACACCTAC  
TTTCAAGATGTTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAAACAA  
ATACGCGTTGGATATCCAGAGTTAGCTGAAGTTTTAGGCAGATTTGTAATATATAAAAAAAGT  
GTATTAAATGCTCGCCTGTCATCAGATTGGGCACATTTATATCTTCAAAGAAAATATAATGAT  
GCTCTTGCATGGTTCGTTTGGAAAAGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA  
CTAGATACAAATATCCTTGCCCCCTGCTACCTGGTCTGCTCATGAGCTGGGTCTATGCTGTAGGA  
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA  
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTAAACATATCTCTTCGGGAGCAACA  
TGTCTAAATAATATCCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAACAAAATTGTGGAG  
GACAATGAGGAATGTGACTGTGGTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA  
AATTGTAAGTTGCAACCAGGTGCCAAGTGTAGCATTGGACTTTGCTGTCTATGATTGTGCGGTTT  
CGTCCATCTGGATACGTGTGTAGGCAGGAAGGAAATGAATGTGACCTTGCAAGTATGAA  
GGGAATTCAAGTTCCTGCCCAAATGACGTTTATAAGCAGGATGGAACCCCTTGCAAGTATGAA  
GGCCGTTGTTTCAGGAAGGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT  
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT  
AACTGTGAGATTACAGGAATTCGAAATTTTAAAAAGTGTGAAAGTGCAAATTCATATGTGGC  
AGGCTACAGTGTATAAATGTTGAAACCATCCCTGATTTGCCAGAGCATACGACTATAATTTCT  
ACTCATTTACAGGCAGAAAACTCATGTGCTGGGGCACAGGCTATCATCTATCCATGAAACCC  
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT  
TTTTAAAAAAATTGCGTCAATAGCTCAGTCTGCAGTTTGAATGTTTGCCTGAGAAATGCAAT  
ACCCGGGGTGTGTTGCAACAACAGAAAACTGCCACTGCATGTATGGGTGGGCACCTCCATTC  
TGTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCCTCCAGGACTGCTCAGAGGGGCG  
ATTCCTCGTCAATTTGGGTGTGTCCATCATAATGTTTTCGCTTATTTTATTAATCCTTTCA  
GTGGTTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAAATG  
CCACTATCCAAAGCAAAAACCTGAACAGGAAGAATCTAAACAAAAAAGTACAGGAAGAATCT  
AAAACAAAAAAGTGGACAGGAAGAATCTGAAGCAAAAAGTGGACAGGAAGAATCTAAAGCAAAA  
ACTGGACAGGAAGAATCTAAAGCAAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG  
AAACAAAAAAAGTAAACCGGGCAATCCATACTCATTAGTAACACAGGCTCATTTATTTAACCA  
GCTAATCATTTATCCAAAGGCTTTCATTCTTCTCCCAATATTTTTTTACTTTAATTTTTCCC  
ACAAGTTTTGATCAGCAAATAAACAGCATTCTTGTGTTTGGAAACAAAA



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**FIGURE 204**

MRSVQIFLSQCRLLLLLLVPTMLLKSLGEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS  
YLLQLKGKKHVLHLWPKRLLLPRHLRVFSFTEHGELLEDHPYIPKDCNYMGSVKESLDSKATI  
STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDDEIEWQMAPYENK  
ARLRDFPGSYKHPKYLELILLFDQSRYSRVNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA  
LEVWTD FNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSFGKVCSL  
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGRLNCIMGSGRTGFSNCSYISF  
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDGSTEECQKDRCCQSNCKLQPGANCSI  
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGT PCKYEGRCFRKGCRSRY  
MQCQSIFGPDAMEAPSECYDAVNLI GDQFGNCEITGIRNFKKCESANSICGRLQCIN VETIPD  
LPEHTTIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNVCVNSSVLQ  
FDCLPEKCNTRGVCNNRKNCHCMYGWAPPFCEEVGYGGSIDSGPPGLLRGAIPSSIWVVSIIIM  
FRLILLILSVVFVFRQVIGNHLKPKQEK MPLSKAKTEQEESKTKTVQEESKTKTGQEESEAK  
TGQEESKAKTGQEESKANIESKRPKAKSVKKQKK

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 684-705

**N-glycosylation sites.**

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

**N-myristoylation sites.**amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,  
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,  
758-764, 767-773**Amidation site.**

amino acids 69-73

**Disintegrins proteins**

amino acids 429-479

**EGF-like domain proteins**

amino acids 650-662

**Neutral zinc metallopeptidases, zinc-binding region proteins**

amino acids 335-345

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**FIGURE 205**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG  
TTGTGGAGGGAAACCACCCATCCTCCTGCCCTCCCACCACCACCATCATCCTGGCTGGACGGAG  
AGGGTGACGGGGCTGGGAAGGGGCAGCTCATGTTTCAAGGTTTCCAGGAGGGGCTACCTGTTGA  
CTGTCTTTCAGGAAGAAGAAAACACCTGAGTGACCAGATGTCCCAGCTCCAGGTGCCTTGCC  
AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTCTGCACACCT  
GGAATGACTGGAACCCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA  
ACAGAAGGCTGTGGACCACCTGTGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGAC  
CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTTCGAGAGTCAGTCAACCGATTGGAA  
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAAATTCTGAATTTCAACCGTACT  
ATGAGGCTTGTGCGAAGGCTGCAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG  
TTGGTATCCTGGGGTTTAACTCTGCAGAGTGGTTTATCACTGCTGTTGGTGCCATCCTAGCCG  
GGGGTCTTGTGTTGGTATTTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC  
ATGCCAAAGTGAACATCTTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTTTCGATTC  
CACAGAGCAGCCTAGAGCCCCATAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAACA  
ACAACCTGTACTCTTGGGATGATTTTATGGAACCTGGCAGAAGTATCCCTGACACCCAACTGG  
AGCAGGTCATCGAGAGCCAGAAGGCGAATCAATGCGCAGTGCTCATCTACACTTCAGGGACCA  
CAGGCATACCCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA  
CAAAGGACTTTAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA  
TTGCAGCACAGATGATGGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC  
AAGCAGATGCTCTCAAGGGCACCTTGGTAAGTACTCTAAAGGAGGTAAAACCTACTGTCTTCA  
TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA  
TGGGCTTGAAGAAGAAGGCATTCGTGTGGGCAAGAAACATTGGCTTCAAGGTCAACTCAAAAA  
AGATGTTGGGGAAATATAATACTCCCGTGAGCTACCGCATGGCTAAGACTCTCGTGTTCAGCA  
AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCCCTCA  
ACCAAGAGACTGCCGAGTTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTTGA  
GTGAGAGCTCGGGACCCACACGATATCCAACCAGAATAACTACAGGCTTCTAAGCTGTGGCA  
AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGAGAACAAGGATGGCATTGGGGAGATCT  
GCCTCTGGGGTAGGCACATCTTCATGGGCTATCTGGAAAGTGAGACTGAAACTACAGAGGCCA  
TCGATGATGAAGGCTGGCTACACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCTCT  
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAAATGTGCCCCCATTC  
CTGTTGAGACCTTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA  
AACTGAAGTTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC  
CTCTGGACAAGCTGAACTTCGAGGCCATCAACTTCTGTCGGGGTCTGGGCAGCCAGGCATCCA  
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA  
ATGCTGTGAACCAGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTGCTCTTGGAGA  
AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAACTTAAGAGACATTTTGTAG  
CCCAGAAATACAAAAAACAATTGATCACATGTACCACTGACTGCTTTGATGGAGCTGCTCTC  
AGCTGTTCTGATGCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAAATGCTGCTCTAGGTAG  
AAGCTCTCCCTGCTGTTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTTGATTGTTTCGTC  
TGTTGGAGAGGTGCTCCCTAGAAGAACCCTGCCATACGTTTTCAAAGCAATAAAATCACTGTATA  
TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCTATTGGGAAGTCTACTAAAACTG  
CCTGATTTACAAGAAAGACCTGAACTTGTGGGCTCCCATTGATTTTTTCTCCTCAGGGGAC  
TCAGACATTAGAAAGAAAAAGCCTCACAGATTTGAAGAACTGGACCCCCAAATCAACTCACCT  
GCCTGGAAGCAACTGGGAAACCTTCCAATAAGTCCTGATAATAAAGCACTTCAGGGTCCCAA  
AAAAA

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**FIGURE 206**

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAASLIKLGLERFHGVGILGF  
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQQLQKILSIPQSSE  
PLKAI IQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGTTGIPKG  
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADALK  
GTLVSTLKEVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY  
NTPVSYRMAKTLVFSKVKTSGLDHCHSFISGTAPLNQETAEFFLSLDIPIGELYGLSESSGP  
HTISNQNNYRLLSGCKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW  
LHSGDLGQLDGLGLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAMLVGDKLKFLS  
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQDPLVYKAIQQGINAVNQE  
AMNNAQRIEKWVILEKDFSIYGGELGPMMLKRHFVAQKYKKQIDHMYH

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 65-86

**N-glycosylation site.**

amino acids 196-200

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 282-286

**Tyrosine kinase phosphorylation sites.**

amino acids 547-555, 608-616

**N-myristoylation sites.**amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,  
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

**Putative AMP-binding domain signature.**

amino acids 177-189

**Putative AMP-binding domain proteins.**

amino acids 173-190

**FIGURE 207**

[illegible]

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**FIGURE 208**

MAYRVLGRAGPPQPRRARRLLFAFTLSLSCTYLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG  
QKLLQKSRPCDPSGPTPSEPSAPSAPAAVPAPRLSGSNHSGSPKLGTKRLPQALIVGVKKGG  
TRAVLEFIRVHPDVRLGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR  
RIFNMSRDTKLIVVVRNPVTRAISDYTQTL SKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM  
YVLHLESWLQYFPLAQIHVFSGERLITDPAGEMGRVQDFLGIKRFITDKHFYFNKTKGFCLK  
KTESSLLPRCLGSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 102-106, 193-197, 235-239, 306-310

**Tyrosine kinase phosphorylation site.**

amino acids 296-305

**N-myristoylation sites.**

amino acids 51-57, 100-106, 121-127, 125-131

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 20-31

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**FIGURE 209**

CTTTCCTTATCTGTGTGTACTCTTATCTCACTGTTCTATTTTTTCTCCTCATTTATATTA  
CTTTCCTTACCTTTTTTCTGAACTTCTAGGCCTTCTCTTCCAGAACTGGTGGAAGACAAATG  
AAACGGCCAAGATGGTAAGAAACAAGCCGATTCTCCTTGGGGAGACTGATAATTTAAAAGG  
TTTGTTGTGTCAGAAACATTCCCAGCTTCATCACCAACCCTTTCCTTCCACCTCTGCCCCACTG  
GAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGCATCACATTAG  
CAGGAGCCAACCTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT  
CCAGACAAGCCGGGGCAGCTCATAACTGGTTCATCTGCTCCCTGTGCGTCCCGCGGGTGCGT  
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCC  
ATCTACTTGGGCTTCTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT  
GAGAAGGGGCCACATCGCAGCCGACACCCGAGCCATCCTTCCCTGAGATACCCCTGGAT  
GGTACCCTGGCCCTCCAGAGTCCCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTAC  
ATTACCCTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCGTGAAGCCCAAGCGC  
AGGAAAAAGCATGCAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTTGGTTCGGACCATCCCTT  
CAGCCGCAGGAAGCGGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAAC  
CTGGTTAAGATTGGAGAGCGACCCTGGAGGTTGGTGCGGGGTCCGGGAGTGCGAGCCGGGGGC  
CCAGACTTCCTGCAGCCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCCC  
TCCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGCGGACAGCGCAGTGGCAGGG  
CTCCGGCCTGTGTCTCTAGGAGCGGAGCCCGTTTGCTGGTGCTGGAGGGGGGCGCACCTGGC  
GCTGTGCTCCGCTGTGGCCCTAGCCCCTGTGGGCTTCTCAAGCAGCCCTTGGACATGAGTGAG  
GTGTTTGCTTCCACCTAGACAGGATCCTGGGGCTCAACAGGACCCTGCCGTCTGTGAGCAGG  
AAAGCAGAGTTCATCCAAGATGGCCGCCATGCCCCATCATTCTTTGGGATGCATCTTTATCT  
TCAGCAAGTAATGACACCCATTCTTCTGTTAAGCTCACCTGGGGAACCTTATCAGCAGTTGCTG  
AAACAGAAATGCTGGCAGAATGGCCGAGTACCCAAGCCTGAATCAGGTTGTAAGTAAATACAT  
CATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTGTACAGATTTATAATCGCTTAGAT  
ACAAATTGCTGTGGATTACAGACCTCGCAAGGAAGATGCCTGTGTACAGAAATGGATTGAGGCCA  
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAAGG  
CATTTGGTTTTTTATAGACAACAAGGGTTCTTTGACAGGAGTGAAGATAACTTAACTTCAA  
TTGTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA  
CGGCAAAACTCTCTCAGTCTCTGTTTCTTGATAAAGTGATTGGGAAAGTCAAGGAGGTAGA  
CAAGGAATGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTCTTATCACCTATATC  
AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG  
TTAGATATATTTATGCATTTTTTGGTTTTTGTAAAAATCAAGCACATCAACCTCAAGCCCGTT  
TAGCAATGAGGCAGTGTAGATGAATACGTAAAATAAATGACTTTAACCAAGTAGCTATAAAGG  
GACTTAGCACTGTATGCATACTTAAAAAGGTTTTGAAAAACAACTACTTGAGAAATATTTGT  
TTATATTTTTCTCTAACATCATGCTATGTGTGCTGAGTCTGAACATCTGACAACAGAAATTTAGT  
TATTATTCTAGCTAAGTTTTGAAAACATTTGTGCTGCTGTTAATAGAAAACCTGCAAACCAGA  
GATACTGACTCCATTAATAAACCATATTTTGTGCCGTTTTGACTGTTCTGACCAAATACTAAT  
GGGAACAATTCTTGACGTTTTTCTGTTGCTGATTGTTAACATAGAGCAGTCTCTACACTACCC  
TGAGGCAACTCTACATTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA  
CATTTAAACAGAAATGCTGGTTTTATTTGCAAATCACCAGTATATTTTCTATTGTGTCTATAA  
AAAATCAGTCATTTAAGTACAAGAATCATATTTTCCATTCCTTTTTAGAAATTTATTTTGTG  
TCCCTATGGAATCATTCACATCTGACAATTTATATGTTAAAGAGTTTTACTCTCTCTATTTT  
GGTCCAATTTGTATCTAGTGGCTGAGAAATTAATAAATTCTAAAGTATGAAGTTACCTATCTG  
AAAATGTACTTACAGAGTATCATTTTAAATGGATGTCTCTTTAAAAATTTTGTACTTTTAC  
CAACAATGTAATATAATTTATGTATATTTTATTAATAATAGTGAATTCCTTAAATTTGTCT  
ATGTACTTATATTTAATTTGATTTAATGGTACTGCCAGATATTGAGAAATGGTTCAAATAT  
TGAGTGTGTTTCAATAA

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**FIGURE 210**

MTCPDKPGQLINWFICSLCVPRVRKWLSSRRPRTRRNLLLTACAIYLGFLVSQVGRASLQHG  
QAAEKGPHRSDTAEPSFPEIPLDGTLAPPESQNGSTLQPNVVYITLRSKRSPANIRGTVK  
PKRRKKHAVASAAPGQEALVGPSLQPQEAAREADAVAPGYAQGANLVKIGERPWRLLVRGPGVR  
AGGPDFLQPSSRESNIRIYSESAPSWLSKDDIRRMRLLDASAVAGLRPVSSRSGARLLVLEGG  
APGAVLRGCPSPCGLLKQPLDMSEVF AFHLDRILGLNRTLPSVSRKAEFIQDGRPCPIILWDA  
SLSSASNDTHSSVKLTWGTYYQQLLKQKCWQNGRVKPKPESGCTEIHHEWSKMALEDFLLQIYN  
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAAIAHIIQRKHDPRHLVFIDNKGFFDRSEDNL  
NFKLEGIKEFPASAVSVLKSQHLRQKLLQSLFLDKVYWESQGGROGIEKLIDVIEHRAKILI  
TYINAHGVKVLPMNE

**Transmembrane domain:**

amino acids 40-56

**N-glycosylation sites.**

amino acids 98-102, 289-293, 322-326

**N-myristoylation sites.**amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,  
287-293, 484-490

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**FIGURE 211**

GTGGGGTGGTGAGCGCAGCGCCGAGGATGAGGAGGTGCAACAGCGGCTCCGGGCCGCCGCCGTGCTGCTGCTGC  
TGCTGCTGTGGCTGCTCGCGGTTCCCGGCGCTAACCGGCGCCCGCGGTGCTGGGCTCCCGCAGCGCCTGGGCCGTGGAGTTCTTCG  
TGACGCTGCTGCAGGCGGACACGGTGCGCGGCGCGGTGCTGGGCTCCCGCAGCGCCTGGGCCGTGGAGTTCTTCG  
CCTCCTGGTGCGGCCACTGCATCGCCTTCGCCCGCAGCTGGAAGGCGCTGGCCGAAGACGTCAAAGCCTGGAGGC  
CGGCCCTGTATCTCGCCGCCCTGGACTGTGCTGAGGAGACCAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG  
GCTTCCCGACTGTGAGGTTCTTCAAGGCCTTTACCAAGAACGGCTCGGGAGCAGTATTTCCAGTGGCTGGTGTG  
ACGTGCAGACGCTGCGGGAGAGGCTCATTGACGCCCTGGAGTCCCATCATGACACGTGGCCCCCAGCCTGTCCCC  
CACTGGAGCCTGCCAAGCTGGAGGAGATTGATGGATTCTTTGCGAGAAATAACGAAGAGTACCTGGCTCTGATCT  
TTGAAAAGGGAGGCTCCTACCTGGGTAGAGAGGTGGCTCTGGACCTGTCCCAGCACAAAGGCGTGGCGGTGCGCA  
GGGTGCTGAACACAGAGGCCAATGTGGTGAGAAAGTTTGGTGTACCGACTTCCCCTCTTGCTACCTGCTGTTCC  
GGAATGGCTCTGTCTCCCGAGTCCCCGTGCTCATGGAATCCAGTCTTCTATACCGCTTACCTGCAGAGACTCT  
CTGGGCTCACCAGGGAGGCTGCCAGACCAGTTGCACCAACCACTGCTAACAAGATAGCTCCCACTGTTTGGGA  
AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCATACATCCTGCGGATAGAAGTGG  
GCAGGTTCCCGGTCTTGAAGGGCAGCGCCTGGTGGCCCTGAAAAAGTTTGTGGCAGTGTGGCCAGTATTTCC  
CTGGCCGCCCTTAGTCCAGAATCTCCTGCACTCCGTGAATGAATGGCTCAAGAGGCAGAAGAGAAATAAAATTC  
CCTACAGTTTCTTTAAACTGCCCTGGACGACAGGAAAGAGGGTGCCGTTCTTGCCAAGAAGGTGAAGTGGATTG  
GCTGCCAGGGGAGTGAGCCGATTTCCGGGGCTTCCCTGCTCCCTGTGGGTCTCTTCCACTTCTTGAAGTGTGC  
AGGCAGCTCGGCAAAATGTAGACCACTCACAGGAAGCAGCCAGGCCAAGGAGGTCTCCAGCCATCCGAGGCT  
ACGTGCACTACTTCTTCGCTGCGGAGACTGCGCTAGCCACTTCGAGCAGATGGCTGCTGCCTCCATGCACCGGG  
TGGGGAGTCCCAACGCCGTGTCTCTGGCTGTGGTCTAGCCACAACAGGGTCAATGCTCGCCTGCAGGTGCC  
CCAGCGAGGACCCCAAGTCCCAAGGTGCAAGTGGCCACCCGTGAAGTTTGTCTGCCTGCCACAATGAACGCC  
TGGATGTGCCCGTGTGGGAGCTGGAAGCCACCTCAACTTCTCAAGGCCACTTCTCCCAAGCAACATCATCC  
TGGACTTCCCTGCAGCTGGGTGAGTGCAGGAGGATGTGCAGAATGTGGCAGCCGCCCCAGAGCTGGCAGTGG  
GAGCCCTGGAGCTGGAAGCCGGAATTCACCTCTGGACCTGGGAAGCCTGAGATGATGAAGTCCCCACAACA  
CCACCCACATGTGCCGGCTGAGGGACCTGAGGCAAGTCGACCCCGAAGCTGCACCTGGCCTCAGAGCTGCAC  
CAGGCCAGGAGCCTCTGAGCACATGGCAGAGCTTACAGGAATGAGCAGGAGCAGCCGCTTGGGCAGTGGCACT  
TGAGCAAGCGAGACACAGGGGCTGCATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCTCTGGGGCCCTTTGG  
AGGTACAGGCGCTGGGCCGAGCTCCAAGCAGCTGGTGCACATCCCTGAGGGCCAGCTGGAGGCCGAGCTGGAC  
GGGGCCGAGGCCAGTGGCTGCAGGTGCTGGGAGGGGGCTTCTTACCTGGACATCAGCCTCTGTGTGGGGCTCT  
ATTCCCTGTCTTTCATGGGCCTGCTGGCCATGTACACCTACTTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG  
CTGGCCACCCTGCAGCTGTAACCACTGGGGAGGAGGCGGAGAGGGAGCTGCCATCTCTAGGCACCTCAAGCCC  
CCTGACCCCATTCCTCCCTCCACCCCTTGCTCCTTGTCTGGCCTAGAAGTGTGGGAAATTCAGGAAAACGAG  
TTGCTCCAGTGAAGCTTCTTGGGGTTGCTAGGACAGAGAGCTCCTTTGACACAAAAGACAGGAGCAGGGTCCAGG  
TTCCCTGTGTGAGGGAGGGCAGCCCGGGCAGTGGGCATAGGGCAGCTCAGTCCCTGGCCTTTAGCACCAC  
ATTCTGTGTTTTTCAAGCTTATTTGAAGTCTGCCTCATTTCTACTGGAGCCTCAGTCTCTCCTGCTTGGTCTTGGC  
CCTCAACTGGGGCAAGTGAAGCCAGAGGAGGTTCCCCAGCTGGGTGGGCTGGAATGGAATCCTCACTAGCTGC  
TGGGGCTCCGCCCACCTGCTCCCTTCCGGACAATGAAGAAGCCTTTGCACCTGGGAGGAAGGACACCCCGGG  
CCCTCTATGCCTGGCCAGCCTCCAGTCTCTCAGACCTCTGGGTGGGGTTTGGCTTCAGGGTGGGGTTTGAAGC  
TTCTGGAAGTCGTGCTGGTCTCCAGGTGAGGCAAGCATGGTTGCTGGGCTGTAGGGTGAAGTGGCTTGGTGGT  
GGGACCTGACGAGTTGGTGGCATGGGAAGGATGTGGGTCTTAGTGCCTTGGCCTGGCTTAGCTGCAGGAGAAGA  
TGGTGTCTTTCACTTCCCCCATTGAGCTCTGCTCCCTTGAGCCTGGTCTTTTGTCTTTTATTTTGGTCTC  
CAAGATGAATGCTCATCTTTGGAGGGTGCCAGGTAGAAGCTAGGGAGGGGAGTGTCTTCTCTCTCCAGGTTTCC  
CTCCAGTGTGCAGAAGTTAGAAGGGTCTGGCGGGGGCAGTGCCTTACACATGCTTGATTCCCAGCTACCCCT  
GCCTTGGGAGGTGTGGAATAAATTATTTTGTAAAGCA



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**FIGURE 212**

MRRCSGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV  
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKA  
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA  
LIFEKGGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFPSCYLLFRNGSVSRVPVL  
MESRSFYTAYLQRLSGLTREAAQTTVAPTTANKIAPTVMKLADRSKIYMADLESALHYILRIE  
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR  
KEGAVLAKKVNWIGCQGSEPHFRGFPCSLWVLFHFLTQVQAAQNVVDHSQEAAKAKEVLPAIRG  
YVHYFFGCRDCASHFEQMAAASMRVGS PNAAVLWLWSSHNRVNARLAGAPSEDPOFPKVQWP  
PRELCSACHNERLDVPVWDVEATLNFLKAHFSPSNIILDFFAAGSAARQVQNVAAAPELAMG  
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAEGPEASRPKLHPGLRAAPGQEPPEHMAELQR  
NEQEQLGQWHLKSRDTGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG  
RGQWLQVLGGGFSYLDISLCVGLYSLFSFMGLLAMTYTFQAKIRALKGHAGHPAA

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 705-728

**N-glycosylation sites.**

amino acids 130-134, 243-247, 575-579

**Glycosaminoglycan attachment site.**

amino acids 6-10

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 644-648

**N-myristoylation sites.**amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,  
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

**Thioredoxin family proteins**

amino acids 62-78

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**FIGURE 213**

GCACGAGGCCGACTTCCAGACCATCTACAACTGCACGGCCTGGAACAGCTTCGGCTCCGACAC  
TGAGATCATCCGGCTCAAGGAGCAAGGTTCCGAAATGAAGTCGGGAGCCGGCTGGAAGCAGA  
GTCTGTGCCGATGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCTT  
TATGGCAACCATCGTGGCGTTCTGCTGTGCCGTTCCCAGAGAAATCTCAAAGGTGTTGTGTC  
AGCCAAAAATGATATCCGAGTGGAATTGTCCACAAGGAACCAGCCTCTGGTCGGGAGGGTGA  
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGTGAATTCAGCAAGACTCAGTCTT  
GAAACAGCTGGAGGTCCTCAAAGAAGAGGAGAAAGAGTTTCAGAACCTGAAGGACCCACCAA  
TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCACTCAACCCCGACCATCTCCCTCTCCAG  
CTGCCAGCCCGACCTGCGTCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCCTTCACCAA  
CATCTACAGCACCTGAGCGGCCAGGGCCGCCTCTACGACTACGGGCAGCGGTTTGTGCTGGG  
CATGGGCAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCAGAGAGGCTCCCTCAGCGACAG  
CAGCTCCTTCCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA  
TGTGCAGTTCGACAAGGCCAGCAAGGCTTCTGCTTCCTCCTCCCACCACTCCCAGTCCTCGTC  
CCAGAACTCTGACCCCACTCGACCCCTGCAGCGGCGGATGCAGACTCACGTCTTAAGGATCACA  
CACCGCGGGTGGGGACGGGCCAGGGAAGAGGTCAGGGCACGTTCTGGTTGTCCAGGGACGAGG  
GGTACTTTGCAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCCAGCGCCTCTGCCAC  
TGCCTTCCTTCGAAGCTCTGATCAAGCACAAATCTGGGTCCCCAGGTGCTGTGTGCCAGAGGT  
GGGCGGGTGGGGAGACAGACAGAGGCTGCGGCTGAGTGCCTGTGCTTAGTGCTGGACACCCG  
TGTCCCCGGCCCTTTCCTGGAGGCCCTCTACCACCTGCTCTGCCCACAGGCACAAGTGGCAG  
CTATAACTCTGCTTTCATGAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC  
ACTGACCACAAGCTCTACCTACCCCTGTGCCTGTGCTCCCATAACAGCCCTGGGGAGAAGGGGA  
TGACGTCTTCCCAGCACTGAGCTGCCCCAGAAACCCCGGCTCCCCACTGCTGCTCATAGCCCA  
TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTACCAGGCTG  
GCCGGGAGCCCACCCCAATTTGTTTGGTGTGTTTGTGTCCATACTCTTGAGTTCTGTCTTG  
GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGGA  
GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCCGGGTGTGCCCCCTCCTGGGCTGTG  
TGACCCCAAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCCTCCCCTCCCCCTCAGCACAAATC  
GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTTCTCTGAACACTTATGGAGAGA  
GTGCTTCCTGGGAAGTGTGGCGTTTGAAGGGGCTGGAGGGCAGGTCTTTAAGATGGCGAGACT  
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTTCAGTAAGGCTCCACGAGAAGA  
GAGGAAGTATATCTACACCTCAACCCTCCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

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## **FIGURE 214**

MAVIIGVAVGAGVAFLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS  
TIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP  
DLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF  
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 150-154

**N-myristoylation sites.**

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 114-125

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**FIGURE 215**

CAGCCTTCCTCCCCAGCCTGAGTGACTACTCTATTCCCTTGGTCCCTGCTATTGTCGGGGACG  
ATTGCATGGGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG  
CCTGCTATTGCATTTATAGACTGACTAGGGGAAGAAAACAGAACAAGGAAAAAATGGCTGAGG  
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG  
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGCTCGGATTG  
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCGGG  
CTGTCCAGAAACGGGCTTCCCCCAATTCAGATGATACCGTTTTGTCCCTCAAGAGCTACAAA  
AGGTTCTTTGCTTGGTTGAGATGTCTGAAAAGCCTTATATTCTTGAAGCAGCTTTAATTGCTC  
TGGGTAACAATGCTGCTTATGCATTTAACAGAGATATTATTCGTGATCTGGGTGGTCTCCCAA  
TTGTGCGAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCTCGA  
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG  
ATGACACAATCACTTCTCGCTTGAACATCTGTGCAGCTTGCTGGACTGAGATTGCTTACAA  
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTTCGTT  
TATTTTCAGCGGGAAATGAAGAAACCAAACCTTCAGGTTCTGAAACTCCTTTTGAATTTGGCTG  
AAAATCCAGCCATGACTAGGGAACTGCTCAGGGCCCAAGTACCATCTTCACTGGGCTCCCTCT  
TTAATAAGAAGGAGAACAAAGAAGTTATTCTTAACTTCTGGTCATATTTGAGAACATAAATG  
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTCGGTGAAGGTTCACTTTTTT  
TCTTTTTTAAAAGAATTTCAAGTGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT  
TTTTGGTGAAAGTAAAAGTTGGAAAATTCATGGCCAACTTGCTGAACATATGTTCCCAAAGA  
GCCAGGAATAACACCTTGATTTTGTAAATTTAGAAGCAACACACATTGTAACTATTCATTTTC  
TCCACCTTGTTTATATGGTAAAGGAATCCTTTCAGCTGCCAGTTTTGAATAATGAATATCATA  
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTTAAGATGGATAAATGAATA  
TCACTACTTGTTCTGAAAACATGTTTGTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT  
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT  
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

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**FIGURE 216**

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKEMAEGGSGDVDDAGDCSGARYNDWSDD  
DDDSNESKSIWVYPPWARIGTEAGTRARARARARATRRARRAVQKRASPNSDDTVLSPQELQKV  
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVLNN  
LSVNAENQRRLLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLF  
SAGNEETKLQVLKLLNLAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN  
FKWEENEPTQNQFGEGLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 68-72, 189-193, 217-221, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-111

**N-myristoylation sites.**amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,  
290-296**Amidation site.**

amino acids 29-33

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FIGURE 217

[illegible]

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**FIGURE 218**

MAIAQLATEYVFSDFLLEKEPTEPKFKGLRLELAVDKMVTCTIAVGLPLLLISLAFQEISIGTQ  
ISCFSPSSFSWRQAAFVDSYCWAAVQQKNSLQSESGNLPWLHKFFPYILLFFAILLYLPPLF  
WRFAAAPHICSDLKFIMEELDKVYNRAIKAAKSARDLDMRDGACSVPGVTENLGQSLWEVSES  
HFKYPIVEQYLKTKKNSNNLI IKYISCRLLTLIIILLACIYLGYYFSLSSLSDEFVCSIKSGI  
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVYVLLAPVVVYTLFVFPFRQKTDVLKVYEILPTF  
DVLHFKSEGYNDLSLYNLFLEENISEVKS YKCLKVLENIKSSGQGIDPMLLLTNLGMIMDVV  
DGKTPMSAEMREEQGNQTAELQGMNIDSETKANNGEKNARQRLDSSC

**Transmembrane domains:**

amino acids 37-55, 108-126, 216-232, 273-290

**N-glycosylation sites.**

amino acids 255-259, 338-342, 394-398

**Glycosaminoglycan attachment site.**

amino acids 357-361

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 61-67, 174-180, 251-257, 393-399

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 218-229

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**FIGURE 219**

CTGTGAGTGACACACGCTGAGTGGGGTGAAGGGAAATGCTGGTGAATTTTCATTTTGAGGTGTG  
GGTTGCTGTTAGTCACTCTGTCTCTTGCCATTGCCAAGCACAAGCAATCTTCCTTCACCAAAA  
GTTGTTACCCAAGGGGAACATTGTCCCAAGCTGTTGACGCTCTCTATATCAAAGCAGCATGGC  
TCAAAGCAACGATTCCAGAAGACCGCATAAAAAATATACGATTATTAAAAAAGAAAACAAAAA  
AGCAGTTTATGAAAACTGTCAATTTCAAGAACAGCTTCTGTCCTTCTTCATGGAAGACGTTT  
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTTGTGGAGGACTTTCATAGCCTTA  
GGCAGAAATTGAGCCACTGTATTTCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA  
GGATGAAAAGAATATTTTATAGGATTGGAAACAAAGGAATCTACAAAGCCATCAGTGAAGTGG  
ATATTCTTCTTTCCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAAGCCAAGTACA  
TTGATTTTACAGTTATTTTGAAATACAATAAGAACTGCTAGAAATATGTTTATAACAGTCTAT  
TTCTTTTAAAACTTTTTAACATAATACTGACGGCATGTTAGGTGATTCAGAATAGACAAGAA  
GGATTTAGTAAATTAACGTTTTGGATATAAGTTGTCACATAATTTGCACATTTTCTGTGTTTTT  
AAATAATGTTTCCATTCTGAACATGTTTTGTCATTACACAAGTACATTGTGTCAACTTAATTTA  
AAGTATGTAACCTGAATTAACGTTGTAATATTTGTGTGTGGAGTGGGATGTGGGGGGTGGAG  
GGGAATGACAGATTTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATGTAT  
ATGATTGTCTGTTTAAAGTGTGTTGAAAATTGTTAATTATGCCCAGTGTGAACTTAGTACTTAAC  
ACATTTTGATTTTAAATTAATAAATTGGGTTTCCTTCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAA



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**FIGURE 220**

MLVNFILRCGLLLVTLSLAIAKHKQSSFTKSCYPRGTLSQAVDALYIKAAWLKATIPEDRIKN  
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSRLRQKLSHCISCAS  
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLLESSQ

**Signal sequence:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 148-153

**Interleukin-10 proteins.**

amino acids 58-94, 74-102, 128-170

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**FIGURE 221**

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCGGCCGGCGGGTGCCGCTCC  
TGCTGCTGCTGTGTTTTGGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCCCAGGA  
TGCTGAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA  
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCTGACGG  
CTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCTGCTGGGGGCAAGGC  
AGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGCAGGTGGAGAGCAACCCCC  
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCT  
TCACCAATTACATCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGA  
ACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGAAGACCTCCTGCCCCGAACCGCGGATCC  
TGCAGAAACTCGCTGTGCCCATCATCGACACACCCAAGTGCAACCTGCTCTACAGCAAAGACA  
CCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGG  
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGGGCCCCCTGGTGTGCCTCGTGGGTCAATCGT  
GGCTGCAGGCGGGGGTGATCAGCTGGGGTGAGGGCTGTGCCCCGCCAGAACCGCCAGGTGTCT  
ACATCCGTGTCACCGCCCACCACAACCTGGATCCATCGGATCATCCCCAACTGCAGTTCCAGC  
CAGCGAGGTGGGGCGGCCAGAAGTGAGACCCCCGGGGCCAGGAGCCCCCTTGAGCAGAGCTCTG  
CAGCCAGCCTGCCCCGCCACACCATCCTGCTGGTCTCCAGCGCTGCTGTTGCACCTGTGAG  
CCCCACCAGACTCATTTGTAAATAGCGCTCCTTCCTCCCCTCTCAAATACCCTTATTTTATTT  
ATGTTTCTCCCAATAAAAACCCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 222**

MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGS  
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA  
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP  
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEG  
CARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGGQK

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 55-58, 79-82

**Casein kinase II phosphorylation sites.**

amino acids 121-124, 165-168, 167-170, 248-251

**Tyrosine kinase phosphorylation sites.**

amino acids 78-86, 197-203

**N-myristoylation sites.**

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

**Amidation site.**

amino acids 219-222

**Serine proteases, trypsin family, histidine active site.**

amino acids 71-76

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**FIGURE 223**

CAAGATGTGGACAGCTCTTGTGCTCATTTGGATTTTCTCCTTGTCTTATCTGAAAGCCATGC  
GGCATCCAACGATCCACGCAACTTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAAGAGGAA  
TGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCC  
TGTCACATTGACCAAAGGGACTTCGGCAGCCACCTCAACTCTATGGAAGTCACAACAGAGGA  
CACAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC  
CATTGCTCCACGGCTGTGGCCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG  
TATGACTGTGGCCTCCAGTGCTCCACGACTGCAGCCTCCAGTACAACGTGTGGCCTCCATTGC  
TCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCACTCCC  
CGCGCCACGTCCACTTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCT  
CAGCACAGCCCTCGCACAAAGTGCCAAAGAGCAGCGGTTGCCAAGAACAGCAACCCTGGCCAC  
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAACACAAGCAGCCCCATGAGCACTCG  
TCCAAGTCCTTCCAAGCACATGCCAGTGACACCGCGGCAAGCCCTGTACCCCTATGCGTCC  
CCAAGCACAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACAAATAA  
ATCCACACCCATGCCCTCAAACACAACCCAGAGCCCCGCCCCACCCCCACAGTGGTGACCAC  
CACCAAGGCACAAGCCAGGGAGCCAACTGCCAGCCCAGTGCCAGTACCTCACACCAGCCCAAT  
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC  
CGCTGGGCCAGGCACATCCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA  
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCA  
GCCCAGCACCCAAGGCCAGTACATGGTGGTCACCACTGAGCCCCTCACCCAGGCCGTGGTAGA  
CAAACTCTCCTTCTGGTGGTGCTGTTACTCGGGGTGACCCTTTTCATCACAGTCTTGGTTTT  
GTTTGCCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCAGGTGGACTACTTAAT  
CAACGGGATGTATGCGGACTCAGAAATGTGAGGGGGGCGGGGGCCTGGCGGGAGGCCTGGCCC  
CTTCCTCGTCCTTTCTTTTGCCTTTGAGACCAAACCAAGTGCTTCCAAATTCTTTGGTGCA  
ATTGAGGAGATATGCCAGATGCTTAAACACATTTAATTGCTGTCAGATTAATTCCATGATCAC  
TAAAGAGTTGCTGCTTTTTTCATATTTATTTTGTAAATGATTCTGTGCCAGGAGCAGCTGG  
GGTTCCACCTCAGGGTGGGGCGGGCAGGACCCCGTCTCCCCAGGTGTCGGAGCCTGACCTGA  
ATTAAAGTACTGACTGCTCGCCA

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**FIGURE 224**

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWGLVKRNASVETVDNKTSEDVTMAAASPV  
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM  
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSLS  
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQ  
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAREPTASPVVPHTSPIP  
EMEAMSPTTQPSMPYTTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP  
STQGQYMVVTTEPLTQAVVDKTL LLVLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLIN  
GMYADSEM

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 396-420

**N-glycosylation sites.**

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

**Casein kinase II phosphorylation sites.**

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

**N-myristoylation sites.**

amino acids 68-73, 354-359

**Aldo/keto reductase family putative active site signature.**

amino acids 195-210

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**FIGURE 225**

GGAAGGCGCTCAAGGTGCGCGGCCCGGGGCGCGCTACTGGGGGCGCCCTCCGCGGTGGGCAGC  
GCGCCAGGGATCGGCCTGGGCAGCCGCGGGGCGCGCGAAGGCTGCGCTTTCCTACGGCCCCC  
CTCGCTTCCTCCGGCACGGCGGCAACGGAGATTTCTCTCGGGGAACTACGCGGATCCTTTT  
CGGGGATCCTCGCCCCGCCCCAGTTCTCCGCCCCCTCCCTTTGCTGGGGCGCCTGGGCTGGC  
CCGCGCAGGGGAGGAGGCTCTGGCAGCCTGGGCAGGGAGGCGGCGGGGGCCGCGGAGCCGCT  
GGCCATCGATTCTCCCCGCCATGTGACGCCGTCTTAGCCCTGCGACCCCAGCGCGTCCCGG  
GCCTGCGCCTCCGCCCCGCGCGCAGCGCACGATGCTTCTGCCGGGACGCGCACGCCAACC GC  
CGACGCCCCAGCCCGTGCAGCATCCCGGCCTCCGCGGCAGGTAGAGCCGCCGGGGCAGCTCC  
TGCGCCTCTTCTACTGCACTGTCTGGTCTGCTCCAAAGAGATCTCAGCGCTCACCGACTTCT  
CTGGTTACCTAACCAACTCCTGCAAAACCACACCACCTATGCCTGTGATGGGGACTATTTGA  
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGGCATTTTATGGGCAAGATTACC  
AAATGTGTAGTTCCCAAGCCTGCCTCCAGAGGGAAGACAGCTTAACCTGTGTGGCAGCCA  
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACCAGCGGGCCTGCCACCTCCTGGTCAATA  
GCCGTGTTTTTGGACCTGACCTTTGTCCAGGAAGCAGTAATAACCTCCTGGTCTCCTTTAAAT  
GCCAACCTAATGAATTAAAAACAAAACCGTGTGTGAAGACCAGGAGCTGAAACTGCACTGCC  
ATGAATCCAAGTTCTCAACATCTACTCTGCGACCTACGGCAGGAGGACCCAGGAAAGGGACA  
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCTTTTCGATTGCTTGTCTTACTCAGCTTTGCAAG  
TCCTATCCCGAAGGTGCTATGGGAAGCAGAGATGCAAAATCATCGTCAACAATCACCATTTTG  
GAAGCCCCTGTTTGCCAGGCGTGAAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGA  
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAAACCTTCTTTGAAGCAGAAAGATG  
GTGAATATGGTATAAACTTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATTCTTG  
TTAGCAACTCTCTGGCAGCCTTTGCTTACATTAGAGCCCACCCAGAGAGAGCTGCCCTGCTGT  
TCGTGTCCAGTGTCTGCATCGGCCTGGCCCTCACACTGTGCGCCCTGGTCATCAGAGAGTCCCT  
GTGCCAAGGACTTCCGCGACTTGCAGCTGGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG  
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTCTGAGTCTGATTTCCAGGGG  
AACTGTGCGGGTCTGTAGGACTTCATATCCTATATACAGTTCCATAGAAGCTGCAGAGCTCG  
CAGAAAGGATTGAGCGCAGGGAGCAAATCATTGAGGAAATATGGATGAACAGTGGTTTGGACA  
CCTCGCTCCCAAGAAACATGGGCCAGTTCTACTGAAACCACATGCATCTTGATGCGATCGCA  
CTTTCTGAAGAAGGAAGGATCCCAAATGCCCCCTCCAGTTCTGGTTCACCTGTACCTTCTATGA  
AGGAGAATTGTCATGTCACTCAACTCGTGAGGCCAGGAAGCTATTAAAGGGATGTTTCAA  
GCTGTTTCTAGCACATTCCAAATAAATGAGGAGGGAGGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 226**

MLLPGRARQPPTPQPVQHPLRRQVEPPGQLLRLFYCTVLVCSKEISALTDGSGYLTKLLQNH  
TTYACDGDYLNLCQPRHSTISVQSAFYGQDYQMCSSQKPAHQREDSLTCVAATTFQKVLDECQ  
NQRACHLLVNSRVFGPDLCPGSSKYLVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA  
TYGRRTQERDICSSKAERLPPFDCLSYSALQVLSRRCYGKQRCIIIVNNHHFGSPCLPGVKKY  
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPGSKVLRKDGILVSNSLAFAFYI  
RAHPERAALLFVSSVCIGLALTLCALVIRESCAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE  
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIIWMNSGLDTS�PRNMGQFY

**Transmembrane domains:**

amino acids 32-49, 322-343

**N-glycosylation sites.**

amino acids 62-66, 165-169

**Tyrosine kinase phosphorylation site.**

amino acids 280-287

**N-myristoylation site.**

amino acids 302-308, 333-339, 428-434

**Amidation site.**

amino acids 191-195

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**FIGURE 227**

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCCAGAATTTCTCATCA  
GGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGCTGGCCC  
TGGAACCACACTTTGAGAACCACTGCTTTAGACCAAACACCAAAGGAAGATGCAGCCACCCTC  
CTTTACATGTCACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG  
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGAAGCGTGTCAACCATGG  
TCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTGCAGTTCTTGTTCTTCCCT  
GGAGGACTCTTGATCGCCTGTGATCTTGGCCAGGAGACCAGGTGCCTGGGTCCCTTCCTGGA  
AGGGGACAAGTTACACACCCCGAGCCCCATTTTCCCACCAACTTCTACATGCCTTGGGAGAACC  
TTCTACATGTTGGCTGCCCCCTTCCCCTATTTTCCAGCAGTGCCCAGTCCTGCTTATAAACCTGA  
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCCAATGTTGT  
TGAGGCCAGATGGATTCCCTGGAAGCAGCTGGCCCATGGATGTGAATCATCACAGTATTCTAGA  
AACAGAGAAGAGGTCTTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCCCT  
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAA  
AGGAATTGTATCTAGGACTAA



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**FIGURE 228**

MVSSWPARKASLLCVC AVL VLPWRTL GSPVILARRPGAWVPSWKGTSYTPQPHFPTNFYMPWE  
NLLHVGCP LPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLEAAGPWM

**Signal peptide:**

amino acids 1-27

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 8-12

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**FIGURE 229**

GGGAAGGGATGCAAGGAAGCCCTCCGGCGCTGCGCTCCGAGGCGGGAGACAGCGTCCCGCTGA  
AAATGTGTGTCTGACATGCAAGCTCAGTGGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT  
CCGGACCTGGATCATGAAGGTGTTGGGAAGAAGCTTCTTCTGGGTGCTGTTTCCCGTCCCTTCC  
CTGGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACGCACCGCGG  
GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGGTCCGGGACAGCTGCAGGAAGCTCTCAGG  
GCTTCTCCGCCAGAAGAATGCAGTTCTGAACAACTGAAAACCTGCAATTGGAGCAGTGGAGAA  
AGACGTGGGCCTGTCGGATGAAGAGAACTGTTTCAGGTGCACACGTTTGAAATTTCCAGAA  
AGAGCTGAATGAAAGTGAAATTCGGTTTTCCAACTGTCTACGGACTGCAGAGAGCCCTGCA  
GGGGGATTACAAAGATGTCGTGAACATGAAGGAGAGCAGCCGGCAGCGCTGGAGGCCCTGAG  
AGAGGCTGCAATAAAGGAAGAAACAGAATATATGGAACCTTCTGGCAGCAGAAAAACATCAAGT  
TGAAGCCCTTAAAAATATGCAACATCAAACCAAAGTTTATCCATGCTTGACGAGATTCTTGA  
AGATGTAAGAAAGGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTTGACGACAA  
TAAATCAGTCAAGGGGGTCAATTTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC  
TAAGCAAAATATAACAAAACGAGAAGTGGAGGATGACTTGGGTCTTAGCATGCTGATTGACTC  
CCAGAACAACAGTATATTTTGACCAAGCCCAGAGATTCACCATCCACGTGCAGATCACCA  
CTTTATAAAGGACATTGTTACCATAGGAATGCTGTCCTTGCCTTGTGGCTGGCTATGTACAGC  
CATAGGATTGCCCTACAATGTTTGGTTATATTATTTGTGGTGTACTTCTGGGACCTTCAGGACT  
AAATAGTATTAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTTGGGGTGTTTTTTACTCT  
TTTTCTTGTGGCTTAGAATTTTCTCCAGAAAAGCTAAGAAAGGTGTGGAAGATTTCTTTACA  
AGGGCCGTGTTACATGACACTGTTAATGATTGCAATTTGGCTTGCTGTGGGGGCATCTCTTGCG  
GATCAAACCCACGCAGAGCGTCTTCATTTCCACGTGTCTGTCCTTGTCAAGCACACCCCTCGT  
GTCCAGGTTCCCTCATGGGCAGTGTCTCGGGGTGACAAAGAAGGCGACATTGACTACAGCACCGT  
GCTCCTCGGCATGCTGGTGACGCAGGACGTGCAGCTCGGGCTCTTCATGGCCGTATGCCGAC  
TCTCATACAGGCGGGCGCCAGTGCATCTTCTAGCATTGTCTGTGGAAGTTCTCCGAATCTCTGGT  
TTTGATTGGTCAGATTCTTTTTTCACTAGCGGCGTTTTTCTTTTATGTCTTGTTATAAAGAA  
GTATCTCATTTGACCCTATTATCGGAAGCTGCACATGGAAAGCAAGGGGAACAAAGAAATCCT  
GATCTTGGGAATATCTGCCTTTATCTTCTTAATGTTAACGGTCACGGAGCTGCTGGACGTCTC  
CATGGAGCTGGGCTGTTTCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCAACGA  
GGAGATCGCCACCTCCATCGAACCCTCCGCGACTTCCTGGCCATCGTTTTCTTCGCCTCCAT  
AGGGCTCCACGTGTTCCCCACGTTTGTGGCGTACGAGCTCACGGTGTGGTGTTCCTCACCTT  
GTCAGTGGTGGTGATGAAGTTTCTCCTGGCGGCGCTGGTCTGTCTCTCATTCTGCCGAGGAG  
CAGCCAGTACATCAAGTGGATCGTCTCTGCGGGGCTTGCCAGGTCAGCGAGTTTTCCTTTGT  
CCTGGGGAGCCGGGCGGAAGAGCGGGCGTCTCTCTCGGGAGGTGTACCTCCTTATACTGAG  
TGTGACCACGCTCAGCCTCTTGCTCGCCCCGGTGTGTGGAGAGCTGCAATCACGAGGTGTGT  
GCCCAGACCGGAGAGACGGTCCAGCCTCTGATGGCTCGGAGATGATGGACCGTGGAAGGGAAG  
CGTCTGTGGGGAGTGAGCGCTTAGATGGCCAGCAGCTGCTCCTTCTGGGAAGCTCGCACCTTG  
GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCCGGCTTTTACAGAATA  
TTCTTGTCCTATTTTAGAATTTTCCGGAGTAGTTTATTTGCAGTCTGTTGATTATGTGCAGTA  
GACCCGGGACACTGCGTTTTACCGATCACCTTGAATGTGGTGCCTGGATGTGCCTTTTTTTTT  
TTTCCCTGAAATTATTATTAATTTTCTATTGTGAGTTCATCAGTTCATAGTTTTTTTTTAGTAA  
GAAGCAAAATTAAAGGCTTTTAAAAATGTACAACTTCAGAATTATAATCTGTTAGTCAATA  
TTTGTATTATAAACATTTCTGTAATATGAAGTTGTAATCCTGGCCGTGAGCTTGGAAGCTTACT  
TTTGATTCTTAAAGCCTATGTTTTCTAAAATGAGACAAATACGGATGTCTATTTGCCTTTTAT  
TGTAACTTTTAAATGAAATAATTTTCATGTCAATTTCTATTAGATATATCACTTAAATATTTG  
GTTTTAAATCACAGAATATGTATTCTTTAATAAGATAATTTATGATCATGGTAAAAAAAAA

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**FIGURE 230**

MKVLGRSFFWVLPVLPWAVQAVEHEEVAQRVIKLRGRGVAAMQSRQWVRDSCRKLSGLLRQ  
KNAVLNKLKTAIGAVEKDVGLSDEEKLFQVHTFEIFQKELNESENSVFQAVYGLQRALQG DYK  
DVVNMKESSRQRLEALREAAIKEET EYMELLAAEKHQVEALKNMQHQNQSLSMLDEILEDVRK  
AADRLEEEIEEHAFDDNKS VKGVNFEAVLRVEEEEANSKQNITKREVEDDLGLSMLIDSQNNQ  
YILTKPRDSTIPRADHHFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLNSIK  
SIVQVETLGEFGVFFTLFLVGLFESPEKLRKVKISLQGPCYMTLLMIAFGLLWGHLRLRIKPT  
QSVFISTCLSLSSTPLVSRFLMGSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQA  
GASASSSIVVEVLRILVLIGQILFSLAAVFLCLVIKKYLIGPYRKLHMESKGNKEILILGI  
SAFIFLMLTVTELDDVSMELGCF LAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV  
FPTFVAYELTVLVFTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR  
ARRAGVISREVYLLILSVTTLSLLLAPVLWRAAITRCVPRPERRSSL

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,  
576-598, 641-660**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 55-59, 673-677

**Tyrosine kinase phosphorylation site.**

amino acids 407-414

**N-myristoylation sites.**amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,  
442-448, 525-531, 530-536**Cell attachment sequence.**

amino acids 404-407

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**FIGURE 231**

GAGAAAAACAACAGGAAGCAGCTTACAACTCGGTGAACAACTGAGGGAACCAAACCAGAGAC  
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAGTGGGCAGAGATTCCACCAGGACTG  
GTGCAAGGCGCAGAGCCAGCCAGATTTGAGAAGAAGGCCAAAAGATGCTGGGGAGCAGAGCTG  
TAATGCTGCTGTTGCTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGGCAGCAGCC  
CTGCCTGGACTCAGTGCCAGCAGCTTTCACAGAAGCTCTGCACACTGGCCTGGAGTGCACATC  
CACTAGTGGGACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC  
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC  
AAAGGATCCACCAGGGTCTGATTTTTTATGAGAAGCTGCTAGGATCGGATATTTTCACAGGGG  
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTTCATGCCTCCCTACTGGGCCTCAGCC  
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC  
AGCCATGGCAGCGTCTCCTTCTCCGCTTCAAAATCCTTCGCAGCCTCCAGGCCTTTGTGGCTG  
TAGCCGCCCCGGGTCTTTGCCCATGGAGCAGCAACCCTGAGTCCCTAAAGGCAGCAGCTCAAGG  
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAATCTACCACCCAGGCACCTGTG  
AGCCAACAGGTTAATTAGTCCATTAATTTTAGTGGGACCTGCATATGTTGAAAATTACCAATA  
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGGAAATT  
TGGGGATTATTTATCCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATTGAAT  
TATGTACTTTTTTCAATAAAGTCTTATTTTTGTGGCTAAAAAAAAAAAAA

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## **FIGURE 232**

MLGSRAVMLLLLLPWTAAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEE  
TTNDVPHIQCGDGC DPQGLRDNSQFCLQRIHQGLIFYEKL LGSDIFTGEPSLLPDSPVGQLHA  
SLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLRLRSLQAFVAVAAARVFAHGAATLSP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Casein kinase II phosphorylation site.**

amino acids 64-67

**N-myristoylation sites.**

amino acids 25-30, 81-86, 122-127

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**FIGURE 233**

CCCACGCGTCCGGCCCTGTAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGGTCTGCAGTGCAG  
CATTAAATGGGCGCTGACATGAATATGGAGTAGTTTTCTCTAGCAAAGAGTAATGGGGCCATGGAGTCAAGGCCA  
CCTCCTCTGGGCTCTGCTGTTTCATGCAGTCCTTGTGGCCTCAACTGACTGATGGAGCCACTCGAGTCTACTACCT  
GGGCATCCGGGATGTGCAGTGAACATATGCTCCCAAGGGAAGAAATGTCATCACGAACAGCCTCTGGACAGTGA  
CATAGTGGCTTCCAGCTTCTTAAAGTCTGACAAGAACCGGATAGGGGGAACCTACAAGAAGACCATCTATAAAGA  
ATACAAGGATGACTCATACACAGATGAAGTGGCCAGCCTGCCTGGTTGGGCTTCTGGGGCCAGTGTTCAGGGC  
TGAAGTGGGGGATGTCATTCTTATTCACCTGAAGAATTTTGCCACTCGTCCCTATACCATCCACCCTCATGGTGT  
CTTCTACGAGAAGGACTCTGAAGTTCCCTATACCCAGATGGCTCCTCTGGGGCCACTGAAAGCTGATGACTCTGT  
TCCCCCGGGGGCAGCCATATCTACAACCTGGACCATTCCAGAAGGCCATGCACCCACCGATGCTGACCCAGCTG  
CCTCACCTGGATCTACCATTCTCATGTAGATGCTCCACGAGACATTGCAACTGGCCTAATTGGGCTCTCATCCAC  
CTGTAAAAGAGGAGCCCTGGATGGGAACTCCCTCCTCAACGCCAGGATGTAGAECATGATTTCTTCTCTCTT  
CAGTGTGGTAGATGAGAACCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCTGCTTCAGT  
GGACAAAGAAGATGAGACATTTCAAGGAGAGCAATAGGATGCATGCAATCAATGGCTTTGTTTTGGGAATTTACC  
TGAGCTGAACATGTGTGCACAGAAACGTGTGGCCTGGCACTTGTGGCATGGGCAATGAAATGATGTCCACAC  
AGCATTTTTCCATGGACAGATGCTGACTACCCGTGGACACCACACTGATGTGGCTAACATCTTTCCAGCCACCTT  
TGTGACTGCTGAGATGGTGGCCCTGGGAACCTGGTACCTGGTTAATTAGCTGCCAAGTGAACAGTCACTTTGAGA  
TGGCATGCAGGCACTCTACAAGGTCAAGTCTTGCTCATGGCCCTCCTGTGGACCTGCTCACAGGCAAAGTTCG  
ACAGTACTTCAATTGAGGCCCATGAGATTCAATGGGACTATGGCCCGATGGGGCATGATGGGAGTACTGGGAAGAA  
TTTGAGAGAGCCAGGCAGTATCTCAGATAAGTTTTTCCAGAAGAGCTCCAGCCGAATTGGGGCACTTACTGGAA  
AGTGGGATATGAAGCCTTTCAAGATGAGACATTTCCAAGAGAAGATGCATTTGGAGGAAGATAGGCATCTTGAAT  
CCTGGGGCCAGTGATCCGGGCTGAGGTGGGTGACACCATTCAAGTGGTCTTCTACAACCGTGCCTCCAGCCATT  
CAGCATGCAGCCCATGGGGTCTTTATGAGAAAGACTATGAAGGCACTGTGTACAATGATGGCTCATCTTACCC  
TGGCTTGGTTGCCAAGCCCTTTGAGAAAGTAACATAACCGCTGGACAGTCCCCCTCATGCGGCTCCTGCTCA  
GGATCCTGCTTGTCTCACTTGGATGTACTTCTCTGCTGCAGATCCCATAGAGACACAAATTCTGGCCTGGTGGG  
CCGCTGCTGGTGTGCAGGGCTGGTGCCTTGGGTGCAGATGGCAAGCAGAAAGGGTGGATAAAGAATTCTTTCT  
TCTCTTCACTGTGTTGGATGAGAACAGAGCTGGTACAGCAATGCCAATCAAGCAGCTGCTATGTTGGATTTCCG  
ACTGCTTTTCAAGGATATTGAGGGCTTCCAAGACTCCAATCGGATGCATGCCATTAATGGGTTTCTGTTCTCTAA  
CCTGCCCAGGCTGGACATGTCAAGGGTGCACAGTGGCCTGGCACCTGCTCGGCCTGGGCACAGAGACTGATGT  
GCATGGAGTCATGTTCCAGGGCAACACTGTGCAGCTTCAAGGCATGAGGAAGGTGCAGCTATGCTCTTCTCTCA  
TACCTTTGTCATGGCCATCATGCAGCCTGACAACCTTGGGACATTTGAGATTTATGCCAGGCAGGCAGCCATCG  
AGAAGCAGGGATGAGGGCAATCTATAATGTCTCCAGTGTCTGGCCACCAAGCCACCCCTCGCCAACGCTACCA  
AGCTGCAAGAATCTACTATATCATGGCAGAAGAAGTAGAGTGGGACTATTGCCCTGACCGGAGCTGGGAACGGGA  
ATGGCACAACCACTCTGAGAAGGACAGTTATGGTTACATTTTCTGAGCAACAAGGATGGGCTCCTGGGTTCCAG  
ATACAAGAAAGCTGTATTCAAGGAATACACTGATGGTACATTCAAGATCCCTCGGCCAAGGACTGGACCAGAAGA  
ACACTTGGGAATCTTGGTCCACTTATCAAAGGTGAAGTTGGTGATATCCTGACTGTGGTATTCAAGAATAATGC  
CAGCCGCCCTACTCTGTGCATGCTCATGGAGTGTAGAACTACTACTGTCTGGCCACTGGCTGCTGAGCCTGG  
TGAGGTGGTCACTTATCAGTGAACATCCAGAGAGGTCTGGCCCTGGGGCCCAATGACTCTGCTTGTGTTTCTG  
GATCTATTATTCTGCAGTGGATCCCATCAAGGACATGTATAGTGGCCTGGTGGGGCCCTTGGCTATCTGCCAAA  
GGGCATCCTGGAGCCCATGGAGGACGGAGTGACATGGATCGGGAATTTGCATTGTTGTTCTTGATTTTTGATGA  
AAATAAGTCTTGGTATTTGGAGGAAATGTGGCAACCCATGGGTCCAGGATCCAGGCAGTATTAACCTACAGGA  
TGAAACTTTCTTGGAGAGCAATAAAATGCATGCAATCAATGGGAACTCTATGCCAACCTTAGGGGTCTTACCAT  
GTACCAAGGAGAACGAGTGGCCTGGTACATGCTGGCCATGGGCCAAGATGTGGATCTACACACCATCCACTTTCA  
TGCAGAGAGCTTCTCTATCGGAATGGCGAGAATACCGGGCAGATGTGGTGGATCTGTTCCAGGGACTTTTGA  
GGTGTGGAGATGGTGGCCAGCAACCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCCATGCTGG  
CATGGAGACCTCTTCACTGTTTTTCTCGAACAGAACCTTAAGCCCTCTCACCGTCACTACCAAAGAGACTGA  
AAAAGTGGCCCCCAGAGACATTGAAGAAGGCAATGTGAAGATGCTGGGCATGCAGATCCCATAAAGAATGTTGA  
GATGCTGGCCTCTGTTTTGGTTGCCATTAGTGTACCCTTCTGCTCGTTGTTCTGGCTCTTGGTGGAGTGGTTG  
GTACCAACATCGACAGAGAAAGTACGACGCAATAGGAGGTCCATCCTGGATGACAGCTTCAAGCTTCTGTCTTT  
CAACAGTAAACATCTGGAGCCTGGAGATATCCTCAGGAAGCACATCTGTAGTCACTCCAGCAGGCCATGGACT  
AGTCACTAACCCACACTCAAAGGGCATGGGTGGTGGAGAAGCAGAAGGAGCAATCAAGCTTATCTGGATATTT  
CTTTCTTTATTTATTTTACATGGAAATAATATGATTTCACTTTTCTTTAGTTTCTTTGCTCTACGTGGGCACCT  
GGCACTAAGGAGTACCTTATTTATCTACATCGCAAATTTCAACAGCTACATTATTTCTTCTGACACTTGGGA  
AGGTATTGAAATTTCTAGAAATGTATCCTTCTCAAAAGTAGAGACCAAGAGAAAACTCATTGATTGGGTTTCT  
ACTTCTTTCAAGGACTCAGGAAATTTCACTTTGAACTGAGGCCAAGTGAAGTGTGTTGCTGCCATGAGCATGTACAACTCTGGAGC  
TAAAGGCTAAGAAATATAGGCTTGATGGGAAATGAAGGTAGGCTGAGTATTGGGAATCCAAATTTGAATTTGATT  
CTCCTTGGCAGTGAACACTTTGAAGAAGTGGTCAATGGTTGTTGCTGCCATGAGCATGTACAACTCTGGAGC  
TAGAAGCTCCTCAGGAAAGCCAGTTCTCCAAGTTCTTAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTTC  
ATGTTTTAGACAGCAACCCCTATCCATTAAAGTACTTGTAGACCAAAAAAAAAAAAA

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**FIGURE 234**

MWAMESGHLLWALLEFMQSLWPQLTDGATRVYYLGIRDVQWNYAPKGRNVITNQPLDSDIVASS  
FLKSDKNRIGGTYKKTIYKEYKDDSYTDEVAQPAWLGLGPVLQAEVGDVILHLKNFATRPY  
TIHPHGVFYEKDESEGLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTDADPACLTWIIYH  
SHVDAPRDIATGLIGPLITCKRGALDGNSPQQRQDVHDHDFLLFSVVDENLSWHLNENIATYC  
SDPASVDKEDETFQESNRMHAINGFVFGNLPENLMCAQKRVAWHLFGMGNEIDVHTAFFHGM  
LTTRGHHTDVANIFPATFVTAEMVPWEPGTWLI SCQVNSHFRDGMQALYKVKSCSMAPPVDLL  
TGKVRQYFIEAHEIQWDYGPMGHDGSTGKNLREPGSISDKFFQKSSSRIGGTYWKVRYEAFQD  
ETFQEKMHLEEDRHLGILGPVIRAEVGD TIQVVFYNRASQPFSMQPHGVFYEKDYEGTVYNDG  
SSYPGLVAKPFEKVTYRWTVP PHAGPTAQDPACLTWMYFSAADPIRDTNSGLVGPLLVCRAGA  
LGADGKQKGV DKEFFLLFTVL DENKSWYSNANQAAAMLD FRLLEDIEGFQDSNRMHAINGFL  
FSNLPRLDCKGDTVAWHLLGLGTETDVHGVMFQGN TVQLQGMRKGAAMLFPHTFVMAIMQPD  
NLGTFEIYCQAGSHREAGMRAIYNVSQCPGHQATPRQRYQAARIYYIMAEVEWDYCPDRSWE  
REWHNQSEKDSYGYIFLSNKDGLLGSRYKKAVFREYTDGTFRI PRPRTGPEEHLGILGPLIKG  
EVGDILT VVFKNNASRPYSVHAHGVLESTTVWPLAAEPGEVVTYQWNI PERSGPGPNDSACVS  
WIYYSAVDPIKDMYSGLVGLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT  
HGSQDPGSINLQDET FLESNMHAIN GKLYANLRGLTMYQGERVAWYMLAMGQDVLHTIHFH  
AESFLYRNGENYRADVVDLFPGT FEVVEMVASNPGTWLMHCHVT DHVHAGMETLFTVFSRTEH  
LSPLTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTLLLVLALGGVVWY  
QHRQRKLRRNRRSILDDSKLLSFKQ

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 1109-1130

**N-glycosylation sites.**amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,  
876-880, 934-938**Glycosaminoglycan attachment site.**

amino acids 871-875

**Tyrosine kinase phosphorylation sites.**

amino acids 82-90, 137-145, 494-502, 513-521

**N-myristoylation sites.**amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,  
843-849**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

**Multicopper oxidases signature 2.**

amino acids 1048-1060

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**FIGURE 235**

GGAAAGAGTGCTGGTACTACAACCAGGAAGTGACAGATAATGTGCTTTAAACTACATTAGAAAAGCTTCTCATAG  
CAAACTGAGAGATTGAAGCAGTGATTATTTTACATAGTTGTCATTAAATATTTGGAGCTCTGCTGTGCATAGA  
GATGGCAACATACTTAGAATACACAGCTTTCTGGGCCAGAAATTGATCTTCTGACTTTTGAGCCTTATCTGATTA  
CTGCTTGGTTCATCTTTATTTTGTAACTACTCTGTAGGCTGAAAGGGAGAGACTCTCCTTGGTTTGCAGAGCC  
TGACTAGACAGGAATTCTGGCAACTGCTCCAGCAGAACTATGGCACTGAGCTAGGTTTAAATGCTGAGGAGATGG  
AAACTTGTCACTGTGATTGAGGATGTGCAGCCAAAGAAGTCCAGGAAGAAGCAGCTTGGATGACTCTGGGGAGA  
GAGATGAAAAATTATCCAAGTCAATCAGTTTACCAGTGAATCAATTAGTCGGGTTTCAGAAACAGAGTCATTTCG  
ATGGAAATTCATCAAAAGGAGGATTAGGCAAAGAGGAGTCCCAAAATGAGAAACAGACCAAAAAGAGTCTCTTAC  
CAACTTTGAAAAGAAGTTAACTAGAGTGCCATCAAAGTCACTGGACTTGAATAAAAATGAATATCTTTCTCTGG  
ACAAAAGCAGCACTTCAGATTCTGTTGATGAAGAAAATGTTCTTGAGAAAGATCTTCATGGAAGACTTTTTATCA  
ACCGTATTTTTCATATCAGTGCTGACAGAATGTTTGAATTGCTCTTTACCAGTTCACGCTTTATGCAGAAATTTG  
CCAGTTCTAGAAATATAATAGATGTAGTATCTACCCCTTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA  
TGACCTACACTATAGTCCCTTAATAGTCCACTTACTGGAAAATGCACTGCTGCCACTGAAAAGCAGACACTGTATA  
AAGAAAGTCGGGAAGCAGGATTTTATTTGGTAGATTTCAGAACTGACACATGATGTCCCCTACCATGATTACT  
TCTATACCGTGAACAGATACTGTATCATCCGATCTTCAAACAGAAATGCAGGCTAAGAGTTTCCACAGATTTGA  
AATACAGAAAACAGCCATGGGGCCTTGCAAAATCTTTAATTGAAAAGAATTCTTGAGTTCTTTGGAGGACTATT  
TCAAACAGCTTGAATCAGATTTGTTAATTGAAGAATCTGTATTAAATCAGGCCATTGAAGACCCTGGAAAACCTTA  
CTGGCTACGAAGGAGAGGCGAACCTTCAACCGAACAGCAGAAACAGTTCCCTAACTTTCTCTCAGCATTCTCT  
CTGGAGATGTGGGCTTAGGTGCCAAAGGGGATATTACAGGAAAAGAAAAGGAAATGGAAGAACTATAACGTCACCT  
TTATTGTGGTAATGAGTATTTTGTGTGTTATTAGTATTTGTTGAATGTGACACTGTTTCTGAAGCTGTCAAAGA  
TAGAACATGCTGCTCAGTCCTTTTACCGTCTCCGCTCCAAAGAGAGAAATCTTAAATTTAGCCTCTGATATGG  
TGTCAGAGCAGAACTATTGAGAAGATAAAGATCAGGCCATCGTTTAAAGGGAGTGCTCCGAGACTCCATAG  
TGATGCTTGAACAGCTGAAGAGCTCACTCATTATGCTTCAGAAAACGTTTGATCTACTAAATAAGATAAGACTG  
GCATGGCTGTTGAAAGCTAGTGATCTGAAGGACTAAAACCGCAGAGATACTTGGAACTTAAAGAAAATACCTGGA  
AGAAAACCAGACGAATGAAGGATTTTGGCATAGAACATTTCTATGTTTTTTCATTATTGAGATTTCTAATATGAA  
CATTCTTTTCAGTAACATTTATTTGATAATTAGTTTCTGCTGGCCTTAATAATCCATCCTTTCTATAGA  
TATTTTAAAGCTGTGAATTTCTTCAGTGAACCATGAAATATATTATAGAACTGAATTTCTCTGATACAAAAGAA  
AATGACACACCCTGAATTGAGTGGTATGGTCTCATTTCTACAGTGAAGTCTGATGCTTTGTTAGCACAGAATCCG  
TACATGTCCAATAGGTCGCTTTTGTAACTGAGATAAGACCAAGAGGATAAACAGGACAATATAAGAAGAAACCTC  
TATGTCTTACTGATTTTAAAGGTTCTGTTTTAGGCAATATAACATTTCCAGGTTTGTGTACTGTAAAGATTATA  
ATGTCTTCATTTATTTAGCATGCAAATTTAATAGTCAAATTTTGAATCTGCATGTTGATGATGATTATCAGAA  
AGGGTCTTCTGCCATGCTGTATCTTTATGAAAGAAATAGTTGTTTTTCTTAAGGTAATATCAGAGGTGGGATT  
ATCTTGCCTCCTCACTTAGAATACCAACAGTCAAAGGAAGAACCATCCTCTGAGTTTTTAAACAGAGGTTA  
TGTTAAATCTGGGCATTTAGTGACAGATCAAATGCATACTTGAACCTAAGATTGGCTTCAGCTTAGCAGTCTTTC  
ATGGTGGAAGTGACACATCTGGTTGAAAATAATTTGTGTATTTTTCAGTAACCATGTATGGCTTCTTTTATGT  
ATGTGTGTGACTTGTTTAATTGGTAAGTTATAAGCCAGACATAGATTTTAGCTCTTTAATAAAAACTTCAGGGG  
CACGTATGTCCAGTACAAGTGTACTGACTATCAAGTTTAACTCAGATGCAAGCTTTGGCTCTTTCATAAAAAG  
TTTTTATGCATATGTGTCTCCATACAAGTGGCTCATTAAAAATAAGAACTTTGTAACTGACTTAAATCAGATAT  
TTTTTCAAGAGTTAGGGAAAGTTGAAGTGTTTTACTGTTTGTCTCTTGAGCCCTTTCTCTGGGGAAAAAATACA  
TATCCATCTATCTATCTATATATAAACTGTGTATACATTTACTGTTTGAACAACATATTGCCTTTAATTAATG  
TTTCATTTTTCTCCAGAGTCCCAAGCCACATGGCATTATTATAGTCATTTTGTAGATGCCTGTAGAGAATGAA  
AGTATTGACTCCGTTAGAGGGAAAATGGGTTTCTCTGGGTGAATTCACGAAGCATACCTAGGGGTAACAGTGA  
ACCTACCTGGGTTGTTTTGTTTGGTAAGGATTTATGTAGTGTCTGGCTGTAAGCAAGAAATGAGTGGATTATAA  
ACTTGAAGATTTCTCTGTTAAAGTCACAAAATGATCGACAAACAATATTTTGTGATGTTTATTTAAACGTTGT  
ATTTTATAACATACTTCAAGGAAGAGTATCGAAGTAAGTTGCTTTATAAATTAAGACTAAATTCGTATGGATGCA  
GAATTCATTAATAAAATTTGAGCCTGTTACGTAAATGAATATTAATAAAATTTGAAAATTTCAAAA



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**FIGURE 236**

MENLSLSIEDVQPRSPGRSSLDDSGERDEKLSKSI SFTSE SISRVS ETE SFDGNSSKGGLGKE  
ESQNEKQTKKSL LPTLEKKL TRVPSKSLDLNKNE YLSLDKSSTSDSVDEENVPEKDLHGRLFI  
NRIFHISADRMFELLFTSSRFMQKFASSRN IIDVVSTPWTAE LGGDQLRTMTYTIVLNSPLTG  
KCTAATEKQ TLYKESREARFYLV DSEVLTHDVPYHDYFYTVNRYCIIRSSKQKCRLRVSTDLK  
YRKQPWGLVKSLIEKNSWSSLEDYFKQLES D L LIEESVLNQAIEDPGKLTGLRRRRRTFNRTA  
ETVPKLSSQHSSGDVGLGAKGDITGKKKEMENYNVT LIVVMSIFVLLL VLLNVT LFLKLSKIE  
HAAQSFYRLRLQEEKSLNLASDMVSRAETIQKNKDQAHRLKGVL RDSIVMLEQLKSS L IMLQK  
TFDLLNKNKTGM AVES

**Transmembrane domain:**

amino acids 352-371

**N-glycosylation sites.**

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 81-85, 307-311

**Tyrosine kinase phosphorylation sites.**

amino acids 202-211, 246-254, 341-349

**N-myristoylation site.**

amino acids 259-265

**Amidation site.**

amino acids 339-343

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**FIGURE 237**

CAGGGGCTGGAGGGCAGGGGAGGGGATGATGTCATTCCCTGCTCGGCGCAATCCTGACCCTGCT  
CTGGGCGCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC  
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTTCCTGGGCAAGAAGGACCA  
CCTGTCCATGTCCACCAGGGCCATCAGGCCCACAGAGGAGGGCGGCCTCCACGTCCACATGGA  
GTTCCCGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGGCTCCGAGGG  
ACACTTCAGAGTCCCGGCCTTGGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC  
CTTCGCCGTCCTTTACATCTACAAGGAGCTGGAGGGGGCCCTCAGCACCATGGTGCAGCTCTA  
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTTCCAGGACTTCTACCCGACCCT  
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCCCAGTCAGATGCATGCAACCCTGAGAGCAA  
GGAGGCGCCCTGACACCTCCGGAGCCCCACCCCCGCCCTTCCCAGGTGGAGCCAAAGCAGCAG  
GCGCCTTTGCCCTGGAGTCAAGACCCACAGCCCTCGGGGACCACCTGGAGTCTCTCCATCCT  
CCACCCCCCGCCTGTGGGATGCCTTGTGGGACGTCTCTTCTATTCAATAAACAGATGCTGCA  
GCCTCA

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**FIGURE 238**

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMASDCRVFLGKKDHLMSSTRAI  
RPTEEGGLHVHMEFPGADGCNQVDAEYLVKGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK  
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

**Signal peptide:**

amino acids 1-20

**Tyrosine kinase phosphorylation site:**

amino acids 110-117

**N-myristoylation sites:**

amino acids 7-13, 79-85, 130-136

**Amidation site:**

amino acids 50-54

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**FIGURE 239**

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCCGAGGCGGTTCA  
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCGTGGATATGGAGCTGGCTGCT  
GCCAAGTCCGGGGCCCCGCGCCGCTGCCTAGCGCGTCCTGGGGACTCTGTGGGGACGCGCCCCG  
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGCATGGCCCTGCTCTCGCGCCCCGC  
GCTCACCTCCTGCTCCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC  
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTCATAAGATAGACACGTACCTGAA  
CGCCGCCTTGGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC  
TAAGCCTTTCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT  
TGGTGTTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTTGCAACCAACACGACAGGTG  
CTATGAGACCTGTGGCAAAGCAAGAATGACTGTGATGAAGAATTCAGTATTGCCTCTCCAA  
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTTCAGGCATGTGAAACAAC  
AGTGGAGCTCTTGTGTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG  
AGCCGCATGCAGGTGTCATTATGAAGAAAAAAGTATCTTTTAAAGGAGATGCCGACAGCTAGT  
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT  
GTCTTATTTTTGTGAAAGGATTATTTTGAACCTTAAAATAATTTATATCTTGATGTTAAAC  
CTCAAAGCAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTTGTCTTCTCAGGTATCTT  
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT  
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAAA  
AAAAGAGATCAAAATATAAAATTCATCATAATGTCTGTTCACATTATCTTATTTGGAAAATGG  
GGAAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA  
GGAACGGACTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT  
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA  
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG  
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTTCAGAA  
GCATAGCCACTCCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT  
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 240**

MALLSRPALTL L L L L L L M A A V V R C Q E Q A Q T T D W R A T L K T I R N G V H K I D T Y L N A A L D L L G G E D G L C  
Q Y K C S D G S K P F P R Y G Y K P S P P N G C G S P L F G V H L N I G I P S L T K C C N Q H D R C Y E T C G K S K N D C D E  
E F Q Y C L S K I C R D V Q K T L G L T Q H V Q A C E T T V E L L F D S V I H L G C K P Y L D S Q R A A C R C H Y E E K T D L

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites:**

amino acids 57-63, 93-99

**Phospholipase A2 histidine active site:**

amino acids 106-114

**Neuraxin and MAP1B proteins repeat proteins Block:**

amino acids 109-137

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**FIGURE 241**

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT  
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC  
GTCTGCCGCTATCTCCGCCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG  
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCCGCGCAGCTGCCTC  
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG  
GTCCCGGGCCGCGCCGCTGGGACCCCTGGCCCGGGCCTTGCACTGGCGCTGGCCGCCTTCC  
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCCTGCGCTCGGATCCCAGCATCCGTGGCG  
TGATGCTGGCCGGCCTGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG  
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT  
GCCGCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCCTGTGCCTGCTGCTTC  
ATGCCGCCGGCGTCCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTGCGCCCTGCTGC  
GAGCCCACACGCCCCTCCACATGGCTGCCCTCCTCCTGCTTCCCTGGCTCATGTTGCTCACAG  
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC  
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG  
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG  
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGGATGGGA  
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTTGACTCCAGGAAGAGCCAGAGC  
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT  
GGACCTTAACATCTGCATTGGACAACCTCCACCCCTTCCTTGGCCTTGCCCCTGCCCGCCTACA  
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG  
GGGCTGCTCAGGCCGCCTAGCTGCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

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**FIGURE 242**

MGQPWAAGSTDGAPAQLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL  
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCL  
LGRCVGFGNYPFLCLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV  
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSYDLGPCHNLQAALGPR  
WALVWLWPFLASPLPGDGITFQTTADVGHAS

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 51-66, 143-160, 174-191, 198-214

**N-myristoylation sites:**

amino acids 2-8, 8-14, 30-36, 81-87, 88-94, 90-96, 206-212

**Leucine zipper pattern:**

amino acids 143-165, 150-172, 157-179, 164-186

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**FIGURE 243**

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC  
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCGGCTTCC  
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTCAT  
CTTCCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT  
CTGTGAACCTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTCTCTGTACAG  
CCAGCTCTGTGTCCTTTTCTTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA  
CCTTTGTGCCCCACTCCTCATTTCCTACGCCTCCCTCTCTCTGCTGGTCCCTCTCTCTCCCTG  
CAAGGTTCCATTCCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT  
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTTGAAGGATTTCACTTCAATCTTTTCTGGT  
TGCGTCTCCACTTGTA CTAGCTTGTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC  
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCCGTGAGATCTGTTGTCAGCCTTC  
GTTTCTCTTTCCTGTGTCCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTCT  
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT  
AGCTGGACTGCTGGGCAGGGGAGCTGTCTAGATAAAATTGGAAAGAAACAGTGACCCAGAGA  
CAGGTGGACAAAGAATTCCGGGACTGATGGGAACTGAGCTTGGGATCCAGACTGAAACTGATT  
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGCCATGGGACCCAGCATTGAGACT  
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG  
CTATGAAGCAACAGCCTCAAGATTCAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT  
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTTATTGAGACAGG  
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTCGTCTTACCCTGCGCAAAT  
CTCCTACCTTGTTTCCCCACCCGAGTGTCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA  
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC  
TATCACATCTGCGTCCTGTAGCTGCCCCACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC  
AAATTTTGTACCACTAATTCTTGCCCCCTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA  
ATTTACAGGACAGGGTTTCTCAATACCACCTTCCCTCCTCATGGGGTGTGCTCGTGAACATAACCA  
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGAAGTGGTCCCTCAACATCTTAGA  
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG  
CCTCCTGTTTGCCTTCAGGGACTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA  
CATAACAAATAAAATAGCAGAGTTCCTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA



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**FIGURE 244**

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRVAFHNWKWLLMRNMVCKLQEGCEE  
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK  
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM  
GCAREHNQLLADFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 117-121, 183-187

**N-myristoylation sites:**amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,  
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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**FIGURE 245**

GTGGAGTTGGGTGGTGTGGGAGCCTCTCCCTGAGGGGCACCGCTCTTCAGGAGCTGGGCCTCCAGTGCGGCGC  
GATGTGAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCGCTGACCGG  
TCCGCTCATGGTGCCGCCACGACGCCATCGCGGGGCAGGAAGGCCAGGGGTGCTGAGTCTTCACCTCCTTTAG  
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT  
GTGTGTATTTGTGATGAACCGAATGAATCCCAGAACAGTGGTTTCACTCAGCGCAGGCGAATGGCTCTTGGGAT  
TGTTATTCCTTCTGCTTGTTGATGTGATATGGGTTGCTTCCTCTGAACTTACTTCGTATGTTTTTACCCAGTACAA  
CAAACCATTCCTCAGCACCTTTGCAAAAACATCTATGTTTGTGTTTGTACCTTTTGGGCTTTATTATTGGAAGCC  
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTGCAGATGCTGAAGGTTACTTTGC  
TGCTTGACACAACAGATACAACATGAATAGTTCCTTGAGTGAACCTCTGTATGTGCCTGTGAAATCCATGATCT  
TCCAAGTGAAAACCTGAGAGCACAAACATTGATACTGAAAAACCCCCAAAAAGTCTCGTGTGAGGTTTCAGTAA  
TATCATGGAGATTTCGACAGCTTCCGTCAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGTCATATCCTGTGAA  
AGAACAAGAATCCATACTGAAAACCTGTGGGAAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTG  
CTTTGTGTGGTTTTTGGCAAATTTGTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT  
ATCTTCAACTTCCGGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCTT  
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAACCTGC  
TGGAAGAGACACAGTAGGTTCCATTGGTCTCTTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA  
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCCAATGTTCTTTGGTTTTGTAGGTTTGTAAATCTGCTGCT  
CTTATGGCCAGGTTCTTTTTACTTCATTATACTGGATTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT  
GTGCATTATCATTAAATGGCCTTATTGGAACAGTACTCTCAGAGTTCCTGTGGTTGTGGGGCTGCTTTCTTACCTC  
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT  
GCAGTTTTCTTGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTCATTTTTTATTGTAACCTCTCCTATGCCA  
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTGCTTTTATATGCAGAAAACATCGAATTCA  
GAGAGTTCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGTTCCTCAGGAGGATGGAGCTAG  
TTAGCTGTCTGTTGTCTGTAGCCCAGCTTGATAATGGAACATAACAGCGAAGAGACAATCTCTGGCAAGTTTTTG  
TAGAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAAACTCTAAATATATTTTTCTC  
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG  
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTGGA  
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTCACATGTTAAATGCTGGAATATATTATGAAAAT  
GTTTTCAAGAAATCACTTAAGTGTTTCATAGACCAGTATTTCTGACAGGTAAAATGCTAAAATAAGCTACCTGTAA  
TAAGTGTGGATTATATTTTTGGGTTTTGTAGAATATTGCAAATTAACCACACAAAAAATGTTTAATTTATGCAAC  
AAGCATGTTTGTGCAATTTTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAATATCTGGTTCACTTACACTA  
CATTTACTGTATTATCTTTTATAGCATTAGGTGCCTTGATTTTAAATCTGTGACAAACCATGGCAAATTTTTTA  
AAGGGGAAGTATTATTATAAATGAAGAAATATGTATTTCTAAAGGCTATATTGCTGTAAACTTAATTGATAAAG  
CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTTCAATTAAGAAATTTTCATAATGGAATGATTTAAAT  
GAAGTGACAAAGAGTATTATTAAATACAATGTTTATAAAAAA

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**FIGURE 246**

MVPPRRHRGAGRPGVLSSSPFRLRS AKFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF  
TQRRRMALGIVILLLLVDVIWVASSELT SYVFTQYNKPFFSTFAKTSMFVLYLLGFIIWKPWQR  
QCTRGLRGKHAFFADAEGYFAACTTDTTMNSSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP  
KKSRVRF SNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF  
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN  
LAGSEKPAGRDTVSGSIWLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWPGF  
FLLHYTGFEDFEFPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALS LTIPLSIIA  
DMCMQKVQFSWLFFAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRPEDS  
EQCESLISMHSVSQEDGAS

**Important features:****Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,  
364-379, 399-419, 453-472

**N-glycosylation sites:**

amino acids 157-161, 255-259

**N-myristoylation sites:**

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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**FIGURE 247**

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG  
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT  
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAAACTGAA  
TCCTGCTACTAAAATAATTCAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT  
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA  
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC  
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT  
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC  
TTCGGGTGATATTGGGGGTTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG  
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACTTCTATTGATCATGACATCATGC  
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC  
AAACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT  
ACAAAGAGCCCGATTCACTGCAAACGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGG  
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA  
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC  
TGTCTTTTGCGGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT  
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTTGAGCTGTGGCAGTTGTGGACCATATGA  
CACAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACCTCCTC

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## **FIGURE 248**

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLPAGVLIHPLWVITAHCNLPKLR  
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLTAEELNDYVKLANLPYQT  
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ  
PCKEVSAAPAICNGMLQGILSFADGCVLRADVGIIYAKIFYYIPWIENVIQNN

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites:**

amino acids 11-15, 156-160, 173-177

**Tyrosine kinase phosphorylation site:**

amino acids 108-117

**N-myristoylation sites:**

amino acids 182-188, 203-209

**Amidation site:**

amino acids 185-189

**Serine proteases, trypsin family, histidine active site:**

amino acids 52-58

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**FIGURE 249**

GCGAGGCGGCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC  
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC  
TGTCGGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT  
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG  
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA  
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG  
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG  
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATTAAACATTCA  
ATAAATGTCTCCATACCATCAA

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**FIGURE 250**

MWLSIGALIGLSVAADVLLAFIVTACVLCYLFISSEKPHTKLDLGLSLQTAGPEEVSPDCQGV  
NTGMAAEVPKVSPLQQSYSCLNPNQLESNEGQAVNSKRLHHCFMATVTTSDIPGSPEEASVPN  
PDLCPVP

**Important features:**

**Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 7-13, 11-17, 62-68, 93-99

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**FIGURE 251**

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG  
GCAGAGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACCATGCGAG  
GCCAGCGGAGCCTGCTGCTGGGCCCCGGCCGCTCTGCCTCCGCCTCCTTCTGCTGCTGGGTT  
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT  
GCCTGCGCTCCCTGCTCTACAACCTCCTTTGGGGGAGTGACACCGCTGTTGATGCTGCCTTTG  
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCCTGG  
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCTACCTGTGTGTCTGCCTCTCATCCTCC  
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA  
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCTGGGTACCCACCCAGGGCAGGAATG  
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCACT  
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCCTGGCTAAACAATTGTG  
TGGGCCACTATAACCATCGGTACTTCTTCTCTTTCTGCTTTTTCATGACTCTGGGCTGTGTCT  
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC  
AGACCCACCCACCTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT  
GGTTCCTGTGAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA  
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG  
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACCTGGAAGGTATTCC  
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC  
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG  
CAGTGTGAGCTGGACTGTGTGAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA  
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA  
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTACCCTGCAGAAGAAAGACACAATGT  
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAACAGAAGTTCCAACCCAGACTAGG  
GGTCAGGCAGCTAGCTACCTACCTTGCCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC  
TGGAGTTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAAACACCTGACTAGTACAGCTGAGA  
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA  
TGCTGCTTAAGGGAGCACAAATAAAGGTATTCGATTTTTAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA



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**FIGURE 252**

MRGQRSLLLGPRLCLRLLLLLGYRRRCPPLLRLVQRWRYGKVCLRSLLYNSFGGSDTAVDA  
AFEPVYWLVDNVIRWFGVVFVVLVIVLTGSIVAIAIYLCVPLILRTYSVPRLCWHFFYSHWNL  
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHCPLN  
NCVGHYNHRYFFSFCFFMTLGCVCYSYGSWDLFREAYAAIETYHQTPPTFSFRERMTHKSLV  
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK  
VFLGVD TGRHWL TRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

**Important features:****Transmembrane domain:**

amino acids 88-100, 202-216, 254-274

**N-myristoylation sites:**

amino acids 55-61, 56-62, 92-98, 210-216, 309-315, 319-325, 340-346

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 201-212

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**FIGURE 253**

GATCAAGCGCCTTCCTTTCCCTTCTCCTACTTGGCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTGGC  
TGCAGGGGCCTGCAGAGCCAGCTGCACTTTTTTCAGGTATGGGGGAGGGCCAGGCACCATGAAGCCAGTGTGGGTC  
GCCACCTTCTGTGGATGCTACTGCTGGTGCCAGGCTGGGGGCCGCCGGAAGGGGTCCCCAGAAGAGGCCTCC  
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG  
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGCTTACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG  
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCAGGAGGACATCATTCTGCTGAGGGAACATGCACGTCAAC  
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGÀ  
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGACCCTGG  
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC  
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTCACTGATCCTCGGGCAATGGCA  
GAAAAAGGCTATGAGACGGGGCCACCATGCGCCGGGCCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC  
CACATCATTAAAGGCCACGCCAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG  
GGAATTTCACTGAAGTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA  
TACCTACAGTTCTGTCTGGGCTGGTTTGCCAACCCCATTTATGCCGGTGACTACCCCAAGTCATGAAGGACTAC  
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTCGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC  
ATTAAAGGCACATCCGATTTCTTGGGATTAGGTCATTTTACTACTCGGTACATCACGGAAAGGAACTACCCCTCC  
CGCCAGGGGGCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT  
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACCTTGCTCAGACTCAATACGGTGATCCTCCC  
ATATATGTGATGGAAAATGGAGCATCTCAAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAATTCAATAC  
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAAGATGGTGCTAATATAAAGGGGTATACTTCCTGGTCT  
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA  
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTTCCCAATCCA  
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT  
TTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCCTCATCACTGCT  
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTGAGACAGGATTATCAATTTTGAGCTTCATAAGAGAATCTT  
CAGGATCTTCCTCCCTTTTCTGCTTTGAGGGTTCCATACATTGCTGTTTTTCAGGTTCTACAATAATTACCTTTT  
TTTCTCTTCTCTTTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAAAATAAGCAGAAATTA

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**FIGURE 254**

MKPVVWATLLWMLLLVPRLLGAARKGSPEEASFYYGTFFPLGFSWGVGSSAYQTEGAWDQDGKGPSIWDVFTHSGKG  
KVLGNETADVACDGYKQVEDIILLRELHVNHYRFSLSWPRLLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI  
VTLHHWDLPLQLQVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTG  
LYKAAHHIIKAHAKTWHSYNTTWRSKQQGLVGISLNCWGEVVDISNPKDLEAERYLQFCLGWFFANPIYAGDYP  
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDRLIELVDPN  
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPPYYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKOGANIK  
GYTSWSLLDKFEWEKGYSRDYGFYYVEFNDRNPKPRYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQ  
MLAAEPLLSHMQMTEIVVPTVCSLCVLITAVLLMLLLRRQS

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 541-558

**N-glycosylation sites:**

amino acids 80-84,171-175,245-249

**Glycosaminoglycan attachment site:**

amino acids 72-76

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 23-27,564-568

**Tyrosine kinase phosphorylation sites:**

amino acids 203-211,347-355,460-468,507-514

**N-myristoylation sites:**

amino acids 44-50,79-85,167-173,225-231,257-263,315-321

**Amidation site:**

amino acids 307-311

**Glycosyl hydrolases family 1 active site:**

amino acids 407-416

**Glycosyl hydrolases family 1 N-terminal signature:**

amino acids 41-56

**Motif name Glycosyl hydrolases family:**

amino acids 37- 67

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**FIGURE 255**

CGCGAAGATGCGAAAGGTGGTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG  
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA  
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTCACCCCACTGCTGAGGTCACCATTGTCCA  
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGCCTCCAAGGAACTTAAGCAAAGGTTTCA  
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAATAAATATCAAAGC  
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTCATATGTTCTCCACAGCTGAAGGCCTGCT  
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG  
CCATTTTATCCTGATTCGGGAACTGGAGCCTCTCCTCTGTCACAGTGACAATCCATCTCAGCT  
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTCAGCCTCGAGGACTTCAGCACAG  
CAAAGGCAAGGAACCCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA  
CAGGAACCTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA  
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT  
TCGCTTTTTTGCAAATGCATTCACTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT  
TTTCCACCAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT  
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA  
TCAAAGTTACTGGAACCTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC  
CAGGCTCAGTGGCTCATGCCTATAATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT  
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAGAAAT  
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG  
GGAGGATCTCTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC  
AGCCTGGGTGACAGCGAGACCCTGTCTCAAAATATGTATATATTTAATATATATATAAAACCA  
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTC  
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

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**FIGURE 256**

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD  
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ  
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSGK  
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLLRF  
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGGRNYIMTQKMDLDEDTAEKFYQK  
LLELEKHIRVTIQKTDNQARLSGSCL

**Important features:****Transmembrane domain:**

amino acids 234-254

**N-glycosylation sites:**

amino acids 37-41, 178-182, 229-233, 263-267

**Glycosaminoglycan attachment site:**

amino acids 12-16

**N-myristoylation sites:**

amino acids 9-15, 13-19, 15-21, 215-221, 224-230

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**FIGURE 257**

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC  
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCTGAGCCCGATGGGGGCCTGATGGTGCTCCCTAAGGACAGCATTAGTTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATT  
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCTCTTCATCCTGCCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCTCCACTAGTCCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGTTCTGCTGC  
TGACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC  
GGCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCCTTGGTGTTGCCTTCTTGCACTCTCCACACATTTCCCTTGGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTTTCACAGGGAAAAA

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**FIGURE 258**

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGKTRQVSLEVIPNWLGPLQNLLHIRAVG  
TNSTLHYVWSSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGASPRGNRSLEFGLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGSPLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFEGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPVPDGLSPLVLGIMAV  
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

**Important features:****Signal peptide:**

amino acids 1-35

**Transmembrane domain:**

amino acids 365-386

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern:**

amino acids 371-393

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**FIGURE 259**

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCCT  
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTGCGCTCTGTTTG  
GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAATAAAATTGAAAGCAAGATTGAAGAGATGGT  
TGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTATC  
AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAACTCAT  
GATGGACGGCCACGAGGTGACCGTGGTGGACAATTTCTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG  
ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCTCTACATCGAGGTTGACCAGATATACCATCT  
GGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATTGGGACATT  
AAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC  
TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG  
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCGAGTGGCCAGAATCTT  
CAACACCTTTGGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG  
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGCGGTTCCAGTACGTACGCGATCTAGTGAATGGCCT  
CGTGGCTCTCATGAACAGCAACGTACGAGCCCGGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT  
TGCTCAGTTAATTA AAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA  
GAAAAGAAAACCAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCCCGCTGGAGGAAGGTTT  
AAACAAAGCAATTCACTACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC  
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAACTCCTCACTTTTAGGACACAAGACTACCATTGTACAC  
TTGATGGGATGTATTTTGGCTTTTTTTGTTGTCGTTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAAC  
TGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCTCAAAAACTGCAGATTTTG  
CCTTGCACTTTTGAATCTCTCTTTTATGTAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT  
CTTGCTGTGAGAGCATATGTTGTGACTGTCGTTGACAGTTTTATTACTGGTTTCTTTGTGAAGCTGAAAAGGAA  
CATTAAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT  
AAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTTTAGGGCAGATAAAAGAATTCTGTG  
TGAGAGCTTTATGTTTCTCTTTAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAAACCTTGACTTTGAAA  
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTGTCTGCGTATCTGGGGCGGGGCAGGT  
TGGGGGGCACAAAGTTAACATATTCTTGTTAACCATGGTTAAATATGCTATTTTAATAAAATATTGAAACTCA



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**FIGURE 260**

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR  
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVDNFFTGRK  
RNVEHWIGHENFELINHVVVEPLYIEVDQIYHLASPPNYMNPPIKTLKTNTIGTLNMLGL  
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHVNPIGPRACYDEGKRVAETMCYAYMKQEGVE  
VRVARIFNTFGPRMHMNDGRVVSFILQALQGEPLTVYSGSQTRAFQYVSDLVNLGLVALMNS  
NVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKMLGWEPV  
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

**Important features:****Signal peptide:**

amino acids 1-32

**N-glycosylation site:**

amino acids 316-320

**Tyrosine kinase phosphorylation site:**

amino acids 235-244

**N-myristoylation sites:**

amino acids 35-41, 101-107, 383-389

**Amidation sites:**

amino acids 123-127, 233-237

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**FIGURE 261**

GCGTGGTGCGGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG  
CATCCTCCGCATCCTCCACATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATC  
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT  
ATAGACAACTGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCCTCCGCGGCCGAC  
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAGTGC  
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT  
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTACACCAAGACATGCCATTACGGCTTGG  
TATAATGAAACCAATTTTATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT  
ACACAGTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTT  
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAATATG  
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAAC  
CTCTGCAGGACTCCACAACCTATTATACCTAACCAAAATCCATTTCTGAAGCCAACGGGGAGA  
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTTTAA  
TGTCATTTATATACAAAAGAAATCTCAAATGTTAAAATAAAGGAATAGTTTATTGCTTAATA

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**FIGURE 262**

MALKNKFSCWLILGLCLVATTSSKIPSI<sup>T</sup>DPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG  
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKS<sup>F</sup>TPRHAITAWYNETQFYDF  
DSLSCSRVCGHYTQLVWANSFYVGCAVAMCPNLGGASTAIFVCNYGPAGNFANMP<sup>P</sup>YARGESC  
SLCSKEEKCVKNLCRTPQLIIPNQNPF<sup>L</sup>KPTGRAPQQTAFNPFSLG<sup>F</sup>LLLRIF

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site:**

amino acids 119-123

**N-myristoylation sites:**

amino acids 103-109, 150-156, 160-166, 161-167, 175-181

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:**

amino acids 136-156

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

amino acids 166-178

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**FIGURE 263**

CGCCCTCCGACCCGCCCCGCGCGCATTGTGGGATCTGTGCGGCTTGTGAGGTGGTGGAGGAAA  
AGGCGCTCCGTCATGGGGATCCAGACGAGCCCCGTCTGCTGGCCTCCCTGGGGGTGGGGCTG  
GTCCTCTGCTCGGCTGGCTGTGGGCTCCTACTTGGTTCGGAGGTCCCGCCGGCCTCAGGTC  
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC  
AACACCAAGAGGTTCCGCTTTGCCCTGCCCACCGCCACCACACTCTGGGGCTGCCTGTGGGC  
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC  
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTGTCATCAAGGTCTACCTGAAGGGTGTGCAC  
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTTGGGGATGTG  
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAAACATTGAG  
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG  
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC  
CAGTGCTTTCTGCTTTTGTCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG  
GAACTGCAGGCCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCCTGCTGATCATCCCCCAAAA  
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA  
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCAATGGTGCAGCTGGCCTGCCATCCC  
AACTTGGACAACTGGGCTACTCACAAAAGATGCGATTACCTACTGAGCATCCTCCAGCTTC  
CCTGGTGCTGTTTCGCTGCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCCCT  
TTCCTCAGAGTTTCAGGTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG  
AACAATATTCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA  
TCTCCCCGTGGCAACAGGTCCAGGAGAGGCCCATGGAGCAGTCTCTCCATGGAGTAAGAAGG  
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCCTTGATAGCATCTTACTCTCACCTT  
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAACTTCACTGTTCAA  
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT  
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA  
TTTCTGTGTGTGTCTCTCTCAGCCCCTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA  
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA  
TATTGAAGA

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**FIGURE 264**

MGIQTSPVLLASLGVLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR  
FRFALEPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP  
EGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGHFNIPNKKSPPEPRVAKKLGMIAAGGTGIT  
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLWFTLDHPPKDWAY  
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

**Important features:**

**Signal peptide:**

amino acids 1-26

**N-glycosylation site:**

amino acids 214-218

**N-myristoylation sites:**

amino acids 22-28, 76-82, 128-134, 180-186

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**FIGURE 265**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA  
ACGCGGCTACAATTAATACATAACCTTATGTATCATAACATACGATTTAGGTGACACTATAG  
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTCGGT  
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCTCAGG  
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC  
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC  
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC  
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA  
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTCGACCCGGAGAAC  
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC  
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTAC  
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGG  
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGTGCTGAAGCCCCGG  
GCCCCGATGACCCCGGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCGCCGAGGACAACAGC  
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAACACGCACGCTGGGGGA  
ACGGGCCCCGAAGGCTGCCGCCCCCTTCGCCAAGTTCATCTAGGGTCGCTGG

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## **FIGURE 266**

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVDG  
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGYDV  
YHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRRNEIPLIHENTPIPRRHTRS AEDDSERDP  
LNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFAKFI

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

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**FIGURE 267**

GGCTGAGGGGAGGCCCGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC  
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC  
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG  
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG  
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCCAGTGGAGGAGGCTGCTTGGCAGCCACCGGCCCTGCAACT  
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG  
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGAAGGACCATGAGG  
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGACGGTTTT  
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTTACCTAAACAGGTACAAGCGGGCGGGCAGTCCCAGGAC  
AAGTGACCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG  
GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG  
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC  
CGCAACATGAACCTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACACCGC  
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG  
GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCCACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG  
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCCGTCCCCAGCCACCCCCGCTGCCCCGCCCCGGGTCTACCAACCA  
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA  
CCCCCTCTGCCCCACTATGCCACTCTCACCAGCTCCCATCTTCCACCGACAAGCCGTGCGGGCCATGGAGAGAC  
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGAGAACACCAACCGCCTC  
ATGCAGGTGTGGTGGCAGCAGACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATGGCTCTGTT  
AACTTCTTCAGGAACCTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG  
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC  
TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC  
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATGTCTACACA  
GGAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGG  
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTTAAGCCAGCTCCCCCTCCTGACCTCTC  
GTGGCCATTGCCAGGAGCCCACCCTGGTCAGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGA  
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT  
GTTTTCTGTCCCTCCTACTTTCCTTCACACCAGACAGCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA  
CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA



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**FIGURE 268**

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ  
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLRKE  
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKYQHLATL  
AHNQSEIIAQLEEHQCRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLP  
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSIYLVKPENTNRLMQVWCDQRHDPGG  
WTVIQRRLDGSVNFFRNWETKQGFQGNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF  
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYQKGGWWYN  
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH

**Important features:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites:**

amino acids 164-168, 192-196

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 124-128

**Tyrosine kinase phosphorylation sites:**

amino acids 177-184, 385-393, 385-394, 461-468

**N-myristoylation sites:**amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,  
473-479**Amidation site:**

amino acids 373-377

**Fibrinogen beta and gamma chains C-terminal domain signature:**

amino acids 438-451

**Fibrinogen beta and gamma chains C-terminal domain proteins:**

amino acids 305-343, 365-402, 411-424, 428-458

**Trehalase proteins:**

amino acids 275-292

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**FIGURE 269**

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA  
GCGGGTCTTACCCCCGGTCTCCGCTCTCCAGTCTTCGCACCTGGAACCCCAACGTCCCCGA  
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC  
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC  
CAAGTCGCGCGCTTTGCGTCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCTGCAGCT  
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGAGTCAGCTGAGCGCGCTGGAGCGGGC  
CCTGAGCGCGTGGGGTCCGCTGTGAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC  
TGAGAGCCGGGTGGACCCTGAGGTCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG  
CAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT  
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCTGGACCACAAGCACCTAGACCATGAGGT  
GGCCAAGCCTGCCCGAAGAAAGAGGCTGCCCGAGATGGCCAGCCAGTTGACCCGGCTCACAA  
TGTCAGCCGCTGCACCGGCTGCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA  
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTTGGTGAAGTCAAGATGAC  
CTCAGATGGAGGCTGGACAGTAATCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC  
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA  
GGTGCATAGCATCACGGGGGACCGCAACAGCCGCTGGCCGTGCAGCTGCGGGACTGGGATGG  
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA  
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT  
ACCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCT  
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC  
CATCCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTA  
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCG  
TCCTGGCTGGGCCTGGTCCCAGGCCACGAAAGACGGTGACTCTTGGCTCTGCCCGAGGATGT  
GGCCGTTCCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAACTTGTGGACAGAGAA  
GAAGACCACGACTGGAGAAGCCCCCTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCCTCCTGA  
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCTTCACT  
CCTTGCTGGCCAGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA  
TGGCGGACTCAGTCACATTGACTGACGGGGACAGGGCTTGTGTGGGTGAGAGCGCCCTCAT  
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC  
GGAGCTCACAGAGTTCTTGAATAAAAGCAACCTCAGAACAC

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**FIGURE 270**

MTVIRFFPAASATKRVLPVLRVSSPRTWNPNVPESPRIPAPRLPKRMSGAPTAGAALMLCAA  
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSLSALERRLSACGSA  
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS  
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFEIQ  
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDENRPWEAYKAGFGDPHGEFWLGLEKVHSITGD  
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQ  
DHDLRDKNCAKSLSGGWFGTCSHSLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT  
MLIQPMAAEAAS

**Important features:****Signal peptide:**

Amino acids 1-13

**Transmembrane domain:**

Amino acids 53-70

**N-glycosylation site:**

Amino acids 224-228

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 46-50;118-122

**N-myristoylation sites:**

Amino acids 50-56;129-135;341-347;357-363

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 396-409

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**FIGURE 271**

CGGACGCGTG GGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG  
AACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGCTG  
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCGCTTCGGCTGAAGCATTTGACTCG  
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTAC  
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT  
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGCT  
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAACT  
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG  
ACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCCAGAAATCCAG  
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC  
TATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC  
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCTTGTCCTCTCGGTG  
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT  
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA  
GCTTCTTCTCTTGTTGTTGTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT  
ACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTTAAAGACAAGTGTAATA  
GACATCTAAAATTCCTCCTCATAGAGCTTTTAAATGGTTTCATTGGATATAGGCCTTAAG  
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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**FIGURE 272**

MAAPKGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK  
EEELYACQRG CRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL  
RQEQLMSLMPKMHLLFPLTLVRSFWS DMMDSAQS FITSSWTFYLQADDGKIVIFQSKPEIQYA  
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFRLRCLSLNSGWILTTTLVLSVMV  
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAGPLPTK  
VNLAHSEI

**Important features:****Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site:**

amino acids 90-94

**N-myristoylation sites:**

amino acids 28-34, 29-35, 31-37, 86-92

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**FIGURE 273**

CCCACGCGTCCGAACCTCTCCAGCGATCGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGTG  
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA  
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGCGCAAGCACGT  
GCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT  
AGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT  
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT  
CACGGAGATCGTGCTGGAGAACAATAACGGCCTTCCAGAACGCCCGGCACGAGGGCTGGTT  
CATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA  
GGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGCCGAGAAGCA  
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGACCAAGCGCACACGGCGGCCCCCA  
GCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCGCCTCCCCACCCCTTTCC  
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC  
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC  
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTCACCCTGA  
TCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC  
GACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCTCGGATCT  
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTT  
GTTTGTTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCCACTCCTCA  
CATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCCCGGAATAAAACCATTTTCC  
TGC

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**FIGURE 274**

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS  
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENN  
YTAFQNRHEGWFMATFTRQGRPRQASRSRQNRQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGS  
APTRRTKRTRRPQPLT

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

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**FIGURE 275**

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT  
TTTTATTCTCTGTCCTATTTGCCATCTCAGAAAGTGCGGAGCAAGGAGTCTGTGAGACTCTGTG  
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG  
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAAACTCCTTCCAGCTCCCACATAAACGTG  
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC  
TTTGGGGTGGACAGATGCCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTTCAGTGATGTCAA  
GACAAGATTTACAAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT  
GCTTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT  
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAAATGATGGCTTTTGGGTAGGCAAAACT  
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC  
AAGGTTAATGAAGTGTCTTTTCAAATTCTACTAATGCTTTGAAATTTCAAATGCTGCGCAA  
ATTGCAATAAAAATGCTATAAA



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## **FIGURE 276**

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGN  
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSKKHSVMSRQDLQTLCTDGC  
SMTDLSALC

**Important features:**

**Signal sequence:**

amino acids 1-18

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 107-111

**N-myristoylation sites:**

amino acids 3-9, 52-58, 96-102, 125-131

**Insulin family signature:**

amino acids 121-136

**Insulin family proteins:**

amino acids 28-46

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**FIGURE 277**

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG  
CCCACAGACCAGAAGCTTCCACTATACTACTTAAATTTACATAGGTGGCTTGTCAAATTTCAATTGATTAGTATTGT  
AAAAGGAAAAAGAGTTCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT  
CAGATGAACAAACTTCTACACTGATTTTTAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC  
AGACACAAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCCAACGCATAGAAGAC  
TTTTTTTTCTCTTCTAAAAACAATAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAAT  
GAAGACTTTTACCTGGACCCTAGGTGTGCTATTCTTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT  
CAAAATTAATAAAATAAAACCAGAGAAGATACCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA  
CACATTCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT  
TAAAGACATGATCACCAGGATGGACCTTGAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT  
TCTGCAACTGGTGGTGGATGTAGATGGAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT  
GAACCTCTCGTGTACTCAACTCTATATGCAATTATACATGAGATTATCCGTAAGAGGGATAATTCACCTGAACT  
TTCCCAACTGGAACAAAATCCTCAATGTCACCACAGAAATGTTGAAGATGGCAACAAGATACAGGGAAGTAGA  
GGTGAATACGCTTCCCTTGAAGTCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAAACAGTGCTT  
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCACTTGTCCAGGTGGTGGCCACAACATATTCCTAACAG  
CCAACAGTATACTCTGGTCTGCTGGGAGGTAACGAGATTCAAGGGATCCAGGTTATCCAGAGATTAAATGCC  
ACCACCTGATCTGGCAACTTCTCCACCAAAAGCCCTTTCAAGATACCACCGGTAACCTTTCATCAATGAAGGACC  
ATTCAAAGACTGTCAGCAAGCAAAGAAGCTGGGCATTGCGTCAGTGGGATTTATATGATTAAACCTGAAAACAG  
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTGAGAAAAGAACAGA  
CGGCTCTGTCAACTTCTTCAAGAAATGGGAAAATTAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT  
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAGTTATTGATTGAATTAGAAGACTGGAGTGA  
TAAAAAGTCTATGCAGAATACAGCAGCTTTCGCTTGAACCTGAAAGTGAATTCTATAGACTGCGCTGGGAAC  
TTACCAGGGAATGCAGGGGATTCTATGATGTGGCATAATTGGTAAACAATTACCACACTGGACAGAGATAAAGA  
TATGTATGCAGGAAGTGGCGCCACTTTCATAAAGGAGGCTGGTGTACAATGCCTGTGCACATTCTAACCTAAA  
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACCAAGATGGAATTTCTGGGCCGAATACAGAGGCGG  
GTCATACTCCTTAAGAGCAGTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAAATGA  
CACAGAAGTTTGTACTTTTACGCTCTTAAAAATGTAATGTTACATGTATATTACTTGGCACAATTTATTTCTAC  
ACAGAAAGTTTTTAAATGAATTTTACCGTAACATAAAAGGGAACCTATAAATGTAGTTTCATCTGTGCTCAAT  
TACTGCAGAAAATTATGTGTATCCACAACCTAGTTATTTTAAATTTATGTTGACTAAATACAAAGTTTGTTTTC  
TAAATGTAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA  
CTTAACAATTTATTTAAATCTAAGATTGCTCTAACGCTAGTGAAAAAATATTTTTTAAATTTAGCCAAATA  
ATGCATTTTATTTTATAAAAAATACAGACAGAAAATTAGGGAGAACTTCTAGTTTGGCAATAGAAAATGTTCTT  
CCATTGAATAAAAGTTATTTTCAATTTGAATTTTGTGCTTTTACACGTAATGATTAAATCTGAATTTCTTAATAATA  
TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAAATACATATCATTTTAAAAATAAAAAAAACCC  
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAGACAAATCTATGAATGAATTTTTCAGTGTATCTT  
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAATCAGCAAAATATTGGTATT  
ACAAAAATGCAGAAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTATTACTTTTTTCTAATTT  
ACTGATCTTACTACTACAAAGAAAAAAAACCCAAACCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC  
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAACTCAAGGAAGTGTGGCTGTTTTCCCGATACTGA  
GAATTC AACAGCTCCAGAGCAGAAAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCAATTTTACAGTGTAT  
GTAAAGCTTAGTCTCAGAGTGTCTTAACTCATCTTTGCAATCAACAACCTTACTAGTGACTTTCTGGAACAATT  
TCCTTT CAGGAATACATATTTACTGCTTAGAGGTGACCTTGCCCTTAATATATTTGTGAAGTTAAATTTTAAAGA  
TAGCTCATGAACTTTTGTCTTAAGCAAAAAGAAAACCTCGAATTGAAATGTGTGAGGCAAACTATGCATGGGAAT  
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAAATCCATCAACATGACCAATGTTTTTCATCTGCCACATCTC  
AAAATAAACTTCTGGTGAACAAATTAACAAAATATCCAAACCTCAAAAAAA

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**FIGURE 278**

MKTFTWTLGVLFFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP  
ICVNTKGQDASTIKDMITRMDLENLKDVLRSQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM  
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNO  
SVMITLLEEQLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGNEIQRDPGYPRDLMP  
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP  
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK  
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGGWW  
YNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYRGGSYSRLRAVQMMIKPID

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation sites:**

Amino acids 160-164;188-192

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 120-124

**Tyrosine kinase phosphorylation sites:**

Amino acids 173-180;387-396

**N-myristoylation sites:**Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;  
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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**FIGURE 279**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGGC  
CCGGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGCCG  
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCAGGTGCGGAGAAGCC  
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA  
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCGAGCAAAAGAAGCGGTGGTGGTGGGCGTCG  
TGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCCGCGAGCGCG  
AGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA  
ACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC  
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC  
TGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC  
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA  
TGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCAAATTCAAAGAAT  
CAGTGTGTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC  
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA  
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC  
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT  
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA  
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA  
CCCCAAAGTTCAAATTTGTGAGTGACATTTACCAAACAAACAGGCAGAGTTCCTATTCTATC  
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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**FIGURE 280**

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVRVKLFGSKKRRRRRPE  
PQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLPVGLRVVAIQGVQTKLYLAMN  
SEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVKKNK  
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

**Important Features:****N-glycosylation site:**

Amino acids 242-246

**Glycosaminoglycan attachment sites:**

Amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site:**

Amino acids 93-100

**N-myristoylation sites:**

Amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 231-239

**HBGF/FGF family proteins:**

Amino acids 78-94, 102-153

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**FIGURE 281**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA  
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA  
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCTCA  
TTTAGAGTGTAGCAAAGGAAAAAACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTGCCCC  
AGTAGGGGTGGGATGAGCGAATATTCCTCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG  
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG  
TCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA  
GGGAAAGGGGACGTTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA  
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG  
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG  
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG  
CGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGGCGCTGGCCAGTAGCCTGAT  
CCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGCGCAGCGGCGCGT  
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG  
ACTGTGCGGGGGGCGGCCCGCGCGGCCGGACCGCGGCCCGGAGCCTCAGCTCAAAGGCATCGT  
CACCAAATGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG  
CACCCCAGAGGATACCAGTCCCTTCACCCCTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT  
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG  
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT  
GTACGCCTCTGCTCTTACCGCCAGCGTCGTTCTGGCCGGGCTGGTACCTCGGCCTGGACAA  
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCCACTTTCTGCC  
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC  
TTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA  
GCCAGCCACCACCACAACCTGT

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## **FIGURE 282**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKLCQKQLLILLSKVRLCGGRPARPDRG  
PEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHYMA  
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK  
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

**Important features:**

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 54-60; 89-95; 131-137

**HBGF/FGF family signature:**

Amino acids 131-155

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**FIGURE 283**

**ATG**CCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG  
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGGCTCTGCAACGGC  
AACCTGGTGGATATCTTCTCCAAAGTGC GCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC  
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA  
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC  
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC  
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA  
TCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT  
AGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA  
ACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT  
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAGTGCG  
TCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAAC**ATAG**



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## **FIGURE 284**

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRLRR  
QDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLYIA  
MNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK  
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

**Important features:**

**N-glycosylation sites:**

Amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins:**

Amino acids 104-155, 171-198

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**FIGURE 285**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCAGGTTTTGCTTTGA  
TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCTT  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCCACTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC  
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCGTGAGTGAGCTCTCACCCCACTCAGCCAAATGAGCCTCTTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTGTAGAAGTTGAGGAACCCAGTGATGGAACATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
TCTGCATCCACTACAACATTGTCTATGCCACAATTACAGAAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACCAG  
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA  
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCT  
CAGTGTCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
GAGCTGTGCACTGCACTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT  
TCAAGGACCTTTTCATCTTCAGGATTACAGTGCATTCTGAAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
ACAGCTCTTTTGGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTAT  
TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC  
GATACGGCTTAGGGTAATGTGCTAGTACAGGAAAAAACTGTGCAAGTGAAGCCTGATTCCGTTGCCCTTGCTTAAC  
TCTAAAGCTCCATGTCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT  
ATGTAAACCAGAACATCTATGTACTACAAACCTGGTTTTTAAAAAGGAATATGTTGCTATGAATTAACTTGT  
GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAGAAGAGAACTACA  
TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG  
TTTCATTGTGTACATTTTATATTTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTCT  
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
TTCTCGTATGGTGTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
GACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA  
AAGTAGACATTAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTTGA AAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCACTAGGAACACATCCTATTTA  
TTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTATGTACA  
GAAGTATGTCTCTTAACCAAGTTCACCTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAATATTTTGTCTGT  
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTGAATCAAAAATGTATTGAATCATCAAATAAAGA  
ATGTGGCTATTTTGGGGAGAAAATTA AAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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**FIGURE 286**

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF  
PHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS  
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNA  
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLYSCTP  
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT  
GVRGLHKSLTDVALEHHEECDVCVRGSTGG

**Important features:****signal sequence:**

Amino acids 1-14

**N-glycosylation sites:**

Amino acids 25-29;55-59;254-258

**N-myristoylation sites:**

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

**Amidation site:**

Amino acids 229-233

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**FIGURE 287**

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC  
CGCTCGGCCTGGCCAGGCCCCGCGCTATGGAGTTCCTCTGGGCCCCTCTCTTGGGTCTGTGCT  
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA  
ATGAGGACTACACCATACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG  
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG  
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG  
CCAAGCATGGCCCCGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCCTGGGCA  
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC  
GCTGCTTGAGGTTGAAGGTGACTGTCACTGAGTGGCAAAATCACTCACAGTCCTCAGGCCCATGACA  
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC  
ACAGTGCTGCCCCACGCCTCTTCCCACCTTGCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC  
TGCAAACCCCGTGAAGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA  
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCAGCCCTGGGAACCACTCCCAC  
CACAGGCATAAGCTATCACCTAGCAGCCTCAAAACGGGTCAATATTAAGGTTTTCAACCGGAA  
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG  
GAGACAGTCCTTTCCCACCATTCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC  
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA  
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG  
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG  
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTGTAGCCAGGTACTGCATTCTCTCCCAT  
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG  
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC  
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCCTGATTTCTACAACCTGGAGTTTT  
TTTATACAATGTTCTTTGTCTCAAAATAAAGCAATGTGTTTTTTCGG

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## **FIGURE 288**

MEFLWAPLLGLCCSLAAADRHTVEWNSSNPKERNEDYTIHVQLNDYVDIICPHYEDHSADAAM  
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFITLGKEFKEGHSYY  
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPPQEKRLAADDPEVRVLHSIGHSAAPRLFPL  
AWTVLLLPLLLLQTP

**Important features:**

**Signal sequence:**

Amino acids 1-17

**N-glycosylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 118-127

**N-myristoylation site:**

Amino acids 10-16

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**FIGURE 289**

CGGACGCGTGCGGCGGACGCGTGCGGCGGCCACGGCGCCCGCGGGCTGGGGCGGGTCGCTTCTTC  
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCCGAAGGGC  
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGGCTC  
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG  
GGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAGGTGGA  
AACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG  
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG  
GAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCCGGACCTCTTCCAGTGGCTG  
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCCCTCGCCTTCCCTGT  
CCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCACTGTGAAGGAGAAGGGACACGAGGG  
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT  
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT  
GCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGCCCTGCAT  
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACTGTGGAGCTGACCAA  
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC  
ATGGGGGCAGGGCCAGGTGCTGTAAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG  
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAGCAGTGTGAAAAC  
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG  
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG  
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC  
TTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTCAGAG  
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCTGTAGGA  
CCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC  
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC  
AGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT  
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTTCCTTAATGGTG  
GCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG  
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCACATCCCCACACCCCA  
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGGAAGTTAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT  
IRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLESEELVESWWFHKQQE  
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQCAGYGG  
EACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTE  
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP  
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVV LQQMFFGIIICAL  
ATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Important features:****Signal sequence:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 342-392

**N-glycosylation sites:**

Amino acids 79-83;205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 290-294

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 321-333

**EGF-like domain cysteine pattern signature:**

Amino acids 181-193

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**FIGURE 291**

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC  
GCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGCGCGGGCTGCCCC  
GGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTTCCAGGCACCCTGTCTGGGGCAGGGAGGGCACAGGCCTGC  
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCCCTCGCCCCAGCATCCAAGTCCCTTGGGCGCCCGTGCCCTG  
CAGACTCTCAGGGCTAAGGTCCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGAAGAGTAGC  
TTGAAGGAGGCACCAATGCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCTGGCTCAGGCCTGCCCTG  
AGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC  
CTGGCTTCCCGGCAATGTGACTACACTGAGCCTGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCCTTCA  
GGGAGGTGCCCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGAGCCCTGGCCT  
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTGCCTGGAGCGACCTGCACAACC  
TCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGCAGCCTTCCGCAGCCTCC  
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGCACACATTGGCCGAGGGCACCTTCACCCGCTCACCG  
CGCTGTCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGAGATGGGCCC  
TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGTTACACCGC  
TGAGCCGCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGCCG  
AGCTGCGGCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCGGCCCTCAGCTTCACTGGCACA  
TCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAACGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCC  
CTGTGGCCAGCTCCCAGCCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCGACTTTGGCAAGCTGG  
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGGCAGTGCTGAGAGCTCAGTGGACGTGGCACTGGCCA  
CGCCCGGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAGGGCTGCTATA  
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC  
CTGAGGCTGCAGTCGAGAAGGGTCCCTGGGCAGCTGCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC  
TCTTCTTCTTCCCTCACCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCTACCAATGCCCC  
TTTAAGTGCTGCAGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC  
TTCTAATCTCTCTAGAGCACCTGTATCCCCAACTTCTAGACCTGCTCCAACTAGTGAAGTACTAGGATAGAATTG  
ATCCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTGCCTGTGCTCTCCTCTCAGGGGCAGCATG  
CTAACGGGGCGACGTCCTAATCCAAGTGGGAGAAGCCTCAGTGGTGGAAATCCAGGCACTGTGACTGTCAAGCTG  
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG  
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCTGCTCAAGCTCCTCCTGCTCCTTG  
CTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG  
CCTTCTTCTCTTACCCTTCTCCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTCCTTTCTCCCCAACT  
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATG  
CCAAAAAAGGGCGCCGCGACTCTAGAGTCGACCT



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**FIGURE 292**

MQELHLLWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPANVTTLSSLNRLP  
GLPEGAFREVPPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLNLSLISDFAWSDLHNLSALQL  
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTCGIV  
WLKTWALTTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV  
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLIP  
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP  
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLLFFFLTSE

**Important features:****Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 403-418

**N-glycosylation sites:**

Amino acids 51-55, 120-124, 309-313

**Tyrosine kinase phosphorylation site:**

amino acids 319-326

**N-myristoylation sites:**amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,  
350-356, 394-400**Amidation site:**

amino acids 355-359

**Leucine Rich Repeat:**

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

**Leucine rich repeat C-terminal domain:**

amino acids 180-230

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**FIGURE 293**

ACTTGGAGCAAGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCCAGGCGCCGCGGCTGCAGCCTTGCCCCCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCGCTGATCCTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGAGCGGTACGCTGGGAGGTCCATCT  
CTAGGGGCGAGACACGCTCGGACCCACCCGACAGCGGCCCTTCTGGAGAGTTCTGTGAGAACAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTGCAATTCTTGACATTGGTCTGATGTCAACCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTCTAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTACGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTCCCTCAGAAAACACCGGATGTGAAC  
ATGAGTGTGTAATGCTGATGGCTCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
CGTGACAAGGATCACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGGTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCTGTGAGTGTCTGAGGGACACGTGCTCCGACGCGATGGGAAGACGTGTG  
CAAAATTTGACTCTTGCTCTGGGGACCAACGGTTGTGAACATTCTGTGTGAAGCAGTGAAGATTCGTTTGTGT  
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCCAACACATTTGTGTTA  
ATAATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTG  
TGAAGCAGTTTGTCACTGGAATTATAGATTTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCCGACGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACACAGAGATTGCCTCTGAGCCACAAACAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG  
ATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCCAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCAACATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAGCTCAGGCTATTGTAAATCAATAATGTTGTGAAGTAAACAATCAGTACTGA  
GAAACCTGGTTTGGCAGAACAAAGACAAGAAGTATACCTAATTTGTATAAATTTATCTAGGAAAAAATCCT  
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AACTTGCTTCTGCCTCATCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAATTCACCACCTCAG

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**FIGURE 294**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIID  
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAVKR  
MRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI  
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF  
CINIPGSYVCRCKQGYILNSDQTTTCRIQDLAMEDHNCQQLCVNVPGSFVCQCYSGYALAEDG  
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGEHECVN  
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTC  
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCEHSCVSSD  
SFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRK  
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF  
EVLKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT  
GLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA  
IEEELQEIASPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS PAGELPKTVQQPT  
ESEPVITINIQDLLSCSNFAVQHRYLFEEFNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM  
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation site:**

Amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 115-119; 606-610; 892-896

**N-myristoylation sites:**Amino acids 133-139; 258-264; 299-305; 340-346; 453-459; 494-500;  
639-645; 690-694;  
752-758; 792-798**Amidation sites:**

Amino acids 314-318; 560-564; 601-605

**Aspartic acid and asparagine hydroxylation sites:**Amino acids 253-265; 294-306; 335-347; 376-388; 417-429;  
458-470; 540-552; 581-593

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**FIGURE 295**

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC  
CATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCCG  
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA  
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAA  
GACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCTGGAGGGGCTGTGCGA  
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG  
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT  
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC  
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCCTGCCGGTG  
CCACATGGGGTACCAGGGCCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG  
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC  
CAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT  
GGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG  
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA  
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG  
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTA  
CGTCTGTGTGTCTCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC  
TGAAGCCACAGAAGGAGAAAGCCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGG  
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCT  
CCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC  
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGT  
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAA

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**FIGURE 296**

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFEGGNTAWEEK  
TLSEYSESEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKV  
CCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR  
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPFPCSAQFCKNANG  
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY  
VCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

**Important features:****Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 190-194;251-255

**Glycosaminoglycan attachment sites:**

Amino acids 149-153;155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 303-310

**N-myristoylation sites:**Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;  
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

**EGF-like domain cysteine pattern signature:**

Amino acids 166-178

**Leucine zipper pattern:**

Amino acids 94-116

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**FIGURE 297**

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAGGAAG  
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCATCATGCTGCTATTCTGCAAATACTGA  
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC  
CACCTTCAAAAAGTACATCAATATTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT  
TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCATATGGCATTTCATCATTT  
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC  
CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA  
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT  
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTTCCAGCCA  
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAGACTTTC  
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAGATGC  
CTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGAACCTGCCTGAAAAATGTCTGTCCGAAGTGA  
ACTTACAAGAACTCTATATTAATCACAACCTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC  
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG  
AGATTCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCAATCTTCGCA  
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACCTAGAAAGCA  
TCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGG  
ATCTAAATAAAAATCCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGA  
TAAATAATATGCCTGAGCTGATTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG  
CTACTAACAACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGACTCCCAAGCTGGAATCACTCATGC  
TGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATAC  
ACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTGGATGAACATGAACAAAACCAACATTCGATTTCATGGAGC  
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTCGAAGTCAGAATGTTCCGCAAGTGCATTTTCAGGGACATGA  
TGGAAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCCCTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT  
CCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTTTGC  
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTAGATATAAATGGCGTAACTCCCAAAGAAG  
GGGTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT  
CTTTCCACAAGATAACAATGGCTCTTTGAATATTAATAAGAGATATTCAGGCCAATTCAGTTTGGTGTCTCT  
GGAAAGCAAGTTCTAAAATTTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCATGCTG  
CGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA  
TTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAGGTTTGCACC  
CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG  
GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACT  
TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAAAGAAAAA  
GTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCTAAAAACCACCAAGGAAACCTA  
CTCCAAAATGAAC

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**FIGURE 298**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF  
PARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN  
KLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDALPN  
LEILMIGENPIIRIKOMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP  
HVALQKVVLNLFDLNKNPINRIRRGDFSNNLHLKELGINNMPELISIDSLAVDNLPDLRKIE  
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNIRCDVIRW  
MNMNKTNIRFMEPDLSFCVDPPEFQGNVRQVHFRDMMEICPLIAPESFPSNLNVEAGSYVS  
FHCRTAEPPQPEIYWITPSGQKLLPNTLTDFYVHSEGLDINGVTPKEGGLYTCIATNLVGA  
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ  
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTLM  
ACLGGLLGIIGVICLISCLSPMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS  
LKVKATVIGLPTNMS

**Important features:****Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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**FIGURE 299**

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT  
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACCTCTGGGGACAGAGCG  
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT  
ACCATGGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCTTGCTGCCA  
GTCCTAGCCTTACTCTGCCACCACTGCCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA  
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT  
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT  
TCTTGCTTCCCATGTACAGTTTGTAATCAGATCAAAAACATAAAAAGTTCCTGCACCATGACC  
AGAGACACAGTGTGTCAAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCCCAGAGATGTGC  
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT  
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACA  
ATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG  
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCT  
GAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC  
AGCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA  
ATTGTGCTTCTGATTGTGTTTGTTGAAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG  
AAAGGTTCAAGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT  
CTGCTGTGTTCCCACAGACAGAAACGCCTGC



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**FIGURE 300**

MARIPKTLKEVVVIVAVLLPVLAYSATTAQQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHT  
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVQCCKEGTFRNENSPEMCR  
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT  
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI  
VLLIVFV

**Important features:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 240-259

**N-glycosylation site:**

Amino acids 77-81;140-144;156-160

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 126-130

**N-myristoylation sites:**

Amino acids 56-62;72-78;114-120;154-160;233-239

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**FIGURE 301**

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT  
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAAGAGACA  
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT  
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAACTAAAGCAAATTGAACAGG  
AAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC  
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT  
GATTACCAAACAGGATTCCCATTTTCGTCAAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT  
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT  
AATCGCAAACCTCAAGACTATCCCAAATATTCCGATGCACATTCAGCAACTCTACCTTCAGTTC  
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC  
CTCAGCCACAACAAAATTAAATCTCAAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT  
CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTTCTCTAAATCT  
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAACTGCAGACAAATGCTATGGATGGG  
CTAGTAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC  
AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA  
ATGCCTCCTGGTTTGCCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT  
ATACCCGAAAAATACTTCGACAAACTTCCAAAACCTTCATACTCTAAGAATGTCACACAACAAA  
CTACAAGACATCCCATATAATATTTTTAATCTTCCCAACATTGTAGAACTCAGTGTTGGACAC  
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAAATAAT  
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT  
TTAACATACATTTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATAACATCTTCTTC  
TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA  
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT  
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT  
TATTATGAAAATCAAGAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA  
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA  
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG  
AACTTACTCAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA  
ATTAACGTTAATGGTTTCTTATGCTCTTTTTAAATATAGAAATATCATGTTAAAGAAAAAA  
AAAAAA

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**FIGURE 302**

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDDYDQEPDDDYQTGFPPFRQNVVDYGVPPFHQYTLGCV  
SECFCPTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK  
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPPLPKSLERLLLGYNEISKLQTNAMDGLVNLT  
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSSIPIPEKY  
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEIKM  
NLTVMCPSIDPLHYHHLTYIRVDQNKLEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ  
VFRFPDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

**Important features:****N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

**Tyrosine kinase phosphorylation sites:**

Amino acids 268-275;300-307

**N-myristoylation site:**

Amino acids 230-236

**Leucine zipper patterns:**

Amino acids 146-168;217-239

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**FIGURE 303**

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC  
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA  
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT  
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT  
ACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT  
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT  
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGGACCTCCA  
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA  
AGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA  
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG  
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG  
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA  
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT  
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCCGAGACA  
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG  
CACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAAGTAGTTTGCATTGCA  
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTTCAGTTT  
TTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACATAAATAATTTGAGTTTAG  
GTGATCCAACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT  
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAAGCAAATAAAAG  
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAACA

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**FIGURE 304**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDLP  
PETVLLYLDSNQITSIPNEIFKDLHQLRVNL SKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ  
SVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF LNAA  
NDADLCNLPKKTTDYAMLVTFMGWETMVISYVVYYVRQNQEDARRHLEYL KSLPSRQKKADEP  
DDISTVV

**Important features:****Signal sequence:**

Amino acids 1-33

**Transmembrane domain:**

Amino acids 204-219

**N-glycosylation sites:**

Amino acids 47-51;94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation sites:**

Amino acids 37-43;45-51;110-116

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**FIGURE 305**

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTCCACTTTGTTGAATTGTTCCCT  
ATACTCAAAATTCACCAAGACACCTTGCTCTCCCAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT  
ATTGCAACATGGGATTTTCAGGAAATGGTGTACAAATTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGT  
CCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA  
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG  
ATAATGTCTGTATAGCTGCAAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAAGAACCTGTGGCTTTGC  
TACAAGAAGTCTATAGAAATTTCTGTGACAGATCTTCCCAACAGATATAATTACATATATAGAAATATTAGCTG  
AATCATCTTCATTACTAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTG  
AATTTGTAAAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA  
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCCAAAAGA  
CCACAGAGTTTGATACAAATTCACGGATATAGCTCTCAAAGTTTCTTTTTGATTCTATATAACATGAAACATA  
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG  
GCAATGTTGCAGTTGCATTTTATATTATAAGAGTATTGGTCCTTTGCTTTCATCATCTGACAACCTCTTATTGA  
AACCTCAAAATTATGATAATTTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCACTCTCAATGAGCTCAA  
ACCCACCCACATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA  
GTCTATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT  
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTGCAATTTTGATGTCTCTGGTCCTT  
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG  
CCATATGCATTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCT  
GTAGCCTATTTCTTGCTGAACCTGTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA  
TTGCCGGACTGCTACACTACTTCTTTTAGCTGCTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCA  
TTGTTGTGGGTGTCTCTACAACAAGGGATTTTGCACAAGAATTTTATATCTTTGGCTATCTAAGCCAGCCG  
TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAA  
ACAACCTTATTATGGAGTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCATCA  
TATACAAAGTTTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAA  
GAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCCTGGATCTTTGGGGTTCTCCATGTTGTGCACGCATCAG  
TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCAATTTTTTATTCTGTGTGTTTTAT  
CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGGTAAACAT  
AGAGAATGGTGGATAATTACAACCTGCACAAAAATAAAATTCGAAGCTGTGGATGACCAATGTATAAAATGACT  
CATCAAAATATCCAATTATTAATACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACT  
GTAGATAATAAGGTAAATATGTATCATATAGATATACTATGTTTTCTATGTGAAATAGTTCTGTCAAAAAATA  
GTATTGCAGATATTGGAAGTAATTGGTTTCTCAGGAGTGATATCACTGCACCAAGGAAAGATTTTCTTTCTA  
ACACGAGAAGTATATGAATGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTTGAAACT  
AGTCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGAATATCAA  
CAGTGAAAAGGGAATGATAAGATGTATTTGAATGAACGTTTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT  
AAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACCTTAAATGTCCACTAAAACAACCTT  
AGACTTCTGTTTGCTAAATCTGTTCTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGA  
AA

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**FIGURE 306**

MKRLPLLVVFTLLNCSYTNCTKTCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC  
TTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS  
VTDLSPTDIITYIEILAESSLLGYKNNTISAKDTLSNSTLTFVKTVNNFVQRDTFVVDKLSVNHRRTHTKL  
MHTVEQATLRISQSFOKTEFDTNSTDIALKVFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAF  
YYKSIGPLLSSSDNFKLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY  
SPDTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW  
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGLLHYFFLAFAWMCIEGIIHLYLIVVGVYIN  
KGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGTTKVCWLSTENNFWSFIGPACLIILVNLLAFGVIIYKVRHT  
AGLKPEVSCFENIRSCARGALALLFLGTTWIFGVLHVHVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEY  
YRLFKNVPCCFGCLR

**Important features:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 431-450; 494-515; 573-594; 619-636; 646-664

**N-glycosylation sites:**Amino acids 15-19; 21-25; 64-68; 74-78; 127-131; 177-181;  
188-192; 249-253; 381-385; 395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 360-364

**Tyrosine kinase phosphorylation sites:**

Amino acids 36-44; 670-677

**N-myristoylation sites:**Amino acids 38-44; 50-56; 52-58; 80-86; 382-388; 388-394;  
434-440; 480-486; 521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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**FIGURE 307**

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT  
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGC  
CCGGAGGAGCGCCTTCCTGCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA  
GGCCGGGCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA  
AGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAGAAT  
GCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA  
ATTCTGTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT  
GCCTCACAGGCATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGCAACACCATTTCTCAAACACCTCAAATGCTATCTTCTTTAAACATG  
TCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTGA  
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC  
TGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAA  
TGGAGGAGCCTGTTTCTACCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA  
ATGCCCCAACCCCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG  
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAAATGCCA  
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC  
AGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGGCGGATCCACCTGAATCCAATTA  
CATCTGGTGAAGTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGT  
GAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC  
TGATATTTACTCTTCCTTTTAAGTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCTTGTTCAGTGCT  
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAATTTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT  
TACAATGCATTTATGGTGTCTGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAA  
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTTCAGATTTTATTGTCAGATATTTAGATGTTGTTAC  
ATTTTAAAAAATGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA  
GTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAAACAATATAATATATTCTAAACACAATGAAATAG  
GGAATATAATGTATGAAGTTTTGCAATTGGCTTGAAGCAATATAATATATTGTAACAAAACACAGCTCTTACCT  
AATAAACATTTTATACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTGGAAAAAATAAAAAA  
AAAAAA



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**FIGURE 308**

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGKM  
APFTHDFRKAQQRMPAIPVNIHSMNETWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLLGT  
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG  
GFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN  
GGTCFYPPGKCICPPGLEGEQCEISKCPQPCRNGGKICIGKSKCKCSKGYQGDLCSKPVCEPGCG  
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDPPESNYIW

**Important features:****Signal sequence:**

Amino acids 1-28

**N-glycosylation sites:**

Amino acids 88-92;245-249

**Tyrosine kinase phosphorylation site:**

Amino acids 370-378

**N-myristoylation sites:**

Amino acids 184-190;185-191;189-195;315-321

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 285-293

**EGF-like domain cysteine pattern signatures:**

Amino acids 198-210;230-242;262-274;294-306;326-338

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**FIGURE 309**

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGCGGCAGCAGAGGTCGCGCACAGATGCGGG  
TTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT  
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATGGAG  
ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG  
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTCGATG  
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG  
TTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTCCCAAGACGGATTCAAGCTGAAGGGCGCTA  
CAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCCTAGGCTGGATCCCAAGTGATAATTCCA  
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATAACAAGACAT  
ATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGGTACCCCGACC  
TACACAATATGGTTTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG  
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT  
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAACTTGATGGGTCTGCGT  
ATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTGCCTTGCTCTGGAAG  
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT  
GTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCTGGCTACAGCCTCACCA  
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTCTTATCAAGTCTACTGCA  
TCAAATCAGAGCAAACGTGGCCCGAGCACCCATGAGACCCCTCCTGACCACGTGGAAGATTGTGG  
CGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA  
CCAAGTTCAAGGCCCCACTTTCCCCCAGGGGGCCTCCCCGGAGTTCAGCAGTGACCCTGACT  
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATGACGAAGCTGTGAGTGGCGGCT  
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCTTACCCGTGGACG  
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGCCCAGGGGAGTCAGAAA  
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGTCCAAAGTCTGTATTACCTCCCAGGTGCC  
AAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG  
CATCCACCAGCCCAGGCATCCATCATGCCCACCTGGGTGTTGTTCCCTAAGAACTGATTGATTA  
AAAAATTTCCCAAAGTGCCTGAAGTGTCTTCAATACATGTTGATCTGTGGAGTTGATTCT  
CTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAAATTGCTATGCTG  
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCCTGTTTCTTCTTGACACAGACTGATTAAA  
AATTAAAAGNAAAAA

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**FIGURE 310**

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGEDDLQVCADPGIP  
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ  
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG  
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS  
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH  
ETLLTTWKIVAFTATSULLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML  
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDSVSGSSEL  
LQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFRLN

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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**FIGURE 311**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG  
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG  
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCGAGGCCGCGAGGCCCCAGCTCAGGCT  
CGTGCCCACCCACCAAGTTCCAGTGCCCGCACCAGTGGCTTATGCGTGCCCTCACCTGGCGCT  
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA  
CCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCAGTGACT  
GCTCTGGGGGAAGTACAAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC  
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT  
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA  
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG  
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG  
ACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC  
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG  
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCCCTGAG  
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA  
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC  
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA  
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC  
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA  
TTAAAGTTGCTTC

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**FIGURE 312**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT  
SGLCVPLTWRCDRDLDCSDGSDEEEECRIEPC TQKGQC PPPGLPCPCTGVSDCSGGTDKKLRN  
CSRLACLAGE LRCTLSDDCIPLTWRC DGHPCDSSDELGCGTNEILPEGDATTMGPPVTLES  
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW  
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Important features:****Signal sequence:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 231-248

**N-glycosylation sites:**

Amino acids 126-130;195-199;213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation sites:**Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;  
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

**Leucine zipper pattern:**

Amino acids 17-39

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**FIGURE 313**

CGGACGCGTGGGCGTCCGGCGGTTCGACAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGGCCCCAGCCCACAC  
CTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC  
TTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGAC  
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCGGTGCCGACGACTGTGCCCTGCCCTACCTG  
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC  
CTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG  
TACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC  
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATTCAGGGCAT  
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCC  
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAG  
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA  
CATGACGCCTGTCTGTGCGCCCGAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG  
TCTCGATGGTGCCTGGTGGTTCTGCGTCGCGGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA  
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCAC  
TGCCCACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA  
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT  
CCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC  
CCTCTAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC  
CAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGCGTCAATGAGTGCGACATCGA  
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTGCGGGCACCACGC  
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATGGGGCGGTGACCCAGCCTCGCCCGA  
CAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGCGCGGGTTCGCTGACGCAGCGCCCCGCCTGGG  
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG  
CACAGCTGCAGATCCCAAGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC  
CAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAG  
TGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCTCCACCTCAGCCTCTCAAG  
TAGCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGT  
TGCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGG  
CATGAGCCACTGCACCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAA  
CCAAAGTATTGATAAAAAAAAAA

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## **FIGURE 314**

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADDCA  
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT  
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**Important features:**

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

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**FIGURE 315**

CGGACGCGTGGGCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT  
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCCAGGAC  
CCAGGGAAGTGAAGCCAGCAAAGTTGTCCTCCTGCCCAGTTGTCCCGGAGCTCCAGGAAGTC  
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA  
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT  
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG  
GGGGCGGCTGGCTGGTGTTCAGAGGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT  
CCTCCTACAGAGCAGGTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC  
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC  
GTACTTTTCGCCCCTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC  
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTTA  
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT  
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG  
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC  
GGATGATGCTTCGATTAGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG  
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT  
CATTTTAGCCCTTTCA



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## **FIGURE 316**

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVVLLPSCPGAPGSPGEKGAPGPQG  
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCMDTEGGGWLVFQRRQ  
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDENGNRTEFAHYATFRL  
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL  
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMLR

**Important features:**

**Signal peptide:**

Amino acids 1-16

**N-glycosylation site:**

Amino acids 178-182

**Glycosaminoglycan attachment site:**

Amino acids 272-276

**Tyrosine kinase phosphorylation site:**

Amino acids 188-197

**N-myristoylation sites:**

Amino acids 16-22;89-95;144-150;267-273

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 242-255

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**FIGURE 317**

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCCAACCCAGGAT  
GCTCCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT  
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA  
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCCTGAGGC  
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGGCTACTTGTGCCTGCCCCGCTCCGC  
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC  
CAACCCCTGCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG  
TGCCCAAGGCCCTGCACGACTGTGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA  
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGGCG  
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCAGGCC  
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC  
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCTGTGTCGCTGCCACCAGGGCTA  
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT  
CTGTGCTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCCACAGGGTTACCA  
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAGTGCTC  
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT  
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCCGCCTCCAACCTCTATGTCG  
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCCG  
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG  
TGCTGGAAACTCGCAGGGGGGACTTTTACATTAGGCAAATCAACAACGTCAGCGCCATGCTGGT  
CCTCGCCCCGGCGGTGACGGGGCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA  
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCTACAC  
CTTCTGAGGAGCAGGAGGGAGCCACCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA  
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCCTGGTGGCTGAGGTGGGCGGGTC  
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTCACCTA  
AATGGGGGTCTCTATATGTTTACGGCCAGGGGCCCCCATTGACAGGAGCTGGGAGCTCTGCAC  
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCGGC  
CCAGAGATTTGGACTTGGCTGGCTTGCAGGGGTCTAAGAACTCCACTCTGGACAGCGCCAG  
GAGGCCCTGGGTTCCATTCTAACTCTGCCTCAAACGTACATTTGGATAAGCCCTAGTAGTT  
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAA

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**FIGURE 318**

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSSQHCRDVNECLTIPE  
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPPVPPAQHPNPPPGYEPDDQDSCVDVDE  
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE  
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSY  
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCSAQTCVNFHGGYRCVDTNRC  
VEPYIQVSENRCPCASNPLCREQPSSIVHRYMTITERSVPADVFIQIQATSVYPGAYNAFQI  
RAGNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF

**Important features:****Signal sequence:**

Amino acids 1-25

**N-glycosylation sites:**

Amino acids 198-202;394-398

**N-myristoylation sites:**Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;  
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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**FIGURE 319**

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC  
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCCTGGCCACCTCCCCGATGC  
CCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG  
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCCGGG  
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG  
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC  
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCAGCTGGGAC  
TGCCCCACCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA  
GGAGGGGGACTGGGGACCCAGCCCCCTTCCAGCCCAAGGACCCAGTTTTCTGGCCTTGTCTCT  
TCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCTGCTCGACCACC  
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG  
CGCCGCCTGTGCCTGTCCAGGCCCTGCCACCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC  
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC  
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCAGGCCCTTGGCTGCAGGCAACACTTTAGC  
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTA  
TGGCAGAGGTGCAAGACCTAGTCCCCCTTCCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT  
GTCCAGGGTCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG  
CGAGCTTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC  
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG  
AGATTCTGGATCTCCTGCTGCCTTTTTCTGGAGTTTGTAAAATTGTTCTGAATACAAGCCTAT  
GCGTGA

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## **FIGURE 320**

MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVLDGCGCCRCVCARRLGEP  
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEG  
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSLP  
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRCLLSRPCPPSRGRSPQNSAF

**Important features:**

Signal sequence:

Amino acids 1-23

**N-myristoylation sites:**

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;

167-173;183-189;209-215

**Insulin-like growth factor binding proteins signature:**

Amino acids 49-65

**von Willebrand C1 domain:**

Amino acids 107-124

**Thrombospondin 1 Homology Block:**

Amino acids 201-216

**IGF binding protein site:**

Amino acids 49-58

**FIGURE 321**

[illegible]

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## **FIGURE 322**

MMGLSLASAVLLASLLSLHLGTATRGSDISKTC CFQYSHKPLPWTWVRSYEFTSNSCSQRAVI  
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 3-9, 26-32

**Amidation site.**

amino acids 68-72

**Small cytokines (intecrine/chemokine).**

amino acids 23-88

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**FIGURE 323**

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA  
TGCCAGCCCCCTCCTGGCTGCTGGCAGCCCATCCTCCTGCTGGTGTGGGCTCAGTGCTGTCAAGGCTCGGCCA  
CGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG  
TCCCCGAGGGCATCCCCACCGAGACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG  
AGTTCGCCAGCTTCCCGACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT  
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA  
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAGG  
ACCTGTACAACCTCAAGTCACTGGAGGTGGCGACAATGACCTCGTCTACATCTCTCACC CGCCTTCAGCGGCC  
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC  
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC  
GACTCAAGGTCTTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAATGCCTCTACGGCCTCAACC  
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC  
GCTTCCTCAACCTCTCCTACAACCCCATCAGCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG  
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCCTCAACTACCTGCGCGTGC  
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACTCA  
TCCTGGACTCCAACCGCTGGCCTGCGACTGTGGCTCCTGTGGGTGTTCCGGCGCCGCTGGCGGCTCAACTTCA  
ACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC  
TGCCCAACTACTTCACTGCGCGCGCGCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCC  
ACACGGTGCAGTTTGTGTGCCGGGCCGATGGCGACCCGCGCCGCCATCCTCTGGCTCTACCCCGAAAGCACC  
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGGTGCGCTACGCCAGGTAC  
AGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGACTCCATGCCCGCCACCTGCATGTGC  
GCAGCTACTCGCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAG  
AGGCCAACAGCACCCGCGCCACTGTGCCTTTCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCT  
TCATCTCTTTCCTGGGCGTCTCCTCTTCTGCCTGGTGTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA  
AGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGAGGCATCAGCTCCGCGACGCGCCCCGCAAGT  
TCAACATGAAGATGATAAGAGCCGGGGCGGGGGCAGGGACCCCGGGCGGCCGGGAGGGGAAGGGGCCTGGT  
CGCCACCTGCTCACTCTCCAGTCTTCCACCTCCTCCCTACCCTTCTACACACGTTCTCTTCTCCCTCCCGCC  
TCCGTCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACCTGG  
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT  
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTTGGGTTTCAATAATTATGGATTTTATGAAAACCTGAAATAA  
TAAAAAGAGAAAAAACTAAAAA



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**FIGURE 324**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL  
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRITGLRSNRLKLIPLGVFTGLSNLTQDI  
SENKIVILLDYMFDQLYNLKSLEVGDNDLVYISHRAFSGLSLEQLTEKCNLTSPTEALSHLHGLIVLRRLRHL  
NINAIRDYSFKRLYRLKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS  
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGVGNLETILDSNPLACDC  
RLWVFRRRWRLNFNRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG  
DPPFPAWLWSPRKHLVSAKSNGRITVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPAHLLHVRSYSPDWP HQP  
NKTFAFISNQPGEGEANSTRATVFPFDIKTLIIATMTMGFISFLGVVLFCLVLLFLWSRGKNTKHNIEIEYVPR  
KSDAGISSADAPRKFNMKMI .

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,  
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,  
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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**FIGURE 325**

CCCACGCGTCCGCCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG  
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG  
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG  
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG  
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG  
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC  
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT  
TGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCCTGGAGGGAC  
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGAGGGCGTTGGGCAGGGGTCC  
CTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGCGCTGGTACTC  
TGGGCTGCACTGGGGGACAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC  
TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA  
GCGTGGAGTCTGTGTGCTGTGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT  
CTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC  
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT  
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC  
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC  
TTCAACCAGGAATCTACGGGAATTTACAGCGCTGCCTCCCGCGGCCCCAATGGCCTGGCCATT  
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCAGTCGCCTCCTTAACCGC  
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG  
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC  
TCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC  
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC  
CGGCCCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGGCAACAGGGACCCCCGGCACCCCGAG  
AGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGATGGTGTCCCCCATGGTCGCTTGAGAC  
TCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT  
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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**FIGURE 326**

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA  
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLTYNTGRHVSFLPAPRPVVNVSGGPPLY  
SHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN  
VASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW  
ILIDRALNITSLQMHSRLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP  
NYRLHVDGVPHGR

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 177-199

**N-glycosylation sites:**

Amino acids 118-122;170-174;260-264

**Eukaryotic-type carbonic anhydrases proteins:**

Amino acids 222-271;128-165;45-93

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**FIGURE 327**

GGACTAATCTGTGGGAGCAGTTTATTCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT  
TTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA  
GTAGTACATGGTGGATAAATTCTACTTTTAGGAGGACTACTCTTCTTGACAGTCTTAGACTGGTCTTCTACACT  
AAGACACCATGAAGGAGTATGTGCTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCAC  
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG  
ATGATGATGAGGACAACTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTCCATTTGATCTGTTTCCAA  
TGTGTCCATTTGGATGTCAGTGCTATTACAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA  
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG  
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCA  
CAAAGAAGTTGCGAAGGCTGTATCTGTCCACAATCACTAAGTGAAATACCCTTAATCTTCCCAAATCATTAG  
CAGAACTCAGAAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACAG  
TTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTCC  
ATATCAGAATTGCAGAAGCAAACCTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACCTAG  
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA  
ACAACAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA  
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCTTCATTCTAATTCAA  
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT  
TATTCAACAACCCGGTGAAATACCTGGGAAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTC  
AGCTTGGAACCTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT  
TTGGAATACTTGAACCTTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGTAAGTCC  
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATTGATACATAAGGGGTTGAGAGAAACA  
AGCATCTATTGCAGTTTCCTTTTGGCGTACAAATGATCTTACATAAATCTCATGCTTGACCATTCCCTTCTTCAT  
AACAAAAAAGTAAGATATTTCGGTATTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGG  
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA  
AGAGTGCATTACACTATTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA  
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAAACTAATTTCTTAAAA  
TAAAGCCTTCAGTAAATGTTCAATACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT  
GCTTTTTTTTTTTTAAATATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACT  
CGCATTTTAATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCACTTCAA  
CTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGACACTAACAATTCTACACC  
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATACTGAATAAGCAGAGCAT  
CAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGTATTTCTTATTGGCATTCAA  
CATATGTAAATCAGAAAACAGGGAATTTTCATTAATAAATATTGGTTTGAAAT

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**FIGURE 328**

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPRS  
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS  
LYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT  
FKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI  
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPPELKYLQI  
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

**Important features:****Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

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**FIGURE 329**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA  
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT  
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGTGTT  
CAGCATGCGCTTGTGGACCCCACTGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACCAGCG  
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT  
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC  
GCTGGAGGAGCAGGTAGAGTGGAACCCCACTATTAGAGGTCCCACCCCAAACCTCAGTTTGA  
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA  
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT  
GTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTCTTTCACCAAC  
CTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTTCGGAATCTGGAGTCCACCCG  
TTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGAGCCATCATCATCCACACTGATGA  
AGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG  
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAAGGTGAAGGA  
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC  
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA  
GAGAGCTGTGGACACATCCTTGACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC  
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC  
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT  
AATGACCCTGGGGATTTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC  
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT  
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA  
TACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA  
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATG

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**FIGURE 330**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVFRHGARSPLKPLPLEEQVE  
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA LGERLRKNYVEDIPFL  
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQ  
PGISED LKKVKDRMGIDSSDKVDFILLDNVAAEQAHNLPSCPMLKR FARMIEQRAVDTSLYILPKEDRESLQMA  
VGPFLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ  
LYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

**Important features:**

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

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**FIGURE 331**

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACATTTTCCCTTTCCCT  
AACAA GTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTTGCTGGAGAAGAAAGGGCTGAGGGCAG  
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT  
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA  
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG  
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGGTGAAC TTCAACAGCCT  
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAAATAAAATTTAA  
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCCCTAAGAGG  
GAGAAAGTATGTTAAAAATAGAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACC  
CTGGGTGAGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA  
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTC  
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTC  
TGGGTGCTGCTGGCCCCCCCCAGCAGCCGGCATGCCTCAGTT CAGCACCTTCCACTCTGAGAATCGTGACTGGACC  
TTCAACCACTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGTCTATAAGCTGACA  
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC  
GTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC  
CGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG  
GAGCCATCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGC  
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCC  
AGCCGGAAGCTGCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT  
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT  
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGACCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC  
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGC  
TGCACCCGGGCCGGGGTGAATACCGCTCCTGCAGGTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAG  
GCCTTCAATATCACAGCCAGGACGATGACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACACCCG  
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAATCAAGGAGCGCCTGCAGTCTGC  
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCC  
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCTG  
TACACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG  
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCCATTACCTCCTCAGCAAA  
GAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA  
AATGGGGAGGTAAGAAGGGGTAAATTTTGTGACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTAT  
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTAAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA



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**FIGURE 332**

MGTLGQASLFAPPGNYFWS DHSA LCF AESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR  
ALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRVYK  
LTGNLTIQVAHKTGPEEDNKSRYPP LIVQPCSEVLTLTNNVNKLLIIDYSENRL LACGS LYQG  
VCKLLRLDDL FILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDYFPTL  
SSRKLPRDP ESSAMLDYELHSDFVSS LIKIPSDTLALVSHFDIFYIYG FASGGFVYFLTVQPE  
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSL AQ  
AFNITSQDDVLF AIFSKGQKQYHHPPDDSALCAFP IRAINLQIKERLQSCYQGE GNLELNWLL  
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT  
KSGKLKKVRVYEFRC SNAIHL LSKE SLLEGSYWWRFNYRQLYFLGEQR

**Important features:****Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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**FIGURE 333**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG  
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTACGC  
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGAT  
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCA  
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTTCAGCTACGGCCAGACCAGCCTGGACAGGCT  
TAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG  
GGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC  
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT  
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT  
GGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA  
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC  
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG  
GGCCCTGGAAGTGTCACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAA  
CAGTGCTCGGAATGTTCTTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT  
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA  
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA  
TGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGA  
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCCCTTCGTGGAAACCTGCTGCG  
GGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGAGGACAA  
GTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA  
GAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGC  
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAGTTGTGGCCACCTT  
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC  
CACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT  
GGACATAG

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**FIGURE 334**

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGO  
TSLDRLRDGLVGAQFWSAYVPCQTQORDALRLTLEQIDLIRMCASYSELELVTSAKALNDTQ  
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF  
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK  
NGGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY  
PVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS  
RLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

**Important features:****N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157



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## **FIGURE 336**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW  
KKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV  
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS  
YTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVALVIS  
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

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**FIGURE 337**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGGCAGCCTCGG  
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA  
TGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG  
CCCTGCGGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG  
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTCATCCC  
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT  
TGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT  
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTACAGCTGCT  
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCTTAGAACTCA  
ATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA  
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC  
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC  
TCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCA  
CTGCCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG  
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCC  
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC  
TGCCCTGGCCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG  
CACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTC  
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAA  
TATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATTGATGACCCCACTCATTGGCTAAAG  
GATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG  
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA  
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC  
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT  
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT  
CTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG  
GTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTCTATTAAACTAACATGAAATATGTGTT  
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAA

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**FIGURE 338**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS  
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD SGPYSC  
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQWDR  
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAAVVAG  
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS  
ARALRPPHGP RP PGALTPTPSLSSQALPSRPLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPV  
MVPAQSQAQGLV

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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**FIGURE 339**

CGGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCTCTCT  
CCCTTCTCATGGGACTTTGGGGACAAAGCGTCCCGACCCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA  
GGACAGCGTCCGGGAACAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCGCGGTTTC  
TGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCACAGC  
AACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC  
CGTGCACAGAGGGTGTGGATTACACCATTTGCTTCCAACAATTTGCCTTCTTGCTGCTATGTACAGTTTGTAAAT  
CAGGTCAAACAAATAAAGTTCTGTACCAGCAGACAGACCCGTGTGTAGTGTGAAAAAGGAAGCTTCCAGG  
ATAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTCAAGTAAATGTA  
CGCCCCGGAGTGACATCAAGTCAAAAATGAATCAGCTGCCAGTTCCTGAGGAAAACCCAGCAGCGGAGGAGA  
CAGTGACCACCATCCTGGGGATGCTTGCTCTCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT  
TAGCTGTGGTTGTGGTTGGCTTTTCATGTCCGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG  
GAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGGCTTCATGTCTTCACGAGTTCCTGGGGCGGAGG  
ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGGTC  
AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCCGAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAG  
CTGAAGGGTGTGAGAGGAGGAGCTGCTGGTTCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTTGCTGG  
ATGCTCCTGGCAACACTGGAAGAGGACATGCAAAGGAAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT  
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTGTGAAGAATCTCTTCAGGAAACAGAGCTTCCCT  
CATTTACCTTTTCTCTACAAAGGGAAGCAGCCTCGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAAACT  
CTACTATCCAATATGGGGCAGCTTACCAATGGTCTTAGAATTTGTTAACGCACTTGAGTAATTTTTATGAAAT  
ACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGTATTAAGG  
GTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT  
GAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAACCTCCATCTCAATTTAAAAAGAAAAAGTGGTTT  
TAGGATGTCAATCTTTGCACTTCTTCATCATGAGACAAGTCTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT  
CTACTGGTGTGTGCAATTAATGACATCTAACTACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTA  
ACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTCAGTTTCGGATATTTTGACTTAATGATGAGATTATC  
AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTGAGCTTTAAGATA  
GGATTATTGGGGCTTACCCCACTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT  
TTCCGATTTTTGTATAATGATGTAACATGGAACAACTTTAGGAAATGCACTTATTAGGCTGTTTACATGGGTG  
CCTGGATACAAATCAGCAGTCAAAATGACTAAAAATATACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG  
AGGCACTTACTGCATTCAGTTCTCCCTCCTGCGCCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA  
AGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT  
ATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT  
GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG  
ATCCGAGACTGCCAAGAGCTTCTTTCAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTTGGG  
CTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGTCTGGG  
AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCTCTCGCTTCTGGTGGTCTGTGAACAGTGAATCCCT  
GGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTTAGGGTACAGATTCCCTGTTTGAAGGAGCTTGGCCCT  
CTGTAAGCATCTGACTCATCTCAGAGATATCAATCTTAAACACTGTGACAACGGGATCTAAATGGCTGACACA  
TTTGTCTTGTGTACGTTCCATTATTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCT  
TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTCTAGGGTTTCAGTCTTTTCCATCTC  
AAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTGGCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTGAG  
ATTGTTGTGTCCATGGAGTTTLAGGAGGGGATGGCTTCCGGTCTTCGCACTTCCATCTCTCCCACTTCCATC  
TGGCGTCCCAACCTTGTCCCTGCACTTCTGGATGACACAGGGTGTGCTGCTGCCTCCTAGTCTTTGCCTTTGCTG  
GGCTTCTGTGCAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCAGCTCCTTTGTCCCTTCTC  
AGAGGCCTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTTAAGCTTATTCCTTTAACATAAGCTTC  
CTGACAACATGAAATGTTGGGGTTTTTGGCGTTGGTTGATTTGTTTAGGTTTGGCTTTATACCCGGGCCAAAT  
AGCATATAACACCTGGTTATATATGAATACTCATATGTTTATGACCAAAATAAATATGAACCTCATRTTAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 340**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEV PQQTVA PQQR  
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKN  
SPEMCRTCRITGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVILAV  
VVVGFSCKRKKFISYLGICSGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQEL  
AELTGVTVESPEEPQRLLEQAEAGCQRRRLVPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE  
EDEAGSATSCIL

**Important features:****Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristoylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139

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**FIGURE 341**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG  
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCAGG  
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC  
AGAAGTCCAACCTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCGAGGCAGCAGCGA  
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGAATGTACTTC  
GCTTCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC  
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC  
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGTGGCTC  
TGTTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCTAAGCCAGGTAAAATGTTTG  
TGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG  
ATTGGAATGACAACCCCCGAAAAATTTCTGGGTATTTCCTGGAGATACTGGTCAAAGAAGATA  
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG  
CTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG  
CCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCAGCTATTCATTAACT  
TCCGGGACCTGGGTGGCACAAGTGGATCATTGCCCCAAGGGGTTCATGGCAAATTACTGCC  
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG  
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC  
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG  
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTTCTTAGGG  
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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**FIGURE 342**

MLRFLPDLAFSFLILALGQAVQFQYVFLQFLGLDKAPSPQKFQPVPIILKKIFQDREAAAT  
TGVSRLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ  
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRSPWPQGAVHFNLLDVAKD  
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRRAA  
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAFMQA  
LMHAVDPEIPQAVCIPTKLSPISMLYQDNNNDNVILRHYEDMVVDECGCG

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 112-116, 306-310

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

**N-myristoylation site.**

amino acids 77-83

**TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364

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**FIGURE 343**

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCATTCTTTTCATTGACAACTGACTTTTTTTATTCTCT  
TTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGTTGTGTGGGAGGGAGACCACGTGG  
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTCTGTCTTTACTTCAAAATACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTTCATGGAAAAAATACTCAGTGCCTGCTGCGGAACCCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACCACTCA  
CACAGCTGCTCTATCTCACACAAATCTACCCCTTGGCTGGCTGGAACAGCTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAGCTGTGCGTCTTAAGGTGCCAGCGCCTTGCCAAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCCATATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAACATTAAAGTCTTTGACGGAACTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTTGCTTCTACTACTTCTTCTCTCTAACATCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACTTGGGAAGGATCCTTACCAGGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC  
AAACAGTGCAATTTGATTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACTCTCTGACTGTGCTGTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACCTGCAGACCAAAATATCAAATGTTGTGGAATTTTCTGTCCCTCTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAATGCCTGGGCAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA  
TTTGAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACTCTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTTGTAAAGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAATGCCTTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTGTATATGTGAT  
AGCAGTGACCAACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTCTGTGAAAAGGGATCGAAGTGAAGTGGCAATTCAGGATTTTCAGCAT  
GAAACACATGCGGAAGAACTCCAACACGCTTTCAACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG  
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

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**FIGURE 344**

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE  
RPNKSIIRIIFSYVQLDPDGSCSENIKVFDTSSNGPLLQVCSKNDYVPVFESSSSTLTfq  
IVTDSARIQRTVFVFFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD  
YKIKLNFKEIFLEIDKQCKFDFLAIDGPSTNSGLIGQVCGRVTPTFESSNSLTVVVLTdYA  
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV  
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGHNSTVEIIYI  
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT  
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD  
SSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN  
SVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Important features:****Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 345**

TGGGGGCCCCCAGGCTCGCGCGTGGAGCGAAGCAGCATGCGGCAGTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC  
GGCCTTGCTGTGTGCTAGGCTCTGGAGCTCTGGGGTGTTCGAACTGAAGCTGCAGGAGTTCTGCAACAAGAAGGGGCT  
GCTGGGGAACCGCAATTGCTGCCGCGGGGGCGGGGCCACCGCGTGCGCCTGCCGGACCTTCTTCCGCGTGTG  
CCTCAAGCACTACCAGGCCAGCGTGTCCCCGAGCCGCCCTGCACCTACGGCAGCGCCGTACCCCCGTGCTGGG  
CGTCGACTCCTTCAGTCTGCCCCAGCGCGGGGGCGCCGACTCCGCGTTCAGCAACCCCATCCGCTTCCCCTTCGG  
CTTCACCTGGCCGGGCACCTTCTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTCGCAACAGA  
AAACCCAGAAAGACTCATCAGCCGCCTGGCCACCCAGAGGCACCTGACGGTGGGCGAGGAGTGGTCCCAGGACCT  
GCACAGCAGCGGCCGCACGGACCTCAAGTACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGGGCTG  
CTCCGTTTTCTGCCGTCCCCGGGACGATGCCTTCCGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA  
CCCTGGCTGGAAAGGGCCCTACTGCACAGAGCCGATCTGCCTGCCTGGATGTGATGAGCAGCATGGATTTTGTGA  
CAAACCCAGGGGAATGCAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG  
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGCAACTGCCAGGAAGGCTGGGGGGGCTTTTGTCAACCAGGA  
CCTGAACTACTGCACACACCATAAGCCCTGCAAGAATGGAGCCACCTGCACCAACACGGGCCAGGGGAGCTACAC  
TTGCTCTTGCCGGCCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTAA  
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGCTACTCCTGTACCTGCCACCCGGCTTCTACGGCAAAATCTG  
TGAATTGAGTGCCATGACCTGTGCGGACGGCCCTTGCCTTAAACGGGGTGGTGTCTCAGACAGCCCCGATGGAGG  
GTACAGCTGCCGCTGCCCCGTGGGCTACTCCGGCTTCAACTGTGAGAAGAAATGACTACTGCAGCTTTCACC  
CTGTTCTAATGGTGCCAAGTGTGTGACCTCGGTGATGCCTACCTGTGCCGCTGCCAGGCCGGCTTCTCGGGGAG  
GCACTGTGACGACAACGTGGACGACTGCGCCTCCTCCCCGTGCCCAACGGGGGCACCTGCCGGGATGGCGTGAA  
CGACTTCTCCTGCACCTGCCCGCCTGGCTACACGGGCAGGAAGTGCAGTGCCCCCGTCAGCAGGTGCCAGCACGC  
ACCTGCCACAATGGGGCCACCTGCCACGAGAGGGGCCACCGCTATGTGTGCGAGTGTGCCCGAGGCTACGGGGG  
TCCCAACTGCCAGTTCCTGCTCCCCGAGCTGCCCCGGGGCCAGCGGTGGTGGACCTCACTGAGAAGCTAGAGGG  
CCAGGGCGGGCCATTCCCCTGGGTGGCCGTGTGCGCGGGGTCACTCCTTGTCTCATGCTGCTGCTGGGCTGTGC  
CGCTGTGGTGGTCTGCGTCCGGCTGAGGCTGCAGAAGCACCGGCCCCAGCCGACCCCTGCCGGGGGGAGACGGA  
GACCATGAACAACCTGGCCAATGCCAGCGTGAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA  
GAACACCAACAAGAAGGCGGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCGCTACCCAGC  
GGTGGACTATAACCTCGTGACGACCTCAAGGGTGACGACACCGCCGTGAGGGACGCGCACAGCAAGCGTGACAC  
CAAGTGCCAGCCCCAGGGCTCCTCAGGGGAGGAGAAGGGGACCCCGACCACACTCAGGGGTGGAGAAGCATCTGA  
AAGAAAAGGCCGGACTCGGGCTGTTCAACTTCAAAAGACACCAAGTACCAGTCGGTGTACGTCAATATCCGAGGA  
GAAGGATGAGTGCGTCATAGCAACTGAGGTGTAAATGGAAGTGAGATGGCAAGACTCCCGTTTCTCTTAAATA  
AGTAAAATTCCAAGGATATATGCCCCAACGAATGCTGCTGAAGAGGAGGGAGGCCTCGTGGAAGTGTGCTGAGAA  
ACCGAGTTCAGACCGAGCAGGTTCTCCTCCTGAGGTCTCGACGCCTGCCGACAGCCTGTGCGCGCCCGGCC  
TGCGGCACTGCCTTCCGTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATATTTAAATGGGT  
GAACTGAATTACGCATAAGAAGCATGCACTGCGTGAAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTTCTTGA  
ATTAGAAACACAAACTGCCTTTTATTGTCCTTTTGTACGAAGATGTGCTTTTCTAGATGGAAAAGATGTGT  
GTTATTTTTTGGATTTGTAAAAATATTTTTCATGATATCTGTAAAGCTTGAATTTTTGTGATGTTTCGTTTTTA  
TAATTTAAATTTTGGTAAATATGTACAAAGGCACTTCGGGTCTATGTGACTATATTTTTTGTATATAAATGTAT  
TTATGGAATATTGTGCAATGTTATTTGAGTTTTTACTGTTTTGTTAATGAAGAAATTCCTTTTTAAATATTT  
TTCCAAAATAAATTTTATGAATGACAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAA

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**FIGURE 346**

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVCLKHYQASVSPEPPCTYGSVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDEHYEGECSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSYTSCRPGYTGATCELGIDECDFSPCKNGGSCTDLENSYSCTCPPGFYKGICELSAMTCADGPCFNGGRCSDSPDGGYSCRCFVGYSGFENCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCDNVDDCASSPCANGGTCRDGVNDFSTCPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGFPWVAVCAGVILVLMILLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGGDDTAVRDAHSKRDTKCQPGSSGEEKGTPPTTLRGGEASERKRPD

SGCSTSKDTKYQSVYVISEEKDECVIATEV

**Important features:****Signal sequence:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 546-566

**N-glycosylation site:**

Amino acids 477-481

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 660-664

**Tyrosine kinase phosphorylation sites:**

Amino acids 176-185;252-261

**N-myristoylation sites:**

Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;  
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;  
676-682;683-689;695-701

**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 552-563

**EGF-like domain cysteine pattern signature:**

Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;  
467-479;505-517

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**FIGURE 347**

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA  
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGATTTCAGGCTCGCCAGCGCCCAGCCAG  
GGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCCTCGCTCCTGCTCCTGCTCCTGCTGT  
TCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT  
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCACGAGG  
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC  
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA  
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG  
CCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTTATAAATCTT  
CATTACGGGAAAAAGACACAGCCACCCTAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC  
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC  
CCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG  
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC  
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG  
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT  
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT  
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA  
AGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC  
ACGCCATCATCGGTGGGATCGTGGCTTTTATTGTCTTCTGCTGCTCATCATGCTCATCTTCC  
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG  
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA  
AGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGCGCCCCCAGGGGCCCTGTGGGG  
ACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT  
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT  
TTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTECGTGGCTT  
CTCTGCATTTGGGTATTATTATTTTGTAAACAATCCCAAATCAAATCTGTCTCCAGGCTGGA  
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACAAACAAAAACA



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**FIGURE 348**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTIVVLKCQVKDHEDSSLQWS  
NPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLVTV  
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT  
VSSSVTFQV TREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL  
HCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN  
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTAEAKGSDDAPDADT  
AIINAEGGQSGGDDKKEYFI

**Important features:****Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 349**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG  
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA  
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTATTTTTTTTTCTTTTCTT  
TTTCCCACCACATTGTATTTTATTTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGG  
CTTTTTCTGAAGTCTTGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA  
GTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG  
AGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGCTGGATTTCCTGCAGAACTGCACAATGTAC  
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATCCCCATGAACCTTCCCAAGAATGTCAGAG  
TTCTCCATTGTCAGGAAAAACAATATTCAGACCATTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGC  
TGCACCTGGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCCTCAAAT  
TGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG  
ATGAAAATCGAATGTGTGCATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG  
GGAACCTCCTGACCAACAAGGTATCGCCGAGGGCACCTTCAGCCATCTCACCAGCTCAAGGAATTTTCAATTG  
TACGTAATTCGCTGTCCCACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTCAGGACAACC  
AGATAAACACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC  
TGCGGATGCTGACTCAAGGGTTTTTGATAATCTCTCCAACTGAAGCAGCTCACTGCTCGGAATAACCTTGGT  
TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCA  
TGTGCCAAGGTCTGAACAAGTCCGGGGGATGGCCGTGAGGAATTAAATATGAATCTTTGTCTGTCCCACCA  
CGACCCCGGCCTGCCTCTCTCACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCAACCTCTCTA  
TTCCAAACCCTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAACTTCCCACGATTCTTGACTGGGATG  
GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATT  
AAGTCAGCTGGCTCTCTCTTACCGTGATGGCATACAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAG  
GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA  
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGCCA  
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCCACAGCATGG  
GCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT  
GCTGGCATATGCACAAAAGGGGCGCTACACCTCCAGAAGTGGAATAACAACCGGGGCGGGCGGAAAGATGATT  
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCCTTAA  
ATAACGATCAACTCCTTAAAGGAGATTTAGACTGCAGCCATTACACCCCAAATGGGGGCATTAATTACACAG  
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTCAGCAGC  
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG  
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA  
TGGGATTTAAAAAAGTGTCTATCTTTCTATTTCAAGTTAATTACAAACAGTTTGTAACTCTTTGCTTTTAAAT  
TCTT

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**FIGURE 350**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE  
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISR  
AALAQLLKLEELHLDONSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE  
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPDLPGT  
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD  
CSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTTPGLPLFTPAPSTAS  
PTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGRERVTPPISERIQLSIHFVNDTSIQVSW  
LSLETVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV  
EDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVLLSVFCWHMH  
KKGRTYSQKWKYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGD FRLQPIYTP  
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Important features:****Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

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**FIGURE 351**

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCCGACCGC  
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC  
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGCTCGCGGGGAACCTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCCATGCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGTAGCCGCTCTT  
CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAAATATTACACTTCTCTCTTGGCTGGAAACAGGATTGTTGAAATATCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAAACTTTTGACCTTAGCAGCAACAATATTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA  
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTTAACTGCCCAACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGCATTTCCAAGCCTTGGTGCTCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCAT  
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCATCACTTATCAAGGTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG  
AACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATTGCATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACCTTTCAGAGCTTTGTA  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGTGTTAGCCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCAGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGCAGTGATTTCCCAATGACTTTTGTCTGGAAAAAAGACAATGAACTACTGCATGAT  
GCTGAAATGGAATAATATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCATCTCCAATCACTTTGGTTCATCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCAGCTTGGAGTGTGCTGCTGTGGGCAACCCAGCCGCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC  
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG  
ATGTCTAACACCCTTGGCACTGAGAGAGGAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTCGCACTCCCT  
CAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTTGTGCTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGCGGAGGAATGAAGATTGCAGCATTACC  
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGCTTCAGAAAAGTGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT  
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCAGATCCTTTTGAACA  
TATCATACAGTTGCACTCTGACCCAAGAACAGTTTAAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAAATCTGTGTCTAACAAGTCC  
TCTTTAGATTTTAGTGAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTTCTTTCATGGGTACCTTTGGAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTAT  
TTGAAAGCTCATTCTTCCCCAGACTTGACTCTGGGTGAGAGGAAGTGGGAAAGAAAGGACAGATTTTCAGGAA  
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTATTTAAAGAGAGAGAAT  
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATTAC  
AAAAAGTTATGAAAATTTTTTACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG  
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGATTTTTTATAATGCCAGA  
TTTCTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACATTTTTTAAATAGAAAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 352**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDCSRKRLARLPEPLPSW  
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETL  
DLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRIAPPKMFKLPLQLHLELNRN  
KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNTLITKGWLYGLMLQELHLSQNAIN  
RISPDWAEFCQKLSELDTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI  
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDSLDAIMSLQGNAFSQMKKLQQLHLNTSSLLCDC  
QLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDFFPKPQITVQPETQSAIKGSNLSFICSAASS  
SDSPMTFAWKKNELLHDAEMENYAHRLAQGGVEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVN  
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS  
CTAONSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDSDPLVVTERHFFAAGNQ  
LLIIVSDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSIV  
WVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSST  
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNGVYGSDPFETYHTGCSPDPRTVLMHDHYEPSYIKKKECYPCSH  
PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHL  
DAYSSFGQPSDCQPRAYLKAHSSPDLDSGSEEDGKERTDFQEEHNICTFKQTLNRYRTNPFQSYDLDT

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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**FIGURE 353**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTTCTCCTTTCCTGGCTTCGGACATTGG  
AGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA  
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTAC  
AGGGGACGTTTGCAAAGAGAAGATCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAA  
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTACCATTATTTCTGCATGGCAATTCCCT  
CACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA  
TGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC  
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT  
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACC  
TGCCAACGTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA  
GGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTGGGACTGCACCTGTGATCT  
GCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCAC  
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAG  
TCTCCCGGCGCCCCCTGCCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA  
AGAGGATCATGCCACACCAGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG  
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCCTAGCTAACAGTTTACCCTGCCCTGGGGGCTG  
CAGCTGCGACCACATCCCAGGTGCGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT  
GAAGCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT  
TGTGGATTACAAGAACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAA  
GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGAGAAATTCGCGGG  
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCCGGGCACTTTCAATGCCAT  
GCCCAAACCTGAGGATCCTCATTTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTC  
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC  
CATCATCCAGATAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA  
ACGCTTGGGTTCGGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTTTAGAAAGGATTTTAT  
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAA  
CAGCACTGGGTGGCGGAGACCGGGACGCACTCCAACCTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT  
GGTCCCGGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTTTATCCTGAGGAA  
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCTCCGAGATTAATTCCCTACAGACAGTCTGTGACTC  
TTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGATGACTGTGGCTCTCACTCGCTCTC  
AGACTAAGACCCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCCGG  
GGCTGGAGGGGCGTGATCCCAAATCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC  
GCACAACCGAAAGGGCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA  
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCTGCTGGAAGAAGTACA  
GTGCCCTCGCCCTCGCCCCGGGGCCTGTGGGGTTGGATGCCCGGTTCTATACATATATACATATATCCACATC  
TATATAGAGAGATAGATATCTATTTTCCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTGGCTACGCAGGGAT  
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACTTTGACTTCTGAC

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**FIGURE 354**

MLLWILLETS LCFAAGNVTGDVCKE KICSCNEIEGDLHVDCEKKGFTSLQRETAPTSQFYHL  
FLHGNSLTR LFPNEFANFYNAVSLHMENNG LHEIVPGAFLGLQLVKRLHINN NKIKSFRKQTF  
LGLDDLEYLQADFNLLRDIDPGA FQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRGNRL  
KTLPYEEVLEQIPGIAEILLEDNPDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ GKDL  
NETTEQDLCPLKNRVDSSLPAPPAQEETFAPG PLPTPFKTNGQEDHATPGSAPNGG TKIPGNW  
QIKIRPTAAIATGSSRNKPLANS LPCPGGCSCDHIPGSG LKMNCNNRNVSS LADLKP KLSNVQ  
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE  
KFAGLQNL EYLNVEYNAIQ LILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN  
YFMYLPVAGVLDQLTSIIQIDLHG NPWECSCTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK  
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT  
SAFTVVGMLVFILNRNRKRSKR RDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS  
LSD

**Important features:****Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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**FIGURE 355**

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCAGAATAAATCAGGGCTGCACCGGGCCTG  
GCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGCCGCTGGGCCCCGGGGGGATTCTTGG  
CAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGAACCGGTTGGGGAAGCCAGCTGTAGAG  
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC  
GGGGCCTCAGAGAAATGAGGCCGGCGTTGCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGGCGCGCGG  
CGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA  
GCGGCAGGCGGGCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCGTGCGGGCGCCGAGCTGCG  
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGGGCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT  
GGAGCGCAGGCGTTCCCACTGCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGG  
CGGTCTCGAAAGCGACAGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT  
CCAGGCCACCGGTGGGGTCGAGCCCGAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG  
CAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGGGCGCCTCTAACTTGAGCTATCGCGCGCCCTT  
CCAGCTGCACAGCGCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCC  
GATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTG  
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCTG  
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCT  
TGGGGGACCGGGGTGCCCACCAGGCGCCCGCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCAAT  
CAGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGAT  
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCCTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC  
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTTGACTCCTCCTC  
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTTGT  
CAAGCTCTGCTTTCACGAAAGCCCTCTTCCCAGCCAAGGAAGGAGTCTATGGGCCCGCCGGGCTGGAGAGTGA  
TCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT  
GCGGGACAGAGCAGAGGTGCCTTGCTGGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACA  
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAAGTACTTGTGTAAGTACAA  
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC  
CCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGATGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATT  
TTCTTATGTTTATTCGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT  
AATTTACATTAAAAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTTGTTGAGGCTAGGAGTATATTGG  
TTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT



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**FIGURE 356**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALST  
VRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD  
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGAASN  
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR  
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATATSPVP  
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS  
KFNSTTSSATPQAFDSSSAVVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPP  
GLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Important features:****Signal sequence:**

amino acids 1-16.

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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**FIGURE 357**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGAGA  
AGACTAAAAATGGTGTTCCTCAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTTAACATAATCCTAATTTCC  
AAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCTGGAGGTATCCCACGAACACCACGAACCTCACCCTC  
ACCATTAAACCACATACCAGACATCTCCCCAGCGTCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTTCTAGA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
TTTAGTGGACTCATTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCG  
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACAACATCTTTTCCATCAGAAAAGAGAATCTAACAGAAGTGGCC  
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA  
GATGCCCTTCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT  
TTGCCATCTACTTTAACAGAAGTATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAAATAAC  
CTCAACCAATTACAAATTTCTGACCTAAGTGAAATTTGCCCTCGTTGTTATAATGCCCATTTCTTGTGCGCCG  
TGTAATAATAATTCTCCCTACAGATCCCTGTAATGCTTTTGATGCGCTGACAGAATTTAAAGTTTTACGTCTA  
CACAGTAAGTCTCTTACAGATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAAGTGGATCTGTCC  
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTCTCCCCAGCCTCATCCAATTGGAGCTG  
TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
AAAAATTCGCGGATCAGAGGATATGCTTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATGCTAACCTCAGCATGTTTAAACAATTTAAAGA  
CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAT  
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTGGAACAATTACATTATTTAGATATGATAAGTATGCA  
AGGAGTTGCAGATTCAAAAAACAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTCAGCATCTTTCTTCTCAAATGCCTG  
AATCTGTGAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACCTTTAGCAGAGCTGAGATATTTG  
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT  
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT  
CTGCAGAACTGATGATGAACGACAATGACATCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
AATCTGTAAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGT  
ATGCCTCCAAATCTAAAGAATCTCTCTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT  
CTAAAGAACCTGGAACCTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAACGTCTCC  
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAAATCAGGAGTCTGACGAAGTATTTCTACAAGATGCCTTC  
CAGTTGCGATATCTGGATCTCAGCTCAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTC  
AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTTGTCTGGTGG  
GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGC  
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTTTTCTCATGGTGATGATGACGCAAGTCACCTCTATTCTGGGATGTGTGGTATATTTACCAT  
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA  
CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAACCTTTCCAGAGCATA  
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTAAGATAGCATTTTAC  
TTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG  
TCCAAGTTCTCAGCTCCGAAAAGGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAACAACCCGCAAGCTCAC  
CCATACTTCTGGCAGTGTCTAAGAAGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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**FIGURE 358**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPDVTLDVPKNHVIVDCTDKHLTEIPGGI  
PTNTNLTTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGL  
TYLKSLYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYRNPC  
YVSYSIEKDAFLNLTKLVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQ  
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINK  
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNELQVYRASMNLSQAFSSLKSLKILRIR  
GYVFKELKSFNLSPLHNLQNLEVLDTGNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE  
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNE\$CYKYGQTLDSLKNS  
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDF\$NNRLDLLHSTAFEELHK  
LEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMESESLRTEFRGNH  
LDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK  
KLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS  
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVWNHTEVTIPYLATDVTCVGPGA  
HKGQSVISLDLYTCELDLTNLILFSL\$ISVSFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ  
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQ  
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLEKPFQKSKFLQLRKRLC  
GSSVLEWPTNPQAHPHYFWQCLKNALATDNHVAYSQVFKETV

**Important features:****Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

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**FIGURE 359**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC  
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG  
AGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT  
GGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA  
AGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC  
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC  
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG  
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA  
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC  
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG  
CTCAGGATTTGCCTTACCTGGTAACCTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT  
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAAACAGAGG  
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCCTTAG  
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAACCTGAGGTCCCTT  
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA  
CCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA  
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACCTCTACCCCATG  
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGCCCTCAGTTT  
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT  
CCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC  
TGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTGAGGGC  
TGAACCTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG  
TGTTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGGTGAAGAGGTGAGCTGTCCCTCTG  
TCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA  
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG  
GCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCACACCTCTCCTGCCCCCTCCC  
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT  
GCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTAGGGG  
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA  
GGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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**FIGURE 360**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL  
AAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC  
GHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLCNYEPPGNVKGKRPYQEGTPCSQCPSG  
YHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRAEASDSRKMGTPSSLATGIPAFLVTEVSGSL  
ATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI  
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLASVFPAQD  
KPGELQATLDHTGHTSSKSLPNFPNTSATAATGGRALALQSSLPGAEGPDKPSVVSGLNSGP  
GHVWGPLLGLLLLPLVLAGIF

**Important features:****Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

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**FIGURE 361**

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG  
GGTGACGGCAGGGCAGGGGGCGCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT  
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG  
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTGCT  
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCGGG  
GCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCGCGATGG  
CCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG  
ACTGCCGGGACCTCGAGGGGACCCGGGCGCGAGGAGAGGCGGGACCCGCGGGGGCCACCGG  
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCCTCAGCGCCAAGCGCTCCGAGAGCCG  
GGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA  
TTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA  
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC  
TTTCTTCCAGTTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGCCATGGTGAG  
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC  
CAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC  
AGTCTTTGCTTAGTGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAAGGAGGGTGTGA  
GGCTGACAACAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG  
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA  
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG  
CAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCACGGTGGGGTGCTCTCTTCCTGGTC  
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT  
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 362**

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG  
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD  
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFQFFGGWPKPA  
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Important features:**

**Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

**FIGURE 363**

[illegible]



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## **FIGURE 364**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGRE  
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD  
TDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATREELT  
AFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQFRDF  
RDLNKDGHLDGSEVGHWWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT  
NYGEDLTRHHDEL

**Important features:**

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

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**FIGURE 365**

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAAG  
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA  
TTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG  
AAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA  
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC  
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT  
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG  
CCTCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCACCATTGGGAACCGGGCAGTGCTG  
ACATGCTCAGAACAAGATGGTTCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG  
ATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA  
ACAGGAGAGCTGGTCTTTGATCCCCTGTGACCTCTGATACTGGAGAATACAGCTGTGAGGCA  
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT  
GTGGGGGTCATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGTTTTTGGC  
ATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG  
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTG  
GTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT  
CTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC  
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC  
CCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTGTTTAAAGTGTTTATTCCTCCTTCT  
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA  
TGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGCTGGCAGGGATCTTTGAATAGG  
TATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA  
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT  
CTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC  
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTTGTGGA  
GAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA  
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT  
CACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA  
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG  
CAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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**FIGURE 366**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYS GFSSPRVEWK  
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVL  
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYV  
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVT LILLGI  
LVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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**FIGURE 367**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
CCACCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGTATGTTCATTTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAGAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACCTCCTTTTTTTTAAAT  
TTTTATTCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACCACTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTTGGTGGT  
GCTGGCTCTTCAACTTCTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTCTCCTGCAGCAA  
CCAGTTGAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
CTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGATACTTGTCTAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGATGATACAGTCCCAGAT  
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCCGTG  
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCTCCACATC  
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGT  
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAATAA  
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTC  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCTCC  
AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTGACAGAGAAAACTT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACA  
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAAATCTCCCTT  
CAACCACACAACAACAGTTAAACACAATAAATTCATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAAA  
GACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA  
AAAAGAAAAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

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**FIGURE 368**

MLNKMTLHPQQIMIGPRFNRALEDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS  
TNTRLLNLHENQIQIIKVNSEFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL  
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLELD  
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH  
NPWNCNCDILWLSWWIKDAPSNNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC  
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTMVTCMVSNSVGNNTASATLNVTAATTP  
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTKFTFTIPVTDINSGIPGIDEVMKT  
TKIIIGCFVAITLMAAVMLVIFYKMRKQHRQNHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHYS  
YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

**Important features:****Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,  
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,  
422-428, 433-439, 531-537.

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**FIGURE 369**

CAAAACTTGGCTCGCGGAGAGCGCCAGCTTGAATGGAAGGAGCCCGAGCCGCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCCTGTGGGGCGCCGCTCGGCCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGCAGGAGGGCTCATGGTGAAGGAGGAGGCGGCTGATCTGCAG  
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAGAGAACGAATTTGCGGAGGAGGAGCCGTGCTGGTACTGAGCCCTGAGG  
AGCCCGGGCCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCCTGTTCCAGGAGGGCGCTGCTGGACTGTG  
GCGGTATTGACCTGCTGAGTTCCCGGGGACCTGCCTGAGCAGCACCACCACTATCTCTGCAGAACCAACAGC  
TGGAAAAGATCTACCCTGAGGAGCTCTCCCGGTGCACCGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
CTTCCCGAGGGCTCCAGAGAAGCGCTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCTGCTTCCGCAAAACGCCCTGATCAGTGTGGACTTTGCTGCCAATATCTCACCAAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGG  
TGCCGGAACAATGTTCAACGGCTCCAGCAACCTGAGGTCTCTATCCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCAGCTGCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCT  
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACCTACCTGACTGACGAGGCGCTGGACAACGAG  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
CGCGCAGCCTGCTGCTGCTGCACTTGAGAGAAGACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCATCC  
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCACTGCGGGAGCAGGGCATCCACCACTGGCCTTCCAGGGCC  
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACCGCTGGAGCGCTGCCAGTGGCTGCTGCGCCGTGC  
GCACCTCATGATCCTGCACAACCAAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGCGACGCTTCCGAAGCTGCGCCTGCTGC  
GCTCGCTGGACCTGTCCGGCAACCGGCTGCACAGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGCGCTGGCGGAGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCGCTGCCCTGGGTGGACCTCGCCCATCTGCAGCTGTGGACA  
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAA  
AGATTAGTGGGTGCGCGCAATGCCTTCGACTCCACGCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC  
TGGCTGTGGGCTCCGTGCTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAAGGAAAGGAGGAGGAGGAAGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTCTGC  
AGCACACGCTGTGTGCTGTGAGCCCCCTACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGCGGTGTCCACGGCCAGACACATGC  
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACCTCCAAACCACACAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGGAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGGCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
GTCCATCTGTCCGTCCGTTCCTTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCTGCCACCCTCT  
GGAACCTCAAAAAGCTGGCTTTTATCCTTTCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCACCCTGCTCCTCCAGGTGCTGGGCAGTCACTGTGTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGACCCAGCTGCACCTAGGAGACACCTTT  
GTTCTTCAGGCCTGTGGGGGAAGTCCGGGTGCCCTTTATTTTTTATTTCTTTCTAAGGAAAAAATGATAAAAT  
CTCAAAGCTGATTTTTCTTGTATAGAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAA

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**FIGURE 370**

MEGEEAEQPAWFHQWPRPGASDSAPPAGTMAQSRVLLLLLLLPPQLHLGPVLAVRAPGFGRSG  
GHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCCGIDLREFPGDLPEH  
TNHLSLQNNQLEKIYPEELSRHRLETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNKLT  
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI  
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK  
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHLSNQLREQG  
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYFLEELNLS  
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALARGALAGMA  
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP  
ANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGLGKEKEE  
EEEEEEEEETR

**Important features:****Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247; 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

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**FIGURE 371**

CACCTTTCTCCCTCTCTTCTTTACTTTTCGAGAAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG  
CCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTTCTGCGAC  
TGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTTTCTTCAACGAGTCTGTGCATCGCCCCGACCTGGCCGG  
GAGGAGGCTTGGCCGGCGGGAGATGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAG  
GAAGATGGGCTCCCGTGGACAGGGACTCTTGTGGCGTACTGCTGCTCCTTGCCCTTGCCTCTGGCCTGGTCTCT  
GAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTGCGCTCCGGACCA  
TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAGGACCAGGGGCTCCCTGCTTCCCGGTGCTT  
GCGCTGCTGTGACCCCGGTACCTCCATGTACCCGGCGACCGCGTGCCCCAGATCAACATCACTATCTTGAAAGG  
GGAGAAGGGTGACCGGGAGATCGAGGCCTCCAAGGGAATATGGCAAACAGGCTCAGCAGGGGCCAGGGGCCA  
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC  
GGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTCTGTGAACCT  
CTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGTACGTGCCCGGCTCTACTTCTTCAAGCCTCAACGT  
GCACACCTGGAACCAAGGAGAGACCTACCTGCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCA  
GGTGGGCGACCGCAGCATCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG  
CCTCTACAAGGGCGAACGTGAGAAGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCACTGGGTACCT  
GGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTCTCTCGCCACCTTCCACCCCTGCGCTGTGC  
TGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTCACTGAGACGCCCTGCACAC  
ACAGAAAGCCAAAGCGATCGGTGCTCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCA  
GGCGGGGACCCGCGAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG  
CGAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGGCGGCACCGCGCTCCAGTCTTGGAAATAATTAGGCAAATT  
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTTGTTATTTTTGTCTTTCCAGCCAG  
CCTGCTGGCTCCCAAGAGAGAGGCCTTTTCACTTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG  
GTCAGGGGAGGGGCGGGGGCAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTTGAGGG  
ATAGGTGGACCTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGTGA  
TGGGGGTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTGGTAGAA  
GCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCAGGCTGCAGATGTTTCTATGAGGGGCG  
AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG  
CCTGCCACCCCTGGCATCGGCTTTCTGTGCCGCTCCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTT  
CTGTTTTTTATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCAG  
TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTGTGCCCCACTGCCCTCATCCAGGCCTCTGACCA  
GTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT  
GTTTCTCAGGCTCCTGTGAGCCTCAGTCCTGAGACCAGAGTCAAGAGGAAGTACAGTCCCAATCACCCGTGTCA  
GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGG  
TTGCGGTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCCATAGCCCC  
TCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCCCCCAAACCCCGCTGCCTCTC  
TTCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCTTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGG  
TCCCTAAGTCCCTCTCTTTAAAGAACTTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAG  
CAGAGCGCCACACTCGTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA



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**FIGURE 372**

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPDHAERAEQHEKYRPS  
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQKYGKTGSAGARGHTG  
PKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFYCYV  
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWRLYK  
GERENAIFSEELDTYITFSGYLVKHATEP

**Important features:****Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

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**FIGURE 373**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG  
TTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGGAA  
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC  
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTAGAGG  
ATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCCAAAG  
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAGCAGAGTTCT  
TCAGTTCTGAAAATGTTAAAGTGTTCGAGTCAATTAATATGGACACAAATGACATGTGGTTAA  
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC  
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTTAAAAAAGGATC  
CATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAATATGTGGGTATGG  
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG  
AAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT  
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA  
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG  
AAGGCTGTTGTTTCAAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA  
TGATGTATGGGGTATACCGCCTTAGGGCATTGCGCATATTTTCAATGATGCATTGGTTTTCT  
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA  
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAATACAGCTGTATGTTTCTT  
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCAACACATTAAAGTCAGTAGTACATTTTAAA  
TGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAGAAGTGTTTTA  
AGAATAATAATTTTGCAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA  
ACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTTAAAAAATTTTAACAGGTCTTTA  
GCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACTTTTAG  
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT  
TTGCCTTCTCAAAATGTACAACCTAAGCAACTAAAGAAAATTAAAGTGAAAGTTGAAAAAT

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**FIGURE 374**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV  
KPKDVSLLWAAVKETWTKHCDKAEFFSSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI  
IENLYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV  
CLKYAGVFAENAEDADGKDVFNKTSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRI.RAFG  
HIFNDALVFLPPNGSDND

**Important features:****Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,  
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,  
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

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**FIGURE 375**

GTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT  
CTATCAGGAAAGAAAGAAAGAAAAAACCAGAACCTGACAAAAAAGAAGAAAAAGAAGAA  
AAAAATCATGAAAACCATCCAGCCAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG  
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA  
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA  
CCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG  
GTGCCTGGATCCTCGCGTGGTCCCTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA  
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA  
GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGATAT  
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC  
GGTTACTTGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA  
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC  
CGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAAGTATCCACCATACATTTTCAAGCCAA  
GGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC  
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT  
GGAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA  
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC  
AGGCGCCGTGAGCGAGGTGAGCAACGGCAGCTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC  
TCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG  
GCTGCCGCCACCACCACCAACAACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA  
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA  
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGG  
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA  
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGA  
GTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAA  
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG  
CGGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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**FIGURE 376**

MKTIQPKMHNSISWAIETGLAALCLFQGVPPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRV  
TRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPKTS  
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ  
GITREQSGDYECASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTQLQCEASAVPSAE  
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHTNASIMLFGPGA  
VSEVSNGTSRRAGCVWLLPLLVLHLLKLF

**Important features:**

**Signal peptide:**

amino acids 1-28

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**FIGURE 377**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGAA  
**ATGT**GGCTCAAGGTCTTCACAACTTTCCTTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG  
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCAC  
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCACACA  
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTTCTGACTTGGAATACCAACAC  
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTTGATGAA  
GGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCAGAAGATA  
CAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCTCTGGGGCT  
GTGGAGTATGTGGGGAACATGACCCGTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC  
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTTCTCCCCAAAAC  
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG  
AACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA  
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGGAGAG  
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG  
ACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTGCATCTGAGAAAGTA  
GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA  
ACTCATTTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGCACAGAAAGGAAAATCA  
TTGTCACTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATTATATCCATGTGTCTTCTC  
TTCCTATGGAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA  
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA  
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGGATTCCAAGCAGGTCTGTTCCA  
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC  
CCTGCCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGGGCTAAACAGTACATTTCGAGTGAA  
ATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGTATATTAATCTGGAATCAGTGAAGA  
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA  
TTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA  
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCCT  
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCACTATC  
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTC  
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT  
ATTTCCAAATTTCTATCTTGTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA  
AAACTATGCCTTCTCTTTTTTTTTCAATCACCAGTAGTATTTTTTGAGAAGACTTGTGAACACTT  
AAGGAAATGACTATTAAAGTCTTATTTTTATTTTTTCAAGGAAAGATGGATTCAAATAAATT  
ATTCTGTTTTTGCTTTTAAAAA

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**FIGURE 378**

MWLKVFTTFLSFATGACSLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS  
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQKIQVTVDPPVTKPVVQIHPPSGAVEY  
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII  
YYGPYGLQVNSDKGLKVGVEFTVOLGEAILEDSCADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD  
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG  
RPETEURKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRPSRVPASDCVSGQDLHSTVYEVIIQHIPAQQQDHPE

**Important features:****Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 379**

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACAA  
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGT  
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC  
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA  
TTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC  
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAACAGCTG  
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAACATTGAT  
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA  
GATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT  
GCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG  
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGG  
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA  
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAAGTTCTTCTGGAAGACCTTCTCCTCCTGCAA  
ATAG



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## **FIGURE 380**

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS  
GATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR  
QEGAPPOQSARRDRMPCRNFFWKTFSSCK

**Important features:**

**Transmembrane domain:**

amino acids 51-69

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

**N-myristoylation sites.**

amino acids 64-70, 75-81, 90-96

**Amidation site.**

amino acids 33-37

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**FIGURE 381**

GGCGCCGGTGACCGGGCGGGCTGAGCGCCTCCTGCGGGCCCGGCCTGCGCGCCCCGGCCCCGCC  
GCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCCGCGC  
CCGCGCCAGGTGAGCGCTCCGCCCCCGCGAGGCCCGCCCGGCCCGCCCCCGCCCCGCC  
CGGCCGGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCCATAAAACATTC  
ATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCCGCCCGCCCTCGCCCTG  
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGCGGAGCG  
CGCCGAGCCTCGTCCCGCGGCCCGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGATGCGGAC  
CCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCCA  
ACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG  
CAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTG  
ACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCCGTGGGCATCCCTGCTGCCAGCCAG  
CGCATCTTCTGACGGAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCCTGCCGC  
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGCGGCTGCCTTCACT  
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCT  
GCCACATTCCACGGCCTGGGCGCCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG  
CTGGGCCCCGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG  
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGCAC  
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC  
CTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCCGCTC  
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGCCCTGGCCCCCTG  
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCA  
CTCTGGGCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA  
CGCCTGGCTGGCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC  
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC  
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG  
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGGTGACAGCCCGCCGGGCAACGGCTCTGGC  
CCACGGCACATCAATGACTCACCCCTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACT  
GCAGTGCGGCCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA  
GGCTGTTACGCAAGAACCGCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGT  
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC  
CTGGGCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCTGACCCCCAGCGGACACAAGA  
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG  
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCTGCCGCCCCGCCACC  
CCCCTCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCCAGAACGCCGCCTC  
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA  
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

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**FIGURE 382**

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIF  
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPATF  
HGLGRLHTLHLDRCLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNR  
ISSVPERAFRGLHSLDRLLHQN RVAVHVP HPAFRDLGRLMTLYLFANNLSALPTEALAPLRAL  
QYLR LNDNPWVCD CRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCAVATGP  
YHP IWTGRATDEEPLGLPKCCQPD AADKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH  
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT  
GDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

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**FIGURE 383**

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTCTGAACTTGTCTG  
AAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTCGCTGCTTTTGTAGGG  
ACTTCTTTCTTGCTTCAGCAACATGAGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGA  
TTGGGGCTTTGATCCCTGAACCAGAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCA  
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA  
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA  
AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCTGCTCTGGGCTATGGAAAAGAAGGAAAAGGTA  
AAATTCCTCCAGAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGCGAAATGGACCAAGATCCCATGAAT  
CATTCCAAGAAATGGATCTTAATGATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT  
TTGAAAACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAGAAGATG  
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCTT  
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTATACAATGTTCTTTCT  
TGCTTTGTTTTTTATTTTATATATTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT  
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTC  
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACCACGACATGA  
GACCAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT  
GAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG  
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT  
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGA  
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAACCCTATCTCTAC  
TAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA  
TCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAA  
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG  
CTCCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTCTTTGTAATAAAATGTA  
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT  
CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA  
GTCTACATTTTCCCATTTCTGTCTCATCAAAAAGTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAG  
CACTTTGGGGGCCAAGGAGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCT  
TGTCTCTACTAAAAATACAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAGGCTGA  
GACAGGAGATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG  
TGACAGAGCAAGACTCCATCTCAAAAAAAAAAAGAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA  
TCCTGGATTTT

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## **FIGURE 384**

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS LF  
HSTHKHNNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI  
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVEDIFD.  
KEDEDKDGFISAREFTYKHDEL

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

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**FIGURE 385**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCTC  
CCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC  
CTGCAGTGACCTACAGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG  
ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG  
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC  
ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA  
CTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCCCTCCCTTCTCCCACCTTCCAG  
CCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG  
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC  
CCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT  
CCTACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGCTGGACTCCACC  
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG  
ATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTCAGCCGCAGGCTGATC  
GCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG  
AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCCCCCTTCCCAGGCCCT  
GAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG  
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC  
TGGATCAGCACCGATTCCCAGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCCGACTCC  
AGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCTGTTCCAGCCTGACCTAGAAGCGTTT  
GTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT  
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG  
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGCCTCATGCCAGTGTGCGGACCCT  
GCCTTCTCCCCTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA  
CGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCAGTGGGGTGAGACTGGGATTCTGGCTT  
CTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACGTGATTCTGGCCCCA  
CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCCAGT  
GACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTGATGAACGCTCACACCCCTTCCAGTAG  
AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCCAATAGATCTGCTCTGTCTGCGACACCA  
GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCAGGTGAGTGCACAT  
TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTGCCCCTCCCTGGNCCA  
TGCCTTCTTGCTTTGGAAAAAATGATGAAGAAAACCTTGGCTCCTTCTTGTCTGGAAAGGG  
TTACTTGCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGT  
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG  
GAGAAGGGGTCGGGGGTGGTGGTAAAGTAGCACTACTATTTTTTTTCTTTTTTCCATTATT  
ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCA  
AACTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG  
GCACGCACCACACACCTGGCTAATTTTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTG  
GCCAGGCTGGTCTTGAACCTCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCG  
GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTG  
TTCAGTATGCAAACTTGGAAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA  
TAGTCTCACCAGAGACTATCATTATTTGTTTTGTTGTAATTCCTTCCACTCTTTTCTTCTTC  
ACATAATTTGCCGGTGTCTTTTTACAGAGCAATTATCTTGTATATACAACTTTGTATCCTGC  
CTTTTCCACCTTATCGTTCATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTT  
ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

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**FIGURE 386**

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCSG  
TIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLT LQDAGEYWCGVEKRGPD ELLISLFVFP  
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPGTSQ  
YGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRILAPV  
LVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGDVISM P  
PLHTSEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

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**FIGURE 387**

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCGGGCTCCCCGGCCGGCACATG  
GCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGAGG  
CGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGG  
**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCACACT  
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA  
GAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAAGTGGTG  
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC  
TTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGCCCAGTGAT  
GAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCATGTCATCTTA  
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT  
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATTACTGGCAGCGA  
ATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCCTCCCAATCTAGGATTGACTACAACCAC  
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTACCAGTGCACAGCA  
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAAGTGTACAGTATGTACAAAGCATC  
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTTGGTG  
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT  
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCT  
CGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG  
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG  
GGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA  
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC  
TTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT  
CACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCAGTGAGCATTGCACGGAACAGATT  
CAGATGAGCATTTTCTTTATACAATAACAAACAAGCAAAAGGATGTAAGCTGATTCATCTGTA  
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT  
TGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAAACTTTTAAT  
GTGGGATATTTTGTATCAGTGCTTTGATTCACAATTTTCAAGAGGAAATGGGATGCTGTTTGT  
AAATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTTCAGACAGTCAAGCAGAAC  
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCCTTCTAAGAACTCCAAA  
AAAGGAAACATGTGTCTTCTATTCTGACTTAACCTTCATTTGTCATAAGGTTTGATATTAATT  
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCCACTCTATACTA  
ATCTCACTATTTGTATTGAGCCCAAAATAACTATGAAAGGAGACAAAAATTTGTGACAAAGGA  
TTGTGAAGAGCTTTCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA  
ATGGAGCAATTGTGGATTTCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTT  
CTGGAAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAA  
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATAACCATTATAGTCTCTTCTTCTGAGAAA  
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA  
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG  
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC



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**FIGURE 388**

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL  
KVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH  
PGRVLLQNLTMSSYGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLIFLLV  
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANSASRSQ  
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

**Important freatures:****Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

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**FIGURE 389**

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG  
CCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT  
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCCTCAAAGCTCCAGTCCCCA  
AAAGGC AAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA  
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC  
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACTGGGAATGTGA  
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC  
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAAGACTGA  
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA  
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATTCAGAGAGAAA  
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG  
AAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA  
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT  
GAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA  
GTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAATGAATGG  
AAATTCTTAAAAAAAAA .

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## **FIGURE 390**

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC  
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC  
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRSSWV  
FIAAKGLELPSEIQREKINHSDAKNNRYSGWP AEIQIEGCIPKERS

**Important features:**

**Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125



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**FIGURE 392**

MSRPGTATPALALVLLAVTLAGVGAQGAALEDPDYYGQEIWSREPYARPEPELETFSPLPA  
GPGEWERRPQEP RPPK R A T K P K K A P K R E K S A P E P P P P G K H S N K K V M R T K S S E K A A N D D H S V R  
V A R E D V R E S C P P L G L E T L K I T D F Q L H A S T V K R Y G L G A H R G R L N I Q A G I N E N D F Y D G A W C A G R N  
D L Q Q W I E V D A R R L T R F T G V I T Q G R N S L W L S D W V T S Y K V M V S N D S H T W V T V K N G S G D M I F E G N S  
E K E I P V L N E L P V P M V A R Y I R I N P Q S W F D N G S I C M R M E I L G C P L P D P N N Y Y H R R N E M T T T D D L D  
F K H H N Y K E M R Q L M K V V N E M C P N I T R I Y N I G K S H Q L K L Y A V E I S D H P G E H E V G E P E F H Y I A G A  
H G N E V L G R E L L L L L V Q F V C Q E Y L A R N A R I V H L V E E T R I H V L P S L N P D G Y E K A Y E G G S E L G G W S  
L G R W T H D G I D I N N N F P D L N T L L W E A E D R Q N V P R K V P N H Y I A I P E W F L S E N A T V A A E T R A V I A W  
M E K I P F V L G G N L Q G G E L V V A Y P Y D L V R S P W K T Q E H T P T P D D H V F R W L A Y S Y A S T H R L M T D A R R  
R V C H T E D F Q K E E G T V N G A S W H T V A G S L N D F S Y L H T N C F E L S I Y V G C D K Y P H E S Q L P E E W E N N R  
E S L I V F M E Q V H R G I K G L V R D S H G K I P N A I I S V E G I N H D I R T A N D G D Y W R L L N P G E Y V V T A K A  
E G F T A S T K N C M V G Y D M G A T R C D F T L S K T N M A R I R E I M E K F G K Q P V S L P A R R L K L R G R K R R Q R G

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**FIGURE 393**

GTCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCATCATTTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCCCTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
TACTTATTTCTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACCTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCCTT  
CCAGGTGTTGAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAATCTCTGAGAGCGCTCTCTGCGAAGCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCCC  
TAACACCCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCTTGATGTGCTTGTGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCTTTTGTGATCTGGTGTAACTGC  
CTATGACAAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGAGCTCCAATGACAATAG  
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAGATGCTGCACCTGGTACGCTTCTCATAAACT  
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCTCCAGAGGT  
GCTGGACACCTTCAGTATGTGATGCCAAGACAGGCCAGGTCTTCTGCGTCGACCTCTAGACTATGAAAAGAACCC  
TGCCTACGAGGTGGATGTTGAGGCAAGGGACCTGGGTCCCAATCCTATCCAGCCCATTTGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCCTCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTATTGCTCTTGTCATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACAATGC  
CACACTGGACAGAGAGCAGTGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTGAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA  
AGTCTCCAGCGGGGAAAACAACCTTACCTCTCTTACCTCATTACCATCAAGGCTCATGATGAGACTTGGGCAT  
TAATGGAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCAGTGAACATGAAAGAGATGGCCGGCTTTGAGTCCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGATCCAGTGTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGCT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCAGAGCTCCCGGCCATT  
CCTTTTGACAACCATTTGTGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCCACCTCTTCATCCTCAACCTCATACCGGGCAGCTGTTGCTCAATGTACCAATGCCAGAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTTGTACCAAGTGTGGACCACTGAGGAGCTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTCATGTCCATCTGCCG  
GACAGAAAAGAAGGACAACAGGGCTTACAACCTGTCCGGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAAACATTCAGAAGGCAGACATCCACCTCGTCTGCTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCACAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCTT  
CCACCTCACCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACAGGGAGCACCGCGGAGAGCCGAGAGGT  
GCTGCAAGACACGGTCAACCTCCTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCAGCTTCCAGGCCTCTGAAGGTTGCAGGCAGCCCCACAGGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCCTGCAACCTGAGACGGCAGCGACATCT  
CAATGGCAAAGTGTCCCTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTCG  
TGCCTTGCCTGATCAGGGCCAATTCAGGCCAAACCAAAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCGG  
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCTCAGTTTGAAGTTGGCCACCACTCAGGCTCAGGCATGAAAGTGAAGGGGACCCAGGTGG  
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGTCCTGTGAACATAACCTCAGACGCCCT  
CTGGATCCAAGAACAGGGGCTGAGGATCTGTGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG  
CGGCGGCTGAGAACTTTAGGGTGAAGTGTGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
TGACCAAGACAGCCCTTGTAGCAGCTCTGAGTCTTCTTGGAGGACAGGACGGTTTGTGGCTGAGATAAGTGTT  
TCTTGGCAAAACATATGTGGAGCACAAGGGTCACTCTTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAATGCTCTCTGACCTAT  
CAATAAGGAAAAGCAGTAATAAAAAAAAAAAAAAAAAA

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**FIGURE 394**

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG  
AAFOVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQVL  
DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD  
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAPFAESSLALE  
IQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPLDYEKN  
PAYEVDVQARDLGPNIPIAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA  
DDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS  
AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVSYRIQDSPV  
AHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLLDANDNAPEVVQ  
PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTIVARDADSGA  
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSPPLOTRALLRV  
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE  
STYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCLOAPFHLT  
PTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPPEQPATGQPRSRPLKV  
AGSPTGRLAGDQGSEEAPQRPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE  
RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGSRSAIPD TDGPSARAGG  
QTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD  
NVISPDAAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLEMLLEQRSSMPVEAASE  
ALRRLSVCGRTLSDLATSAASGMKVQGDPPGKGTGTEGKSRGSSSSSRCL

**Important features:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 395**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG  
CTCCAGAATCGTGTAACAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC  
AGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGGACGCCCCCGACCTCGTGCG  
GCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG  
GAGGACAAGGTGCTGGGGGGTCA TGAGTGCCAACCCATTTCGCAGCCTTGGCAGGCGGCCTTG  
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTG TAGGTGGCAACTGGGTCTTACAGCT  
GCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAAGAT  
GGCCCAGAGCAAGAAATACCTGTGGTTT CAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT  
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC  
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA  
GGCTGGGGCACTGTCACCACTCCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTA  
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC  
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT  
GATGGTGC ACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT  
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC  
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC



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## **FIGURE 396**

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV  
GGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQL  
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCEDAYP  
GQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLDWI  
KKIIGSKG

**Important Features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

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**FIGURE 397**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC  
TACTGGGCCTGATTGGGGGCTGACTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT  
ACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTCACCCCCCATCCGCAACGTCACTG  
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA  
GCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG  
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC  
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG  
TGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC  
CTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC  
AGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA  
TGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA  
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCCCTGGCAGCCGGG  
AGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC  
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG  
AGGGCGAGGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGCCCCTGGGGACTACCA  
AGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCC  
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCT  
TCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG  
CCTTCTCCTCACTGCCCTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA  
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTCACAGTGGAGCTTCCAGGACC  
CAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 398**

MSDLLLLGLIGGLLLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGRL  
FTESCSISPKLRSIAVYYDNPHMVPPDKCRAVGSI LSEGEESPSPELIDLYQKFGFKVFSFP  
APSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCLARQGD  
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAA TLSPGASSRGW  
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE



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**FIGURE 400**

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHEG  
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWLPL  
AHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI  
TGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC  
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLSCRKNR  
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

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**FIGURE 401**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG  
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT  
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC  
AACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGGTACC  
AGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC  
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCTGTGTCC  
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT  
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTTCTGCCCCCTGA  
CCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGGTAAATAATA  
TTCAACATGTCAACAAC

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**FIGURE 402**

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS  
APRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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**FIGURE 403**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGAAAGCAGCGAGTTG  
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC  
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGG  
GCGGTGCGACGGCGGTAATTTCTGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG  
ACAGTGAACAAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTTCGATCA  
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC  
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG  
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGCCAGTGGTCTATCCAGCCCTGTTTGTGGTTTCAGATGGTCA  
TACCTACTCTTTTCAGTGCAAACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG  
ACATTGCCCATGTCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT  
CAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAAGTCAAAACAAGAAGACAAA  
AACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT  
GTTTAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAA  
TGAACAGTGTAACAGGCATTCTTCAATTCTTGTGACACATACAAGGACAGTTAATATCTAATAATGAGTGGTG  
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCAAGGGGTAA  
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT  
TGGACAGTGCTGGTGTGTTGACAGATATGAAATGAAGTCATGGGATCCAGAATAAATGGTGTGTCAGATTGTGC  
TATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA  
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTATGA  
CCATGATGTATACATTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTACAAAATGATAG  
CCTATTTAAATTTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA  
AAATTGCAGCTAAAGTTATAGAAGTTATGTTTAAATAAGAATCATTGCTTTGAGTTTTATATTCCTTACACA  
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTTGAAGTGTACTATAATAAATTTTCACGAGA  
ACAACTTTGTAAATCTTCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAGAT  
AATTCTAAGTGAATTTAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT  
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA  
AAAAAAAAAAAAA



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**FIGURE 404**

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD  
EVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV  
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPGPSDK  
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTKLLRPERSRFDTSILPICKDS  
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNEWCYCFQRQQDP  
PCQTELSNIQKRQGVKKLLGQYIPLCEDGYYKPTQCHGSGVQCWCVD RYGNEVMGSRINGVA  
DCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

**Important features:****Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins.**

amino acids 353-365 and 339-352

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**FIGURE 405**

[illegible]

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**FIGURE 406**

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRCSQRNQTHRSSLHYKPTPDLRISIENSEE  
ALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQHQE  
ESLAQGPPLLATSVTSWWSPQNI SLPSAASFTFSFHSPHTAAHNASVDMCELKRDLQLLSQF  
LKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH  
SRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGEKVLGI  
VVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCE  
CNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVP LPCRKRPRDY  
TIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLEGYNLYRLV  
VEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIYPSMCWIRDS  
LVSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLGLSLVLGLPWALIFFSF  
ASGTFQLVVLYLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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**FIGURE 407**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG  
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC  
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA  
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC  
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC  
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC  
TCTCAGAAGGCGGTGGTGGCCAGCTGGGATC**ATG**TTGTTGGCCCTGGTCTGTCTGCTCAGCTG  
CCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA  
CTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTCAC  
AAGCGTTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT  
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAACGTGTGCCGGAT  
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC  
CCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT  
CACTGAATGGGTGGATGGCTGTGACTTC**TAG**GATGGACGGAACCATGCACAGCAGGCTGGGAA  
ATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG  
TGAAA

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**FIGURE 408**

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY  
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGYWE  
AWRHHCQGKDLTEWVDGCDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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**FIGURE 409**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
CTCTTTAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCGTGCTCCTTCTGGCC  
GCTCTGCCTCCGGTGCTGCTGCCCTGGGGCGGCGGCTTACACCTTCCCTCGATAGCGACTTACCTTTACCCTT  
CCCGCCGGCCAGAAGGAGTGCTTCTACAGCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTAT  
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTGAACAAAGAAAA  
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTAGCACCATT  
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG  
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
AGACTAAGCAAAAAGTGGGCACATACAAATTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGC  
AAGTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGCAGCCATTCAAGTTTAT  
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAAGTAACTTAACTCCAACTAGAGTACGTAACATTGAAA  
AATGAGGCATAAAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
AAAGTAGGAAACAGGTATAATTTAATGTGAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
TTGTACTTAAGTGTGTAAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATACTGCAT  
TTTCTTAACCTTGAAGAAATTTGCAAAATGTCTTAGGTGATTTAAATAAATGAGTATTTGGGCCTAATTGCAACACC  
AGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTGTAAATGCGGCAGTTACAAATTAAGTATTTGGAAGTTT  
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCAA  
CTTTTCTTATTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
AGATTTTTATAACCAAAATACATTTTCACTGTACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC  
CCAAAGCTGACATTTTCAAGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
AAATGAAGAATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTTCTCTAACCTTAACTTAAAGTGTAGGA  
TTTTAAATTAATGTGAGGTAAAATAAGTTTATTTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
TAATCATGTTATGTTAATTTAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA  
TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
AGAATTTAGAAAACCTTGAGAAAACCTAATCCAAAATAAAATTCACTTAAGTAGAACTATAAATAATCTAGA  
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
AACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTGAATTATTTTGTAAAGCAGGTACATTTTATA  
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAATAAATTTTATTTATAACAACTTTTAT  
TAAATGGCCTTTCTGAACACTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT  
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGTCTTAC  
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTTTAAAGTTATGCCATTTATAACGTTGTTTAT  
GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCTCAACAGGTTAGTAATGCTGGAATT  
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAATGAGGTAATGCCGTAT  
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGGCTGTAAATTTGCAATGAGAAGCAAAATTACA  
GTACCATAACTAATAAGCAGGTACAGATATAAACTACTGCATCTTTCTATAAACTGTGATTAGAATTTCTA  
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTGACTCCTTACCTAACAAATGAATTTGTACATAATCTTCT  
ACATGTATGATTGTGCCACTGATCTTAACTTATGATTACGTAACCTTCTTACCATATAAAAACGATAATTGCTT  
TATTTGGAAGAAATTTAGGAATACTAAGGACAATTTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT  
CATATGCTTTTTTAAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT  
AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATTTTAACTAAGGCCCAACCGATTTT  
CATAATGTAGCAGTTACCGTGTTTCACTCACACTAAGGCCTAGAGTTTGTCTGATATGCATTGGATGATTAAT  
GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGTGTTTGAATTTTATGGTAAATTAATCCTTCTTA  
CACATAATGGTGTCTTAAATTGACAAAAATGAGCACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTAT  
GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTCTCATCTGAAGTACAATAATGCACATCAGTGTTG  
CTCAAAGTCTTTTATACTTATAAACAGGCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATA  
AAATTATCAAAGGAAAA

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**FIGURE 410**

MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEYQ  
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL  
DNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE  
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 411**

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTCA  
GTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCACAGGGCTTGGGGGAAAGATGGTGGGGACCAAG  
GCCTGGGTGTTCTCCTTCTGGTCTGGAAGTCACATCTGTGTTGGGGAGACAGACGATGCTCACCAGTCAAGTA  
AGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCCTGGAGAGCCCTGGTGAG  
TGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAGGGCGACTATGAGCGGCTGGAGCGCCATTGCGTTCTAC  
TATGGGGACCGTGTATGTGCCCGTCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCGGGCAGCACT  
GGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGGCCTCAACAGGGAGCAGCGGCCCTGGCCAGAAGTGC  
TCTAATTACACCGTACGTTCTCTGCCCCAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGAGCCCATGG  
TCTCCCTGGAGCAAGTGTCTCAGTGCCTGTGGTCAAGCTGGGGTCCAGACTCGCACACGCATTGCTTGGCAGAG  
ATGGTGTGCTGTGCAGTGAAGCCAGCGAAGAGGGTCAAGCACTGCATGGGCCAGGACTGTACAGCCTGTGACCTG  
ACCTGCCAATGGGCCAGGTGAATGCTGACTGTGATGCCTGCATGTGCCAGGACTTCATGCTTCATGGGGCTGTC  
TCCCTTCCCGAGGTGCCAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGTGTGACCCAG  
ACAGACAGTGAAGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAAGCATCCTGAAGATCACAAAGGTC  
AAGTTTGCCCTTGTACTCACAATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGGCAGAGTTTGTGAGG  
GCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCACGGAGAGCTGGGCAGAGCGTGTCTGTGTGCTGT  
AAGGCCACAGGGAAGCCAGGCCAGACAAAGTATTTTGGTATCATAATGACACATTGCTGGATCCTTCCCTCTAC  
AAGCATGAGAGCAAGTGGTGTGAGGAACTGACGACACAGGCTGGGGAGTACTTTTGAAGGCCAGAGT  
GATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAGACTCCTTGCAACCCAGT  
CCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAGAATGCCACCAACTCCTTCTACTATGACGTGGGA  
CGCTGCCCTGTTAAGACTTGTGCAGGGCAGCAGGATAATGGGATCAGGTGCCGTGATGCTGTGTGAGAACTGT  
GGCATCTCCAAGACAGAGGAAAGGGAGATCCAGTGCAGTGGCTACACGCTACCCACCAAGGTGGCCAAGGAGTGC  
AGCTGCCAGCGGTGTACGGAACTCGGAGCATCGTGGGGGCGGTGTGCTGCTGCTGACATGGGGAGCCCATG  
CGCTTTGGCCATGTGTACATGGGGAACAGCCGCTGTAAGCATGACTGGCTACAAGGGCACTTACCCCTCCATGTC  
CCCCAGGACACTGAGAGGCTGGTGTCTCATTTTGTGGACAGGCTGCAGAAGTTTGTCAACACCACCAAAAGTGCTA  
CCTTTCAACAAGAAGGGGAGTGCCGTGTTCCATGAAATCAAGATGCTTCGTGCGAAAGAGCCCATCACTTTGGAA  
GCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACCCCATGGCTGAACCTGGAGATTCCATCC  
AGGAGTTTCTACAGGCAGAATGGGGAGCCCTACATAGGAAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCCGG  
AATATTCCACAGCCACAGCTGCCAGACTGACCTGAACCTTCATCAATGACGAAGGAGACACTTCCCCCTCCGG  
ACGTATGGCATGTTCTCTGTGGACTTCAGAGATGAGGTCACTCAGAGCCACTTAATGCTGGCAAAGTGAAGGTC  
CACCTTGACTCGACCCAGGTCAAGATGCCAGAGCACATATCCACAGTGAACCTCTGGTCACTCAATCCAGACACA  
GGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAAATCAAAGGAGGAACAAAAGAGAAGACAGAACCTTCTGT  
GTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACTGGATGTTCTGTAAAGCAGGCGGTGCTTTGTAAAG  
GTGAGGCTCAACGGAGTGAGAGTTCTTGCTAGTGAGCAGATCCAGGGGTTGTGATCTCCGTGATTAACCTG  
GAGCTAGAAGTGGCTTCTGTGCCAACCTTAGGGCTTGGGGCGCTTGACAGTGTCTACAGGCCCAACGGG  
GCCTGTGTGCTGCTTCTGTGATGACCACTGCCCTGATGCCTACTCTGCCTATGTCTTGGCAAGCCTGGCTGGG  
GAGGAAGTCAAGCAGTGGAGTCTTCTCTAAATTAACCCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAAC  
AAGCTCAACTACCGTCGGACGGACCATGAGGATCCACGGGTAAAAAGACAGCTTTCCAGATTAGCATGGCCAG  
CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCCCTATGCTTGTGAGAACCTCCGGGCATGTGAAGAGGCA  
CCACCCAGTGCAGCCCACTTCCGGTTCTACCAGATTGAGGGGGATCGATATGACTACAACACAGTCCCCCTCAAC  
GAAGATGACCCTATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTAGGGCCTGCTAT  
ATCAAGGTGAAGATTGTGGGGCACTGGAAGTGAATGTGCGCATCCCGCAACATGGGGGGCACTCATCGGGGACA  
GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACCAAGCCCAATGTCTCAGTGCCTGT  
CTGGAGTTCAAGTGCAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCCCTGGTGAAGGTGATCCCCAG  
GGCAGCTGCCGTGAGCCAGTGTGAACCCCATGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCAGTCAAC  
AACGACACCACTGAGTACACCATGCTGGCACCCCTTGAGCCCACTGGGGCACAACATATGGCATCTACACTGTCACT  
GACCAGGACCCCTCGCACGGCCAAGGAGATCGCGCTCGGCCGCTGCTTGTGATGGCACATCCGATGGCTCCTCCAGA  
ATCATGAAGAGCAATGTGGGAGTAGCCCTCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTC  
CAGTACCTCCAAAGCACCCAGCCAGTCCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGCCTCGAGGAGGCAG  
CAGCGAGCGAGCAGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCCTCTGTGAGATTCTCTAGAGTTGCTCAACAG  
CCCCTGATCAACTAAGTTTTGTGGTACTTCAACCTCTTGGCCCTCATTTTCATGTGACAGCCATTGTGAGACTGA  
TGCAAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTTCTGTAATTTGCTTGTGTTTCTTTCATGCCTTTA  
CTTACTTTGTCCATGCTACTGATTGGCAGTGGCCCCCACAATGGCACAATAAAGCCCCCTTTGTGAACTGTTC  
TTTAAATGAAACACAAGAAATGGCCACTGGTAAACTCTGACAGTTCAACTGTACTTCATTTAATGCCATTAAT  
GCAAAATATACTTCTCTTTTTCATGTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA  
ATAACCAATATAAAGCATATTTCTTGGCCTTGCTCCACAGGACATAGGCAAGCCTTGATCATAGTTTCATACATAT  
AAATGGTGGTGAATAAAGAAATAAACAACAATCTTTTACTTGAATGTAAATAACTTATTTATTTCTTTGCTA  
AATTTGGAATCTAGTGCACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTCCTCTACCAAGTCTGG  
AAAGAACATCTCCTGGTATCCACAATTACACCAGGTTGCTAACTGTATTTGTACATTTCCCTTTGCATTGCTTT  
TGTTCTTGCTAGAAACCCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA



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**FIGURE 412**

MVGTKAWVFSFLVLEVTSVLGRQTM LTQSVRRVQPGKKNPSIFAKPADTLES PGWTTWFNID  
YPGGKG DYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP  
GQNC SNYTVRFLCPPGSLRRDTERI WSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS  
EEGQH CMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTKTPKL  
LTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPYMVMNP  
ETKARRAGQSVSLCCKATGKPRPD KYFWYHNDTLLDPSLYKHESKLVLRLQHQHAGEYFCKA  
QSDAGAVKSKVAQLIVTASDET PCNPVPESYLIRLPHDCFQ NATNSFYDVGRC PVKTCAGQQ  
DNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKESCQRCTETRSIVRGRVSAADNGEP  
MREGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFNKKGS AVFHE  
IKMLRRKEPIT LEAMETNIIPLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV KASVTFLDPR  
NISTATAAQTD LNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHLDSTQVKMPEHI  
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLE NLDVPESRRCFVKV  
RAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACVPAFCDDQSPDA  
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPRVKKTAFAQISM AKPR  
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYD YNTVPFNEDDPMSWTE DYLAWW  
PKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF  
KCSGMLYDQDRVDRTL VKVIPQGSCRRASVNPMLHEYLVNHLPLAVNNDTSEYTM LAPLDPLG  
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT FNCVERQVGRQSAFQYLO  
STPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVAQQPLIN

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**FIGURE 413**

GCCACGTTGTCTTCTTTCTTCACCAACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC  
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCCCTCTTGCCTCCTTCTC  
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCCCTTAGACTCCGTT  
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG  
AAGCTCTCGTGTGCTAGTGTCAAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT  
GTCACTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTCAGCTGGAAACCACCTGC  
CACTGCCAGTGCAAGTGTGGTGGACTGGACCACTGCCCCGCTGCTGCCACCTGACCTGACAGGGA  
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT  
CTAACTCAAACGTCCCACCTTCATTTGTTCCATTCCTGATTCTTGGGTAATAAAGACAACTTT  
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 414**

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS  
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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**FIGURE 415**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGTG  
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA  
GTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGCAGAACCTGAGCACCTTTTGCC  
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTGGGGG  
TGCCTCGAAGTGCCTCTATAAAGGATATTA AAAAGGCCTATAGGAACTAGCCCTGCAGCTTC  
ATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTT  
ATGAGGTTCTGTCAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAAGGATTAA  
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTTTGGTTTCA  
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG  
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAAC  
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGATGCGGACCACCC  
AGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA  
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG  
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC  
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA  
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA  
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG  
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT  
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT  
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTT  
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTGTGTGTGTTTTTGTTTTTA  
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG  
GCTTAAGAATTTGTCCATTTGCATTTCGGAAAAGAATGACCAGCAAAGGTTTACTAATACCTC  
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGTTTCAAGAATTAAAGCTGCAAGAGG  
ACTCCAGGAGCAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATCAAATG  
CCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTATTTTTTA

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## **FIGURE 416**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKALQLHPDRNPDDPQAQEFQDLGAAYE  
 VLSDSEKRKQYDITYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTFRQQDRNIPRGSDIIVDLEVTLEEYAGNF  
 VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCECPNVKLVNEERTLEVEIEPGVRDGMETPFI  
 GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW  
 KKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

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**FIGURE 417**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCACAGCAGGA  
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCGGGGCAG  
**GATG**ACCAAGGCCCGGCTGTTCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCTGCT  
GATCATCGTGTACTGGGACAGCGAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCTCTAG  
GCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCGGACAGGGACAGGGAGCTCACGGCCGA  
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC  
CAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA  
CTGGTCCCCGCGCGACGCCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG  
CGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTCGA  
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTG  
CTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT  
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGC  
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCCGCCACCTCAT  
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTCGTGCGCGACCCCTTCGTGCGCCTGAT  
CTCCGCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCCGTGCC  
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGCGCGAGGCCTTCCGCGC  
TGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT  
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA  
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA  
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA  
GGACTGGTTCGCCAAGATCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA  
CTTTGTTCTCTTCGGCTACCCCAAGCCGAAAACCTCCTCCGAGACT**TGA**AAGCTTTCGCGTTG  
CTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCCAGTTTTTTTTATGACCTACGATTT  
TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT  
TTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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**FIGURE 418**

MTKARLFRLWLVLGSEVEMILLIIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTAD  
SDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEEESVRGYDWSPRDARRSPDQGRQQAERRS  
VLRGFCANSSLAFPTKERAFDDIPNSELHIVDDRHGAIYCYVPKVACTNWKRMIVLSGSL  
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI  
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL  
APFNEHWRQVYRLCHPCQIDYDFVGKLETLEDAQAQLLQVDRQLRFPPSYRNRTASSWEE  
DWFAKIPLAWRQQLYKLYEADFVLEFGYPKPENLLRD

**Important features:****Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

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**FIGURE 419**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG  
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT  
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA  
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA  
ACACCATTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA  
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTCGGGCA  
CGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAATGCCATCG  
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG  
GGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT  
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGATCGCAAGACGG  
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCAGTGTG  
AGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC  
TGCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT  
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTAGAAATAATGAAAATCCAA  
CACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCAC  
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA  
AGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGAGACGCCCATGGTGCCCC  
CCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCTCGCTGGTGCTCTACCCTTTCT  
TCCAGTTCCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG  
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAATTGACAAGGGCT  
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTGACTCAGGGAGGTGTCACCAT  
CCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA  
AGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT  
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTCCCATGTGCTTTAGTGGGC  
TTTGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACCTTGTTT  
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA  
AGTTCCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCTTGGTTGCCAGAGATAAAGTGA  
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAAATTAAAGTGCTTTTCT  
GGGTCAAAAAAAAAAAAA



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**FIGURE 420**

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM  
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGSKVLAKKEL  
AYVPIIGWMWYFTEMVFC SRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHEISM  
QVARAKGLPRLKHHLLPRTKGFAITVRSLRN VVS AVYDCTLNFRNNENPTLLGV L NGKKYHAD  
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA  
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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**FIGURE 421**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC  
GCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC  
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC  
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGCG  
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGGGTGCC  
CTGAAGGAGGAGGTGGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC  
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA  
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT  
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCGTGCCCCACG  
TCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG  
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCCTGGATGAGCAG  
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGGGCTGTGCGCCAT  
CTGGGCAAGGTTACAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC  
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTCATGATGCTGCACACGGGGCTG  
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC  
TGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCGAGCATGTCGTATCCTGGGGGCTGCTCA  
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCTCATCCACCGCTGCTGAG  
TCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA  
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACCTCCACTAGCTCCAAAATCC  
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG  
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGCAGCCTGAGG  
AAGCATCAATAAATATTTGAGAAATGAAAAA

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## **FIGURE 422**

MDTTRYSKWGSSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL  
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALREL  
RERVTOGLAEAGRGREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA  
QDHCADASAPHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFHWNQ  
GEPNDAWGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:**

**Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

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**FIGURE 423**

GC GCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGGC  
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCGCCGAGAAGCCTCGCTCGGC  
GCCCAACATGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGATCGC  
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCGCGCTGCCGCCGGAGCAGAGCCGGGTCCA  
GCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTTTACGC  
CCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAATGGTGA  
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT  
CTTTGTCACCACTCTCCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG  
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC  
TCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGCTGGAATGGCTGGTCTTTTTAGCAT  
CTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATTCCTGCTTGGTG  
TTCTTATGTGTTTTTCGTGATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT  
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA  
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA  
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGATAGATGATGAAGAAGAGAAAGAAGATCTTG  
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTGCTGGTGTGGATGAGGA  
GAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA  
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGCTGACACAGAGGTGGTGGGA  
AGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGT  
TTTCAAGAATACACACCAAAAACAATATGTCAGCTTCCCTTTGGCCTGCAGTTTGTACCAAATC  
CTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCTCTCTAGTCATTTGGTCTCATG  
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC  
AAACGTAGTGTTGGGATCTGTTGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA  
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCATAATCAGCACCTTCCAGAGACAAGGCTGC  
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACTG  
AGAAGCCTTGATCCTTTTTCTTGTGTAAAGTATTTATTTTTGTCAAATTGCAGGAAACATCAG  
GCACCACAGTGATGAAAAATCTTTCACAGCTAGAAATTGAAAGGGCCTTGGGTATAGAGAGC  
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAATT  
TTTCCAGCATTTCCACCATGGGCATTCCAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA  
GAGGACTCCAATAACAGCCAGGTTTACATGAACTGTGTTTGTTCATTCTGACCTAAGGGGTTT  
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG  
GCCATCAGAGACTCAAAGGAAGTAAGGATTTTACAAGACAGATTAAAAAAAATTGTTTTGT  
CCAAATATAGTTGTTGTTGATTTTTTTTAAAGTTTTCTAAGCAATATTTTTCAAGCCAGAAG  
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTT  
ATCTCAAGGGGTTCCCTGGGTCTTGAACACTTTAATAATAACTAAAAAACCACTTCTGATTT  
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAACCTCCAGTACCTGAAAGTGAAAGATT  
TGATTTTGTTCATCTTCTGTAATCTTCCAAGAATTATATCTTTGTAAATCTCTCAATACT  
CAATCTACTGTAAGTACCCAGGGAGGCTAATTTCTTT

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**FIGURE 424**

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAPW  
CPSCQQT DSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG  
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY  
VFFVIATLVFGLFMGLVVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEKDDSN  
EEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTREEVEPE  
EAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide  
isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

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**FIGURE 425**

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG  
CTGGGCCGTCGGAGAGTGCCTGTCTCTCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA  
GGGTTTGGAGATGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA  
AGTATTAGAAATGAGCTGAAGACCATTACAGATTATATTTTTGGGGACAGATTTGTGATGCTTGATTCACCTT  
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
TTAAATCAGAACTTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG  
AGTGTCAAAACCTGCAAGCAGTAGAGAAATAAGACAAGCTTCAAGAAATTTGGCATTGAAGTTACATCCTGATAA  
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGAACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC  
TGCTGTTAATCTGGAGAACTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTACACTGCCATGATTTAGCTCC  
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTTGGAGCTGTTAACTGTGGTGATGATAGAAT  
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAAGCTTG  
GACAGGAAATTTTTGTCAACTCCATACAACTGCTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTTTGTCAA  
AGGAGGAGATTGTTTGACTTCACAGACAGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA  
AGAAATATATTTGGAAAGTAAATACATAATCTCCAGATTTTGAAGTACTTTCCGCAACACACTAGAGGATCGTTT  
GGCTCATCATCGGTGGCTGTTATTTTTTCATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAT  
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCTCTGCAACAGACATCTGTAGTAA  
TCTGTATGTTTTTCAGCCGCTCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAATATGAAATTCATCATGGAAA  
GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATCTCATGTTACCACGCTTGGACCTCAAAA  
TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGCGAGCTTTACT  
ACCAGAGTTACGAAGAGCATCAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTATGA  
GGGACTCTGTAACATGTATAACATTCAAGGCTTATCCAACAACAGTGGTATTCAACAGTCCAACATTCTAGTA  
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCTAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
ACCCACCACCTTCAACGAAGTGTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATCTCCGTG  
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAGAAATGGCCCCGACATTAAGTGGAGTGAACAGTGGG  
CAGTATAGATTGCCAACAGTATCATTCTTTTGTGCCAGGAAAACGTTCAAAGATACCCCTGAGATAAGATTTTT  
TCCCCCAAATCAAATAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT  
CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAAGTTCTACAAGG  
GAAAAATCATTTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT  
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA  
AGCTGGGATCAGGGCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTCAAGAAGAGCA  
GATAAATACCAGAGATGCAAAAGCAATCGTGCCTTAATAAGTGAATAATTTGGAAGTCTCCGAAATCAAGGCAA  
GAGGAATAAGGATGAACCTTGAATAATGTTGAAGATGAAGAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG  
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGAGTTGTACTGCCA  
GAATTATCTACAGCACTGGTGTAAGAAGAGGGTCTGCAACCTTTTCTGTAAAGGGCCGGTTATAAATATTTTA  
GACTTTCAGGCTATAATATATGTTTACACATGAGAACAAAGATAGAGTATCATGATTTCTTTGTTATTTGCT  
TTTAACAACCTTTAAAAAATATTAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTACGTCATG  
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGACATGAGTCTGCTGTGCT  
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTACAGTTTTTTGGCTGACCTGAAAAGAGGTAAGT  
TAGTTTTTGGTCACTTGTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTAAAAACACCCAT  
GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCAATGTTTTCTTCTCTCA  
AAGGTTGAAAAATGCTTTTAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTCTGTATCATCCAGGAAAACCTGAGGGAATAAATA  
TAGCAATTAAGTGGCATTTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
TGTGTTTATGATTTTCTGAAATGCTTTTCATAGAAATTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
TTACATATTTGCCCTCTGAACCTTTGTTTTGACCTGTATCCTTTTATTACATTGGGTTTTCTTTTATAGTTTGG  
TTTTTCACTCCTGTCAGTCTATTATTATTCAAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT  
AATGATACTGTAGTTATTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTCAAGATAAATATTGACATAATA  
ACTGAAGTTATTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGA  
CTCAAAGAATCAAAATTTGTGAGTAAATGAGTTGTTTAGTTATAATTCAGAGTGTACAGAAATGGTAAAAAT  
CCAATCAGTCAAAAGAGGTCAATGAATTAAGGCTTGAACCTTTTTCAAAAAAAAAAAAAAAAAA

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**FIGURE 426**

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKLH  
PDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYRDFGIYD  
DDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD  
RMLCRMKGVNNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA  
FAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR  
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLAVFK  
GQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPNFPANDKEPWLVDFFAPWCPPCRALL  
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFNQSNIEYEGHSAEQILEFI  
EDLMNPVSVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS  
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLT  
PQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDCQAYAQTCQKAG  
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRNKDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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**FIGURE 427**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA  
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTTGA  
GTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGGTAG  
CGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTCAATT  
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG  
TCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACAACCTACC  
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC  
GCGGAGGGGACGCAGGCGTGAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC  
GTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTTTCTGATCAAA  
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT  
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG  
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT  
CCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT  
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA  
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTAAACCAGCT  
ATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC  
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA  
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTGTGATTGCAGTAAATTACT  
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAACTTTTAATTATTTTCT  
AAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAAATTTTGTACACATTGATTGTTAT  
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTAGCTTATAGTTCTTAAAAG  
CATAACCTTTACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGAATGACAAAT  
GATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG  
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAAATAAAATTTAACATTTAAAAAAA  
AAAAAA



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## **FIGURE 428**

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA  
PGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRHAM  
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC  
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQKDDH  
QASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

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**FIGURE 429**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCC  
TTTCCTAACCCAACCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC  
CAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT  
CCTGGTAACTTGGGTTTTTACTCCTGTAACAAGTAAACAAGTCTTGCTACAGAGAATAT  
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGTCTGTT  
CAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATTTCCAAA  
TGAAAATCAAGTAGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA  
CAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA  
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAGTGACCCCAT  
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTGG  
ATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA  
TGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAGATATAGTGGCGA  
CAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC  
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTTGTCGAGAAATAAC  
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTCTCATACTCTTTCACATGAA  
AGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAA  
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA  
GAAACTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG  
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCGTATTTGACTTACATTCTGG  
AAACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGATACAGCCCCAGGAGAGCAAGC  
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG  
GTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTGAAAAACAGTTTGTAAGCCTTTC  
AACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTATATTTTCATAATTCTATGTGTAT  
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 430**

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM  
LHPIFEEASDVIKEEFPNENQVVFEARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ  
RSVKALADYIRQQKSDPIQEIRD LAEITTLDRSKRNIIGYFEQKDS DN YRVFERVANILHDDC  
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN  
GEELTEEGLPFLILFHKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP  
ADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV  
ASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:****Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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**FIGURE 431**

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA  
GGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG  
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGCGTG  
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG  
CGGGGTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG  
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG  
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCCAACGGCGTGAGTGCTACAGC  
TGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCGTGAGCTGCTACAAC  
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG  
ACTGTGTCCCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA  
GGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC  
AACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCGGGTGCCCCCTCCAGAGCCCACG  
ACTGTGGCCTCAACCACATCTGTCAACCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC  
ACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC  
CGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG  
CAGTATCCTGCAAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCCACAGCT  
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTAGAGCTTCTCCACCTGGA  
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCCTGTTCCCA  
CCACTGGACTGGGCTGGCCAGCCCCTGTTTTTCCAACATTCCCCAGTATCCCCAGCTTCTGC  
TGCGCTGGTTTTGCGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA  
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTGTGATG  
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC  
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC  
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC  
TTACTAGACTGTGAGCTCCTCGAGGGGGGGGGCCGGTACCCAATTGCCCCATAGTGAGTCGTA

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**FIGURE 432**

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVCAPGVDVCTE  
AVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQAQDRCNAKLNLTSRALDP  
AGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCFDGNVTLTAAANTVSLP  
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTTVAST  
TSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSGOYPAK  
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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**FIGURE 433**

[illegible]

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**FIGURE 434**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSGILLILSRCKC  
SFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRRLLLEPLDANVDA

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**FIGURE 435**

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTCACTCTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA  
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGCAGGCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG  
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCACAGCCACCACCC  
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT  
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC  
TCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTTTTGCCAACAATTTTA  
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGA<sup>AAA</sup>  
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG  
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT  
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 436**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTEFLH  
YDCGNKTVTPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

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**FIGURE 437**

GTTCCTCTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG  
TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGTCTACCTCACGGCGCAAGTGTGGATTCTGT  
GTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCCAGAACTGCCCCCTCCGTTTGCTCGTGCAGTAACCAGTTCA  
GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC  
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG  
GCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCTCAACACCCTGGAGCTGTTTCG  
ACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA  
ACCCCATCGAAAGCATCCCCTCTTACGCCTTCAACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCA  
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCA  
ACATTAAAGACATGCCAATCTACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG  
AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAACTCACAGGTACAGCTGA  
TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACCTCAACTTGGCCACAATAACCTCTCTTCTTTGC  
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTG  
ACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTC  
CCATGCACATGCGAGGCGCCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCTTCATCATGG  
ACGCACCTCGAGACCTCAACATTCTGAGGGTCGGATGGCAGAACTTAAGTGTGCGACTCCCCCTATGTCTCCG  
TGAAGTGGTTGTGCCCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCAAGGATCTCTGTCTCAACGACG  
GCACCTTGAACCTTTCCACGTGCTGCTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCA  
ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAG  
TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTACCACGTCCACTG  
GTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGCTACCCGTGTGCCAAGCAGGTGGCAGTAC  
CCGCGACAGACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT  
GCTTTGTGGCAGTGACTCTGCTAGCTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGC  
GGAGTACAGTCACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG  
CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTATGACCATATTAACCT  
ACAACACCTACAAACAGCACATGGGGCCACTGGACAGAAAACAGCCTGGGGAACCTCTCTGCACCCCACAGTCA  
CCACTATCTCTGAACCTTATATAATTACAGACCATACCAAGGACAAGGTACAGGAACTCAAATATGACTCCCCCT  
CCCCAAAAAAGCTTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT  
TTCTTGTATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGACAAAA  
AGTCAAAACA

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**FIGURE 438**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR  
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN  
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE  
GAFEGLENLKYLNLMCNKDKMPNLTPLVGLLEEMSGNHFPEIRPGSFHGLSSLKKLWVMNS  
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHPWNCDCDILWLAWWL  
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP  
MSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSNASAYLNV  
STAEINTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV  
AVPATDTTDKMQTSLDEVMKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE  
IIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTEENSLGNSLHPT  
VTTISEPYIIQTHTKDKVQETQI

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**FIGURE 439**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG  
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC  
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA  
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC  
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATTAGTGAAAAAAT  
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTCAACGACACCCTGATC  
TTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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**FIGURE 440**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEVK  
HCTDQISFKKRLSLKKSWWK

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**FIGURE 441**

GAACATTTT TAGTTC CCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG  
GGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC  
ACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG  
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG  
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA  
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGAAGGGGC  
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT  
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC  
CAAAGAGGCCCCAGCCGACAAGTGATCGCCCAAGCCTTACTCACCTCTCTCTAAGTTTAGA  
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG  
AGGCGAATAAATGTTCAAACCTGTA

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**FIGURE 442**

MPSPGTVCSSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG  
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 443**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG  
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTC  
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTGCTC  
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT  
ATGTCCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACA  
CCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCAGCCTGGGGCCAGAGTCTTTGTCCCC  
CGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCCAGAAGTGAGATCATGGACAAAAAGGGCAAA  
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACTCACGCCG  
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGAGACAATGGA  
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC  
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCACTAACCAAACTGAAG  
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTCAGTCATGTTGCT  
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC  
CTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG  
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGACACGGGCAGCAGAGTG  
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA  
GAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCCTGCCTGCAG  
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAAGAGCCTCCTTGTTTCATAACC  
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGATGTTTTAAACACACACCTC  
TAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC  
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAA



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**FIGURE 444**

MNTWLLFLPLFPVQVQTLIVVIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGWV  
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ  
QEAELTPRPAGVVPGA

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**FIGURE 445**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTGC  
TGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA  
GGAAGGGGCAAGGGCGGCCTGGGCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACCTGG  
TGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG  
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA  
TGTCACAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCCGTATCC  
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG  
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCGCCTCTGCC  
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT  
GCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGACCATCCTCCT  
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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**FIGURE 446**

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE  
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSPRI PVDLPEARCLCLGC  
VNPFTMQEDRSMVSPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

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**FIGURE 447**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA  
TGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT  
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC  
CCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTGGATG  
GAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAAGTGGGAGACTGGGGATGACCGGT  
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAGAACCAG  
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC  
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA  
TGGAGAAGGCTTCCCTCCCCCTCCCCTCCCTTGGGGGCTTTGTGGCAAAAATCCTATGGTTATCC  
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC  
TTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAAGTGAAGCGCCTTTGCTGCTGTTTCCTCT  
GTCCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTCTTCCAAGCGACT  
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTGGGCCTTCTACATG  
GCCTGGCTCTCCTTACCTGCTGCATGGCGTCGGCTGTCACCACCTTCAACACGTACACCAGG  
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAACCCGAAGTGCCTACCA  
CATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCACCCTGGGTCTTTGACC  
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC  
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA  
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT  
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA  
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTGCGGTGCCA  
CTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCACCCACATCTCACACATCCAGAA  
TTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGCTAAACCATGGAGATAAAAAGAAG  
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 448**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV  
SLDGDNTSTQEVVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE  
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQLP  
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLTTCLELWLG  
LLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

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**FIGURE 449**

CCACACGCGTCGCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC  
ACGCGTCCGCTGCAAGCTCGCGCCGACACTGCCTGGTGAGGGAAGGACGCCGGCGCTCTCGCCGCTCCCG  
CGCGCGCTCGCAGCTCCCCACCGCCCGCGCGCGCGCGCGCAAGCATGACTGAGCCGCTCTCTG  
GCAGCTGCCCGGGGCGCAATTGGCAGGCTGTTTCCGCGGAGTAAAGGTGGCGCGGTGACTGGTGGTTTCCAAT  
GACGGACATTAACCAAGCTGTCAAGTCTGGGAGTCCGAGCGCCGAGTTTGGAGTTTTCCTCCCGCAACGCT  
CACAGTCCGAATCGAGAGGAAGGAAGGCGGAGGAAGCAAGCTCGGGTCCGGCAGTATGTTGGAAACT  
TGCGGGTCTTAGAAGTCGCCTCCCGCCTTGCCGGCGGCCCTTGACGCCCGAGCGAGCAGCAAGTGAGACAT  
TGTGCGCTCGCAGATCCGCGCGCGGACCGGGGCTGCTCGGAAACACAGAGGGTCTTCTCTGCCCGCTGCA  
TATAATTAGCTTGACACAAAGGGAGCAGCTGAATGGAGTTGTCACTCTGTGAAAAAGGATTTCTGACCGAGCG  
CTTCCAATGGACATTTCCAGTCTGTCTGAAAGATTCTCGTAATGGATTCTGCTGCTGCTCGGTCTCTGTCTA  
ACTGGTGTGAGGAGGCCCTCGGGGCTGTTCTGTGTCTGCTGGGGCTGTTCTAGATGCTGCCCGCGCC  
CCAGCGGGTGGCCGAGCTGTGCGGTGCGAGGGGCGGTGCTGTACTGCGAGGCGCTCAACCTACCGAGGCGC  
CCCAACAACCTGTCCGGCTGCTGGGCTGTCTGCTCGCTTACAACAGCCTCTCGAGTGCGCCGCGCGAGTTCA  
CGGGGTTAATGCAGTCACTGGCTCTATCGATCAACATACATCTGCTGCTGCGAGGGGACGCTTTTCAGA  
AACTGCGCGAGTTAAGGAACTCACGCTGAGTTTCAACACAGATCACCCAACCTGCCAACACCACTTCCGGCCCA  
TGCCCAACCTCGCGAGCTGTGACCTCTGTGTAACAAGCTGACGGCGCTCGCGCCGACCTCTTCCACGGGCTGC  
GGAAGTCCACACGCTGCATATGCGGGCCAACGCCATCAGATTGTTGCCGTGCGCATTTCCAGGATCGCGCA  
GCCTCAAGTTTCTCGACATCGGATACAATCAGCTCAAGAGTCTGGCGCGCAACTCTTTCGCCGGCTTGTTAAGC  
TCACCGAGCTGCACCTCGAGCACAACGACTTGGTCAAGTGAACCTCGCCCACTTCCCGCGCTCATCTCCCTGC  
ACTCGCTCTGCTCGGAGGAAACAAGGTGCCATTGTGTGTCAGCTCGCTGGACTGGGTTTGAACCTGGAGAAAA  
TGAAGTTGTGCGGCAACAGATCGAGATCAGATCGAGGCCCATGTGTTTCGAGACCGTGGCGACCTGCAGTCCCTGC  
AGCTGGACTCCAACCGCTCACTACATCAGAGCCCGGACTCTCAACTCTTGAAGTCCCTGACAAGCATCACCC  
TGCGCGGGAACCTGTGGGATTGCGGGCGCAGCGTGTGTCCCTAGCTCGTGGCTCAGCAACTCCAGGGGCGCT  
ACGATGGCAACTTGAAGTGCGCCACCGCGAGTACGCACAGGGCGAGGAGCTCTGGACCGCGTGTACGCTTCC  
ACCTGTGCGAGGATGGGGCGAGCCACAGCGGCCACTGCTCTCGGCGCTCAACCAACGAGTGTATGGGGG  
CCCCTGCCAGCTCGGCCACACGCTCGCGGACGGCGGGGAGGGGAGCAGCAGCGGCACATTTCAGGCTGCCACCG  
TGCTCTTCCAGGCGCGAGCAGCCGAGAACCGTGCATGCAACAGTTGGTCAACGAGGTCAGCGGCACCTTCA  
CTTCTCTCTTCTCATCGTGTGTCTGGTGCTCTACGTTCTGCTGGAAGTGTTCGACGAGCCTCAGGCGCTCA  
GACAGTGCTTTGTACGCGAGCGCAGGAAGCAAAAGCAGAAACAGACCATGCATCAGATGGCTGCCATCTGTGCC  
AGGAATACAGTTGATTACAAACCAACCACTTGAAGGAGCCCTGGTATCATCAACGAGTATGGTCTGTGTA  
CCTGCCACCGCAGCGCCGCGAGGGAATGCGAGGTGTAATTGTCCAGTGGCTCTCAACCCATCGCTACCAATA  
CGCTGGGACCGCGGAGCGCGCGCGGCGGACCAAGCTGGGCTCTTGTCTGTCTGATATGCTCCTTGAC  
TGAAACTTTAAGGGGATCTCCGAGGACTTGCATTTAGCTTTTGTGTTTAAAAACAAAGGAATTA  
AACACAACAAAAAACCCACCCCAACCTTCAGGACAGTCTATCTTAAATTTATATGAGAATCCTTCTCTCC  
TTTGAAGATGTCCATATCTCAGGAATCTGAGAGTGTAAAAAAGGTGGCCATAAGACGAGAGAGAAATATCGTG  
CTTTGTTTTATGCTATCTCTCCACCTCGGCATGATTAACATCATGTATGTAAGAATCTTAAGTCCATACGC  
ATTTCAATGAAGAACCTTGAAGAGGAATCTGCAATCTGGGAGCTTAAGAGCAATGATGACCATGAAGACTA  
TGTTCTTACTTTGTGTGTGTCTGTATGTTTCTGCTGTGTGCTCTTGTAGGCAAGTACAAACGTTGCTACACA  
AACGGGAATTTAGCTCACATCATTTTCATGCCCTGTGCCCTAGCTCTGAGATTTGGTGGGGGAGGTGGGGGA  
AACGGCAGGAATAAGGGAAGTGGTAGTTTAACTAAGTTTAACTAAGTCTGAACTCTTTTCTTCTCAAAATTA  
ATTATCTTTAAGCTTCAAGAACTTGTCTGACCCCTTAAGCAACTACTAAGCATTTAAAGAGAACTCAATT  
TTAAAGGTGTAGCACCTTTTTTTTTTATCTTCCACAGAGGGTGCTAATCTCATTATGCTGTGCTATCTGAAA  
GAACTTAAGGCCAATTCAGTCTCTGCTCGGGCATTTGATGATGATGACCTCCATTTGTCAGTACCTTCCAG  
CTGATTAAGTTTCAGCAGTGTATTGAGTTTTCGAATTTATATAGAAAAAAGTCTTTTTCATGACAAAT  
GACACTCTCACACCACTTTCAGCCCTAGTAGTTTTTGTAGTTTGGACCAAGGAAGCAGTTAAATGAGACCTGTC  
CTCTGCTGCACTCAGAAAAATAGGCAGTCTCTGATGCTAGATCTTATGATTTAATAGTTGAGACCACT  
TACCACAATGACGCTATCTCCAAAGACTACAAAGTTTACCATCGCAAGGAAGGTTATTCAGTAAAGGAA  
ATAGTTTTCTCAACCAATTTAAAAATATCTTCTGAACATCAAAAGTAGAAGAGCCCCAACCTTTTCTCTGCG  
CTTCAAGAAGGCACATTTGGTATGATTTAGCATCAACAACATTTATGATATATGATATAGTAAATCAGAGGGG  
CAATGCCACTTGTATTCTCTCCAAAGTTTTCAAAGCAAGTACACACAGATCTCTGGTAGGATTAGGGGCCACTT  
GTGTTTCCGGCTTATTTTAGTGCAGTCTGTGACGAAGTTTATGCTGATCTATGATCTGAGCCAGTAGAACG  
GGCATTGATGATCAGATGAGTGGTAGGAAGAACATCATACATACCCCTCTCACAGAGAAATATCAAGAA  
CCAGAAATATATCTGTTTGGAGCAAGAGTGTATAATGTTTCAGGGTAGTCAAAATAAACATAAATATCTCC  
TCTAGATGAGTGGCGATGTGGCTGATTGGGTCTGCCATTGACAGATGTCAAAATAAAGGAATTAGCTAGAA  
TATGACCAATTAAGTTGTCTTGAATAATATTTTGAATAGGTTTGAAGTGTCA

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**FIGURE 450**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN  
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQIT  
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLKF  
LDIGYNQLKSLARNSFAGLFKLTLEHNDLVKVNFAHFPRILSLHSLCLRRNKVAIVVSSL  
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSITLAGNL  
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSGHLLSAV  
TNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI  
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVII  
NEYGSCTCHQQPARECEV

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**FIGURE 451**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCCTCCAGTCACCCTCCCGCCGTTAC  
CCGCGGCGCGCCCGAGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAAACTAATACGGA  
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT  
ACCATCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAAATGACTTCG  
AAATTTATCTTGGTGTCTTCATACTTGCTGCACTGAGTCTTTCAACCACCTTTTCTCTCCAA  
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA  
GTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT  
GTTTTTATTACAAAACCTACCCTAACCATTATACTTTGGTAACTGGCCTCTTTGCAGAGAAT  
CATGGGATTGTTGCAAATGATATGTTTGATCCTATTCGGAACAAATCTTTCTCCTTGGATCAC  
ATGAATATTTTATGATTCGAAGTTTTGGGAAGAAGCGACACCAATATGGATCACAACCAGAGG  
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGAACAGATGTAAAAATACATAAGCGCTTT  
CCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT  
GAATGGTTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTTGGGAAGACCCTGATGAC  
ATGGGGCCACCATTGTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAAG  
AAGTTAGGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC  
ATCACAAGTGATCATGGAATGACGCAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCAGTAC  
CTGGATAAAGACCACTATACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA  
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCCTAATCTTACTGTTTACAAA  
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCAACCAATCATAGCA  
CTGGCTGATGAAGGGTGGCACATTTTACAGAAATAAGTCAGATGACTTTCTGTAGGCAACCAC  
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTGCCTTCAGA  
AAGAATTTCTCAAAAGAAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTC  
AATATCACTGCCATGCCACACAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCA  
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTAAACCAGCA  
GAATATGACCAAGAGGGGTCATACCCTTATTTCATAGGGGTCTCTCTTGGCAGCATTATAGTG  
ATTGTATTTTTTTGTAATTTTCATTAAAGCATTTAATTCACAGTCAAATACCTGCCTTACAAGAT  
ATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAAATGTTACTTTGAAGTGGATTGTCAT  
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATCTGGGAAACCAGTT  
CCAAACATCTGCAGAAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACA  
CACATACACACACACGACCAAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT  
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTTGGCGCAGAT  
AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT  
CTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAACTTGATTG  
AAAATGACAACTTTTTGCACCCATGTCACAGAATACTTGTTACGCATTGTTCAAACCTGAAGGA  
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA  
GGTGATAAGTGTTGAAAATTAAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTC  
CAACAGCAGAATGCAACTGTGGGCATTTCTTGCTTATTTCTTTCCAGAGAACGTGGTTCAT  
TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTGCTTCTAAATATATTGTTTCTGT  
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCATAAATAATGAAGACAC  
CATGAATATACTTTTCTTCTATATAGTTCAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT  
CTCAGCAATGTTTTCTCTTGTGTAATTATTTGCTCCTTTGAAAATTAAATCACTATTAATT  
ACATTA AAAATCAAATTTGGATAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 452**

MTSKFILVSFILAAALSLSTTFSLQLDQQKVLVSEFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ  
VTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIWIT  
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWETSKEPINLGLLYWED  
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL  
DQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKEDVPERWHYKYNRIQP  
IIAVALDEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC  
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSPYPYFIGVSLGS  
IIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Important features:****Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,  
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

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**FIGURE 453**

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC  
TATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT  
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGACCAA  
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA  
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC  
TGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAACTCCA  
ATATGAGGACAAGTTCCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCAACACCTA  
CACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGGCAGAGATGGAGAGTTC  
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGAGGAACTGAA  
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT  
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGGAAGAGAAGATTGCTGCGCTCTTTGATCTTGA  
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT  
GATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC  
TGCTTTTTCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT  
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCCGTGTTTGCCTGTG  
CTCCCTGCTGCGCCACTTCCCCTATGCCCAGCGGCAGTTCCCTGAAGCTCGGGGGGCTGCAGGT  
CCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT  
CTACGACCTGGTCACGGAGAAGATGTTGCGCCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC  
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCTGTGGGAACAGGGCTG  
GTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGATGCCCGTGAGAAGGTGCTGCA  
GACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG  
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA  
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGCTGAAGGAGCTGAGATTG  
AGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG  
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCTTGGCCATTAAATGGAAACCTGAAGG  
CCAA  
AA

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**FIGURE 454**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEELD  
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY  
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI  
NKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAFLGA  
AFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGLQV  
LRTLVOEKGTAVLAVRVVTLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPGLWEQGW  
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE  
DEGYFQELLGVSNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

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**FIGURE 455**

CCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAGT  
GGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCCTA  
CCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT  
CTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC  
TCCTATCTTCTGAATTCTATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCCTTG  
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA  
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTTCTCGCCA  
ACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG  
GAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCAATGGATCCG  
ACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT  
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAGGAAGAAAGTTT  
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCC  
AGGGGGTCAAATCCATCCCCACCCTGGCTACTCCACCCTGGCCACTCTAACGACCTCATGC  
TCATCAAACCTGAACAGAAGAATTTCGTCCCCTAAAGATGTCAGACCCATCAACGTCTCCTCTC  
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCAAG  
TGCACTTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG  
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT  
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCTT  
GGGGAGATTACCTTGTGCCCCGCCCAACAGACCGGTGTCTACACGAACCTCTGCAAGTTCA  
CCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCTATCCAGGACTCAGCACACCGG  
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTAGACCCTCATTCTTCCAGAGA  
TGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC  
CCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTCCAAAACCTGTCCAG  
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTT  
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAATAAAAAA

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**FIGURE 456**

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS  
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV  
YESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRIPTKDVRPINVSSHCPASAGTKCLVSG  
WGTTKSPQVHFVKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSSGGPVVCN  
GSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 457**

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTTGCTTCCTGAACT  
AGCTCACAGTAGCCCGCGGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGG  
CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG  
CCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA  
CCCTGCTGACTTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACCAGC  
TCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCCAAGAGTTGCAATCTC  
TTCAAGTCCAGAATATAAAGCTTGCAAGGAGTCTGCAGCATGTGGCTGAAAACTCTGTCGTGAGCTGTATAACA  
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA  
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAAC  
AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCC  
CTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATG  
TCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA  
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG  
AAGGTGACTGATTTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG  
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCGTGTTCCTGTT  
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC  
CAAACAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAA  
TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCTTACACTTGGTGGAAATAAGAACTTTTGAAGTAGAGGAAA  
TACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTAC  
CAGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC  
CATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
GCATTCCCTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATAT  
ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGT  
GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT  
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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**FIGURE 458**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL  
KRCVCERRAGMVKPESLHVPPETLGEGD

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**FIGURE 459**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCGAGGCCTGCGCAGGGCAGGAGCAGCTGGCCCAC  
TGGCGGGCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCTGT  
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGTGGT  
CAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA  
GTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA  
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA  
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC  
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACT  
ACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGTGCTTTGAAG  
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA  
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC  
ACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGCTGGTGGCCTCCTACGACG  
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTGGGGAGTTCTCTACG  
CAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA  
GCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACGAGGGATGGCCAGAGC  
TGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCCTCAG  
CCAGGGGCCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA  
GGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCTTGCACGCTGTGTGCGCCTCTCCTC  
CTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACCAGCCTCAGAGGGTCTTCT  
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGGACTGCTGACGGCTGGTCCTG  
AGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGTGCTGGTTTTGAAAAA  
AAAAAAAAAAAAA



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## **FIGURE 460**

MRVSGVLRLLALIFAIVTTWMFIRSYSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA  
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV  
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRG  
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

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**FIGURE 461**

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA  
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC  
TAGAACCCGACCCACCACC**ATG**AGGTCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT  
CCAGTGGTCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTATTAA  
GGAGCCTCAAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA  
GTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA  
GCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCACCGGAGA  
CAGAGGAAAGGAGGCCAACAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCACACAGCACA  
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAAACCATGGTGAACACACTGTCACCCAGAGG  
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA  
GACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTGAGAGAA  
GCACCAGGGCAAAGCGGCAACCCACAGCCAAGACGCTCATTCCCAAAGTCAGCACAGAATGCT  
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC  
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAGAGCCCCACGACGCA  
GAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA  
ATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC  
CAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTCTTCCTGGACTCCAGACA  
CTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACCCCTTTGGCTTCATGGAGCT  
CAACTACTCCTTGGTGCAGAAGGTGCTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT  
CCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG  
CATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG  
CGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTCGGACATCCTTCTACGGCTTTAC  
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAACGTGCCCTCT  
TGGGAAGGACGTCCGCTACTTGCACTTCCCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC  
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTCAGGCACAGACCCCAGGA  
AGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTCTCCGATA  
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGCCCACTGGAGGATATACCGCCC  
CACCCTGGGGCCCTCCTGCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG  
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT  
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA  
AGGGATAATCCGGCTGTACCAGCGTCTGGTCCCGGAAGTCCCAAAGCCAAGAAG**TGA**CCGGG  
GCCAGGGCTGCCATGGTCTCCTTGCCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC  
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAGGAGTTCCAAGGGAACAC  
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCA  
GTACATTGCTGTAGGTCTGAGGCCAGGGATTTTAAATTAAATGGGGTGATGGGTGGCCAATA  
CCACAATTCCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCC  
TGGATTTACAGAAACATATAGATCTGGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCT  
TGAAGGTATTACTTAACTTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC  
TAGAAGGTCTATACTTGTCTTGTCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAAAC  
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAACAAAA  
AAAAAAA

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**FIGURE 462**

MRSCLWRCRHLSQGVQWSLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK  
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS  
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNQGQTRKLTASRTVSEKHQGKAA  
TTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPEKKPQATPPPAPFQSPTTQRNQRLK  
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW  
DRLEHFAPPPFGFMEINYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGGILNNSH  
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVPLGKDVRV  
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFAREALHMDRYLLLHPDFLRVMKNRFL  
RSKTLGDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDYTSWKRLIFYINH  
DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

**Important features:****Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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**FIGURE 463**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGGCGCAAGGGTGAGGGCGGCCCGAGAAC  
CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTGCCCCCTCAAATGGTCCCTTGCAACCATGTG  
ATTTCTACTTTCCTCACTGTTGGCTCTCTTAAGTGTGTCCACTCCTTCATGGTGTGACAGCAC  
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCTTGGAATAAAATACGACTTCCTGA  
GTACGTCATCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG  
GGGAACCACGAAAGTAGAAATCACAGCCAGTCCAGCCACCAGCACCATCATCCTGCATAGTCA  
CCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC  
CCTGCAGGTCTTGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAGCCCCCTCCT  
TGTCGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTTCGGAGACTTTCCACGG  
ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGAAGGATACTAGCATCAACACAATT  
TGAACCCACTGCAGCTAGAATGGCCTTTCCTGGCTTGTGATGAACCTGCCTTCAAAGCAAGTTT  
CTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAAATC  
TGTGACTGTTGCTGAAGGACTCATAGAAGACCATTGTGATGTCACTGTGAAGATGAGCACCTA  
TCTGGTGGCCTTCATCATTTTCAAGTTTGTAGTCTGTGAGCAAGATAACCAAGAGTGGAGTCA  
GGTTCTTCTTTATGCTAAGGGAGACAAAGATAAATCAAGCAGATTATGCACTGGATGCTGGGT  
GACTCTTCTAGAATTTTATGAGGATTATTTTCAAGCATACCGTATCCCTACCCAAACAAGATCT  
TGCTGCTATTCCCGACTTTTCACTGCTGGTGTATGGAAAACCTGGGGACTGACAACATATAGAGA  
ATCTGCTCTGTTGTTTGTATGCAGAAAAGTCTTCTGCATCAAGTAAGCTTGGCATCACAGTGAC  
TGTGGCCCATGAACCTGGCCCAAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGAAATGA  
TCTTTGGCTAAATGAAGGATTGCCAAATTTATGGAGTTTGTGTCTGTGAGTGTGACCCATCC  
TGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGACGCAATGGAGGTAGATGCTTT  
AAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTGCTCAGATCCGGGAGATGTTTGA  
TGATTTCTTTATGCTAAGGGAGCTTGTATTTGAAATATGCTAAGGGAGTATCTTAGCGCTGA  
CGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAGCATAGCTATAAAAATACAAAAACGA  
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT  
TTGCTCTAGAAGTCAACATTCATCTTCATCCTGCATGGCATCAGGAAGGGGTGGATGTGAA  
AACCATGATGAACACTTGGACACTGCAGAGGCTTTCCTTAATAACCATCACAGTGAGGGG  
GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTCTGACGGCGCCCCGGACACTGG  
GTACCTGTGGCATGTTCCATTGACATTCATCACCAGCAAATCCAACATGGTCCATCGATTTTT  
GCTAAAAACAAAAACAGATGTGCTCATCTCCAGAAAGAGGTGGAATGGATCAAATTTAATGT  
GGGCATGAATGGCTATTACATTTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT  
TTTAAAGGAACACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAAACATGCATT  
TCAGCTCGTCAGCATTGGGAAGCTGTCCATTGAAAAGGCCTTGGATTTATCCCTGTACTTGAA  
ACATGAAACTGAAATTATGCCCGTGTTCAGGTTTGAATGAGCTGATTCCTATGTATAAGTT  
AATGGAGAAAAGAGATATGAATGAAGTGGAACTCAATTCAAGGCCTTCCTCATCAGGCTGCT  
AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG  
GAGTGAACACTACTCCTCGCCTGTGTGCACAACATATCAGCCGTGCGTACAGAGGGCAGAAAG  
CTATTTAGAAAGTGGAAAGGAATCCAATGGAACTTGAGCCTGCCTGTGACGCTGACCTTGGC  
AGTGTGTGTGGGGGGCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT  
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGA  
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAAATAAAACTCAGGAGTTTCC  
ACAAATTCCTTACACTCATTTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG  
GAAAACTGGAACAACTTGTACAAAAGTTTGAACCTGGCTCATCTTCCATAGCCACATGGT  
AATGGGTACAACAAATCAATCTCCACAAGAACACGGCTTGAAGAGGTAAAGGATTCTTCAG  
CTCTTTGAAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATGGAAGA  
AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAGCT  
TGAACGTATGTAAAAATTCCTCCCTTGCCCGGTTCCCTGTTATCTCTAATCACCAACATTTTGT  
TGAGTGTATTTTCAAACCTAGAGATGGCTGTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTC  
AACTCATTTTTTACTATCCCTGTGAAAAGAAATAGCTGTTAGTTTTTTCATGAATGGGCTTTTT  
CATGAATGGGCTATCGCTACCATGTGTTTTGTTCATCACAGGTGTTGCCCTGCAACGTAAACC  
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 464**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTFPWNKIRLPEYVIPVHY  
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP  
PQEQIALLAPEPLLVLGYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM  
AFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS  
DFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAAIPDFQ  
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDLWLNNEG  
AKFMEFVSVSVTHPELVKVDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG  
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDFGCSRSQHS  
SSSSHHQEGVDVKTMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL  
TFITSKSNMVHRFLLKTKTDVLIILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTLGLLKGHTA  
VSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRD  
EVEVTFKAFILIRLLRDLIDKQWTWDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE  
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALCRTQNKELQWLLD  
ESFKGDKIKTQEFQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHVMVGTTNQF  
STRTRLEEVKGGFSSSLKENGSQLRCVQQTIETIEENIGWMDKNFDKIRVWLQSEKLERM

**Important features:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

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**FIGURE 465**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACT  
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA  
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACAC  
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC  
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA  
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC  
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG  
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCT  
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG  
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGAACTGCAATAG  
GAAAGATTTTCTGACCTGTCTATCGGGGGACCACCATTTATGACACACGGAACTTGGCTCAAGA  
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCTCAGGAGAC  
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT  
TGGGGCTCAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGGGTGCTTGTGGCCTC  
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA  
CTCCCTCCCTCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC  
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA  
TGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAATGAGCATTGAGGGCTGCGT  
GGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA  
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC  
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTC  
CTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTC  
TGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTCCCATTTCTGTCCATGAATCATCTT  
CCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC  
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC  
CCTGTCCTTTCA

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**FIGURE 466**

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLIE  
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA  
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCNLLN  
GTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETLLIID  
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQ  
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS  
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVCPSC

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**FIGURE 467**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTG  
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTTCG  
AGGAGCTTCTGCATTGCTGGTTCCTTGCAGCTTTTCTGCCCCCGCCGAGTGACCCA  
GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGGAAAA  
ATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCGAAGAGTTCTCAAAAAATATATCTGT  
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTTGGCACT  
GAGAGTTGAACGTGCCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTGACGAGTG  
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA  
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAAAT  
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAA  
GGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAACATACGGGCATT  
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCCTGGCAGGGAAAC  
AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT  
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGGCCG  
AGCATTGGTTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT  
CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGG  
CACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATT  
CCTCTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC  
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTTCTTCCCCAA  
GAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAAGAGATAAGCAGCTCTATGCCTGGAA  
TGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAATGCAT  
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC  
CCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGT  
ATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC  
ATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAAACCTCCTGGCTCTCAAGGATGACCAC  
ATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACTGCTCCCCAGCATTTACTGTAACCTCTG  
CCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCAATATTACCACTGGCTTTTCTC  
TCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTTCAAATGTCTATTGATATTCTCCATTTT  
CACTGCCCCAACTAAAATACTATTAATATTTCTTTCTTTCTTTTCTTTTTTTTGGAGACAAGGT  
CTCACTATGTTGCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT  
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAATACTATTTCTTATTG  
AGGTTTAAACCTCTATTTCCCCTAGCCCTGTCTTCCACTAAGCTTGGTAGATGTAATAATAAA  
GTGAAAATATTAAACATTTGAATATCGCTTTCAGGTGTGGAGTGTGTCACATCATTTGAATTC  
TCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGT  
AACACAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG  
CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTCATCGTT  
TCAGCCTAAAAATAATAGTCTGTCCCTTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAAT  
AGGCCTTTCAAATGATAATTCCTCCAGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCC  
TCCTCTTGTCTGTCTGCTGCTGTTTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTG  
AGCAAAAAAAAAAAAAA



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**FIGURE 468**

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEF  
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE  
AEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTVWEF  
ANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL  
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDTPCRSQ  
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK  
QLYAWNEGNQIIYKLQTKRKLPLK

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**FIGURE 469**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC  
AGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC  
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG  
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG  
CGGGAAGGGCAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC  
CACACCTGTCCCTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTACCGCTGC  
TCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCCCTGGTCTCAGGATACCCACCATCCT  
TTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGACTCTCCCAG  
TCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA  
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG  
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA  
GGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCCCTGGGCCCTGCCCCCTCTCCCCA  
CATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG  
TCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT  
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT  
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC  
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA  
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCCTGAAGCCCCCA  
ATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT  
ATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTCCAAGGATCAGCCCTGAGAGCAG  
GTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC  
AGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGGCAACTACACACCAACATGCTGG  
CTTTAGAATAAAAGCACCAACTGAAAAA

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**FIGURE 470**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHPG  
SHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Important feratures:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

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**FIGURE 471**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTCC  
TCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG  
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGCCC  
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTCAAAGCAA  
AGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT  
GTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC  
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG  
GAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA  
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAGGCTTCTCTG  
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTTCGTGGTGGGATCAGGAAAGCAGG  
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG  
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGATTGTGTGAACTG  
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTG  
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA  
TATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA  
CTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAATTGACTGCCAGGCTGG  
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG  
GTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA  
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA  
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG  
GGTACTGAGACTCTAACTAA

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**FIGURE 472**

MSFLQDPSFFTGMWWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT  
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP  
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEGLGGVFVVGS  
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 473**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT  
TGGGATTTTAAATTTTCAAACACAGCAGAATGACATTTTCTGTCACTATTATTATTGTTGGT  
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC  
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC  
CAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT  
AATTCTTGCTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAACACTTAGATTCAATGATTGTA  
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA  
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT  
TTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT  
TTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAAATGCGATACA  
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA  
TGTTGCCAAGGAAAAAAAAA

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**FIGURE 474**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG  
IVKGRNLDSRGLILGAEWGRGVKKNT

FIGURE 475

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCAT  
CTCCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCCTC  
AGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGCATG  
CAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCCTGAAG  
CCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGCTCAGC  
GATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATCTTCACC  
TACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAGCTCTCAC  
AGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTCAACCTGACCAAGTTCACCCAGTACGAC  
AAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAGAAGGTGCC  
GAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCGAAGACATCTACCAG  
ATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGGCGATGAAGAAG  
TTTGAAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGCCGGCCGGCCGTG  
CAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTTCGCCGAGGCCCTC  
CGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGGGTGGCTGGGACCTG  
CTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAACGCGCCCGTGGTGGCG  
ATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCCCCGGCGCGGAATCTG  
AAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGGCGGTGAAGCGCATCACC  
TTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGGCTGCACTACGTGCCGGCC  
ACCAAGGTGTTCTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGAGCACATTGAAGGCGGCCAC  
TCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGCCGCGCGAGGGCGCGCTGCTG  
CTGGCCTCGTACACGTGGTTCGGACGCGGCGGCAGCGTTCGCCGGCTTGAGCCGGGAAGAGGCG  
TTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCCTGTGCTGCGCCAGCTCTGGGAC  
GGCACCGGCGTCTCAAGCGTTGGGCGGAGGACCAGCACAGCCAGGGTGGCTTTGTGGTACAG  
CCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACGGTCCCTTATGGCCGCATCTACTTT  
GCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGAGACGGCGGTCAAGTCGGCGCTGCGC  
GCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCATCGGACACGGCCAGCCCCGAGGGGCAC  
GCATCTGACATGGAGGGGCAGGGGCATGTGCATGGGGTGGCCAGCAGCCCCCTGCATGACCTG  
GCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGGCCAGTTATCTCTCCAAAACACGACCCAC  
ACGAGGACCTCGCATTAAAGTATTTTCGGAAAAA



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**FIGURE 476**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRVI  
VVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRI LHK  
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMALNQ  
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALRAHSC  
LSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA  
DVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGGHSNTDR  
PSRMIFYPPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV  
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKI  
NSRKG PASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQNTTHTRTSH

**Important features:****Signal peptide:**

amino acids 1-21

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**FIGURE 477**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT  
GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
GAACTCAGAGCCGGGAAGCCCCATTCACTAGAACACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCTT  
GCTGCTGTTCAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT  
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA  
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGTTTCCAGAGAACAATGACCTAACAAAGTTGCTG  
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC  
CTGTCTCTTGATATAAGGTTATAAATCATCACCAGACAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG  
GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAAGC  
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT  
AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA  
GCAAAGAGGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGCACTTCAG  
AAAACCTGTGCTCTAGCCCAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG  
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGC  
CACTCTGTGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA  
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
CACATTGTTTCCGCGGTTGCCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCT  
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
TTTCTGGGACAAGCTCATCTTGTCAAAGATCCAGGACAGCCTGGGCGGAAGGTTTCGTGTAATTGTCACTGGAGC  
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGACGAATGGGATGTGAGGTGTATGAAGCTTATGGTCA  
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTACGTTGGGGTGCCCTGGC  
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACCTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG  
GCTTCACACAGGAGACATTGGTCTGGCTCCGAATGGAACCTCTGAAGATCATCGACCGTAAAAAGAACATTTT  
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTTACA  
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTTGACACAGATGTACTTCCCTC  
ATTTGCAGCCAGCTTGGGGTGAAGGGCTCCTTTGAGGAACGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTCTTCATCC  
AGAGCCATTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG  
TGCACTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTGTTTTGCCTTTCTCCTATTTTTTTTTAAACC  
TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAGTCTAGTTCCCAATAAATCA  
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAAGGCTACTTTTATCAACATGCCTGTCTTCAA  
GATCCCAAGTTTATGTTCTGTGTCCTTCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
CAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA  
TCTTCTACTGTTCAAATAAGAGATTTTTAAATCTGAAAACTGCTTACAAATTCATGTTTTCTAGCCACTCCAC  
AAACCACTAAAATTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
CTGCGTAAATTAATTTGTGTACTGAAGGGAAGTTTGATCATACCAACATTTCTTAACTCTCTAGTTAGATA  
TCTGACTTGGGAGTATTAATAATTTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
CAGTAGGAACCTGGGAGTAAATCTGTTCCCTACAGTTTGTCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
GGTGGGCCCAGTGAACTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCTGAACTGGGAACAAAGATCT  
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCTTGGATT  
AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAAC  
TATTACAGATAAAAAA

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**FIGURE 478**

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFKLLFTKMLFIFNF  
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTSCC  
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ  
FVGIFAQNRPEWIISELACYTYSMAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG  
NVEKGFTPSLKVIIIMDPFDDDLKQERGEKSGIEILSLYDAENLGKEHFRKPVPSPEDLSVIC  
FTSGTTGDPKGAMITHQNIVSNAAFLKCVHAYEPTPDDVAISYLPLAHMFERIVQAVVYSC  
GARVGFFQGDIRLLADDMLTKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE  
LQKGIIRHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTEC  
TGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT  
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVH  
GESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ  
VKAIFLHPEPFSIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

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**FIGURE 479**

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCGAGCGGGGC  
CCGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC  
GGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC  
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCAGACA  
GGGGCCGTGCTTTTCCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACACTCGG  
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC  
CGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCCTGGACGTAGAGGTGTAT  
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATGAGGCCCGG  
GAGCAGGGCCGGGGCATCCATGTCAATTGTCCTCAACCAGGCCACGGGCCACGTGATGGCAAAA  
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCAACATGGTA  
GCGCCCGGGCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA  
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA  
TGGGCCTTCTGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC  
CTCTCTTCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG  
GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT  
GAGGGCTATGGAAGTGATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA  
CTCCCAGACAACAAGTCTCTCAATGTGCCTGTGGCTGTCAATTGCAGGGAACCGACCCAATTAC  
CTGTACAGGATGTGCGCTCTCTGCTTTAGCCCCAGGGGGTGCTCTCCTCAGATGATAACAGTT  
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTGGTCTGAGGGGCATC  
CAGCATACTCCCATCAGCATCAAGAATGCCCGGTGTCTCAGCACTACAAGGCCAGCCTCACT  
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTTCTGGAAGAGGACCTGGACATT  
GCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACAGCCTG  
TACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCTACTG  
TACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTCAGGAGGTCTTGTAAGAAGGAG  
CTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCT  
GAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACGTTTCCCGATCCTACCCTTTGGCATC  
GTCGGCCTCAACATGAATGGCTACTTTCACGAGGCCTACTTCAAGAAGCACAAGTTCAACACG  
GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAAGTT  
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC  
CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTCGAATGGAGAAAGATGATGACTTC  
ACCACCTGGACCCAGCTTGCCAAGTGCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT  
CGGGGCCTGTGGAGATTGTTTCGGAAGAAGAACCACTTCCTGGTGGTGGGGTCCCGGCTTCC  
CCCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTCTGGAGCCACCCCAAGGAG  
GAGGGAGCCCCAGGAGCCCCAGAACAGACAT**GAG**ACCTCCTCCAGGACCTGCGGGGCTGGGT  
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTA  
GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC  
CTGCTCCAACACCCCGTTTCTGAGTTAAAAGTCTATTTATTTACTTCTTGTGAGAAGGGC  
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCAC  
TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTGACTGTCCTGAGGGCCTTGAAAACAGGC  
CGAACCTGGAGGGCCTGGATTTCTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC  
TTACTCAGGAACTGCTGTGCCCAACCCATGGACAGGCCCTCCTCTCAGCCTTCTCTTTGTCCAGA  
AGACTCACTCAGAGACCCTTAGACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA  
TTTCCAAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAA  
AAAAAAAAAAAAAAAA

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**FIGURE 480**

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVIVNIKLILDTRR  
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE  
QGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFLLNMVAPGRVLICTVKDEGSFHLKDTA  
KALLRSLGSQAGPALGWRDWAFFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSSAEEA  
ECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL  
YRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHYKASLTA  
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLY  
RVETMPGLGWLRRSLYKEELEPKWPTPEKLWDWDMWMMPEQRRGRECIIPDVSRSYHFGIV  
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVD SLKKEAYEVEVHRL LSEA EVLDH SKNPCEDSFL  
PDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDL D VRGNHRGLWRLFRKKNHFLVVGVPASP  
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

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**FIGURE 481**

GAAAGAAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCA  
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT  
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAAAGTT  
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCA  
TTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA  
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTCTGGAA  
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT  
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC  
TGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA  
AACATGATCACAATTGAAAATGGCATCCCCCTGATCCCCTGGACATGAAGGGGGGCATATTA  
ATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC  
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT  
CATATATTTTGTTCACCATTCTTCTTTTGAATAAATTTTGAATGTGCTTGAAAGTGAAAAG  
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAA  
AATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTAA  
GCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACTTCAAAGACCTAAGGAAAA  
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT  
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA  
AATGGATGGATAAAAATGGAATTACTCATATACAGGGTGAATTTTATCCTGTTATCACACCA  
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT  
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTTTAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 482**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN  
REATEISHVLLCNVTQRVSEFWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTLEFL  
KIPSTLAPPM DPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENM  
ITIENGIPSDPLDMKGGILMMPS

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**FIGURE 483**

CGTCTCTGCGTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC  
CCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGTGGTGT  
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGCACCCG  
GGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA  
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAAGATTCTGTGCGA  
CGGCGTGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGCTGCGAGTG  
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA  
CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTA  
CCGGGGCCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCCGCGGCCACAGTCGTGCGTCGT  
GGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGAGCGGCGCCCTGCCCTGTGCCCTCCAG  
CCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGCCACATGCGCCA  
GGCCACCTGCTTCTTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC  
TGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAACTTCGT**TGAG**CGCTGCAGGAC  
AGGCCTGGGCCTGGTGCCGAGGCCCCCATCATCCCTGTTATTTATTGCCACAGCAGAGTC  
TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTTGGGGATCCCAGAACC  
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCCGGCTGGTGGGTGGGAT  
AGACCTGCGTTCGGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCCCT  
ACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA  
TTATTGCTACTACTAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC  
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA  
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT  
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT  
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT  
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG  
GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACACTGTGACCTTAGCCC  
AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCCTGCCAGCCCAAGAACT  
CCAGCTTCCCCACTGCCTCTGTGTGCCCCCTTTCGCTCCTGTGAAGGCCATTGAGAAATGCCCA  
GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC  
CACCCAGCGTCTCCCCTGCTGCTGTCCACGTCACTTCATGAGGCAACGTGCGGTGGTCTCAGA  
CGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTG  
GGGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG  
CCAAGACTCACGCATGTGTGACATCCGGAGTCTGGAGCCGGGTGTCCAGTGGCACCCTAG  
GTGCCTGCTGCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCACAACCTGCCCC  
GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG  
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCTCCCCCTCCAT  
CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTA  
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC  
TTGGGCATCCTCCTCCAGCCTCCTCCAGCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAA  
AGTCCCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCC  
CTGCCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA



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## **FIGURE 484**

MRPGAPGGLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC  
CA  
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPDCS  
GLPARLQVCGSDGATYRDECELRAARCRGHPDL SVMYRGRCRKSCHEVVCPRPQSCVVDQTGS  
AHCVV CRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG  
GESAE EEEENFV

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 73-77, 215-219

**Osteonectin domain proteins.**

amino acids 97-130, 169-202

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**FIGURE 485**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC  
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGA  
AACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC  
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG  
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGAAGAAC  
GAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC  
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAATAACATC  
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC  
GGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC  
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA  
ATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC  
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG  
CCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAAACAGCAAGTCCCAGACACCA  
GCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG  
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG  
GTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC  
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA  
GACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAAC  
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA  
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG  
AAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA  
CTGGAATCACATATTTCAACAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA  
ATACTGAAAACCTGTGAAATGTACTAAATAAAATGTACATCTGA

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**FIGURE 486**

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGAV  
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT  
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD  
LSENNDQRQQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCRQVEK  
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEM  
EGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF  
NVEDQKRDITINLLDQREKRNHTL

**Important features:****Signal peptide:**

amino acids 1-29

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**FIGURE 487**

AACTCAAACCTCTCTCTGCGGAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG  
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTAT  
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT  
ATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG  
TTAAAATGCACTTTCTCCAGCTTTGCCCCGTGTTGGGTGATGCTCTAACAGTGACCTGGAATTTT  
CGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC  
ATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC  
ATCCTTCTCTGGAACTGCAGTTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA  
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT  
GAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT  
GTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG  
GAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA  
GACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT  
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTCCAACCAGTTC  
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT  
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAA  
GTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTGCCCTTAAGACACTACTTACAGTGT  
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTTACATTT  
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC  
TTCCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAATC  
CTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACATATGAGACACATC  
TTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATTTTTTGTCG

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**FIGURE 488**

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW  
NFRPLDGGPEQVFVYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK  
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFQHYRKKRWAERAHK  
VVEIKSKEEERLNQEKKVSYLEDTD

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**FIGURE 489**

[illegible]

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**FIGURE 490**

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFDGRLTFHPGSQVVKLPFINFM  
KTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF  
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNWLRK  
EAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP  
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIYSSDHG  
ELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSVLVDIYPTMLDIAGIPLPQNLSG  
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD  
LSSDPDELNTNAVVFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQYNSNVIA  
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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**FIGURE 491**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA  
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGC  
CTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT  
TGCCATGCTGCTCCCCAGCTGGAAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGT  
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA  
CATCTATAGCACCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC  
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT  
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGG  
AGGCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC  
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTC  
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCCTGCTCATCCAGAGAAATCG  
CTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG  
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAAGAAC  
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA  
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG  
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA  
GGATGCTCGCCATGCCAGCCTTCTGTTTTCCCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC  
AACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT  
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGACCCTCTGTGATCAA  
AGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT  
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC  
TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG  
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA  
GGCAGCCTGGGACATTTAAAAAATA



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**FIGURE 492**

MASLGLQLVG YILG LLG LGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ  
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFI  
LG LLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR  
NRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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**FIGURE 493**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT  
TATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA  
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC  
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCACCTTC  
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTGTGAAG  
CTGAAGGTTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC  
AGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATCTCAGAAA  
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT  
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA  
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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**FIGURE 494**

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDIVSLSET  
RQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Important features:**

**Signal peptide:**

amino acids 1-25

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**FIGURE 495**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT  
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA  
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTTGCT  
ATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGAGTCT  
GCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG  
CCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTTAATGGAACATCAGGGGAACGATGA  
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGA  
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCTTCATTCTGTGACC  
TGTCTGAGGCCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGA  
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCCTCCTGATGACCCCTATG  
GCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCCTTCACCCTTCTGTGAGATT  
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA  
CTTTATAAATGAAAA

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**FIGURE 496**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL  
ARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Important features:**

**Signal peptide:**

amino acids 1-24

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**FIGURE 497**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC  
CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCTGGC  
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCCCTCA  
GAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG  
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA  
GGAGACTTCAAACCTTCGGATTACAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT  
GGTCTTCTCTCCATTTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC  
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAGCCCGGGCT  
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAGTGGGCCTCTC  
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC  
CAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCACAGGCCAAAAG  
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAAATCCCAAAGTGTGATGAGAT  
TAATCCTGAAACCAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGAAATGGTTGACCCC  
ATTTGACCCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTACAAGACCATTAAGGT  
GCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAATTTTCGTTGTGATGT  
CCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCATGGAGAAAATGGGTGA  
CCACCTCGCCCTTGAAGACTACCTGACCAAGACTTGGTGGAGACATGGCTCAGAAACATGAA  
AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA  
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTGCTGACCTTAGTGAACCTCTC  
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA  
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAAGTCTTATTCCATGCCTCCTGT  
CATCAAAGTGGACCGGCCATTTCAATTTATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT  
TCTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGGACATGCATAAGCACTTCGTGCTG  
TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG  
AGTGTTCCCTTTTGTCTTAACTAGTTTAGGGTGTCTCAAATAAATACAGTAGTCCCCACTTA  
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT  
TATATATATTTTTTCTACACATACATACCTATGATAAAGTTTAATTTATAAATTAGGCACAG  
TAAGAGATTAACAATAATAACAACATTAAGTAAAATGAGTTACTTGAACGCAAGCACTGCAAT  
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA  
CAGTGTGGAGACATTGGGCAAGGGGAGAATTACATCCTGGGTGGGACAGAGCAGGACGATGC  
AAGATTCCATCCCACTACTCAGAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG  
AATTTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA  
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAATTTGATACATATTTTTTAAAAAAA  
AAAAAAA

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**FIGURE 498**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E E  
E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I K R  
G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F D T E  
C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P V F T E  
V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L A L E D Y  
L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A T G R N L Q  
V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F L G R V V N P  
T L L

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**FIGURE 499**

[illegible]



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**FIGURE 500**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLAT  
LQEAATTQENVAWRKNWMVGEGGASGRSP

**Important features:**

**Signal peptide:**

amino acids 1-18

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**FIGURE 501**

[illegible]

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**FIGURE 502**

MGPSTPLLILFLLSWSGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML  
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGRRN  
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF  
TLAMAARKASRVVRVFPFWGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLANRTVV  
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQQWDTP  
CPRENAEAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN  
PRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

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**FIGURE 503**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT  
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC  
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA  
CGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTCAGCA  
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGGGTGTT  
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC  
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT  
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGCCTGGGCTT  
CCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG  
AGTGCTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC  
ACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

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**FIGURE 504**

MGGLLLAAFLALVSVPRQA VVLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVG VVTL  
TPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAII FTQLEF  
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Important features:**

**Signal peptide:**

amino acids 1-20

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**FIGURE 505**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA  
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC  
CTGCTTGCTCTGGCAACAGGGCTTGAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAGTGC  
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGGGGCG  
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTT  
CACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG  
TCCTTCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG  
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA  
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCCAG  
TTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAG  
AACGCCTACCCCGGAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG  
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC  
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA  
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA  
TCACCTCCATTTCCACTTGGTGTTTGGTTCTGTTCCTGTTCACTCTGTTAATAAGAAACCTAAGCC  
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC  
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG  
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT  
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAA

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## **FIGURE 506**

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC  
LKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV  
RPLTLSSRCVTAGTSCCLISGWGSTSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTMVCA  
SVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

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**FIGURE 507**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAGG  
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA  
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC  
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC  
CAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCATCCTT  
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCCGAGCCC  
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCCGTTG  
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC  
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA  
CTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAAAAAAAAAAAAA  
AAAAAA



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**FIGURE 508**

MRRLLLVTSLVVLLWEAGAVPAKVPPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVLF  
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP  
RLWVMPNHQVLLGPEEDQDHIYHPQ

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**FIGURE 509**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC  
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCGCG  
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCCATG  
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG  
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA  
ACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCT  
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC  
AAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC  
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCATTCTGAAGCA  
AAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTT  
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTTCGGTATCGAACC  
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT  
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCTCTTTTTGAAAATA  
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG  
TAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT  
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCTGGGGTGGGGGCATTGG  
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA  
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGTAGCTCACATAAAGAACTT  
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA  
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAACTGTAGTAGTT  
GGTCTAGAAACAAAATACTCC

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**FIGURE 510**

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPDHT  
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS  
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM  
YYSRRGIRYRTIDEHDAII

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**FIGURE 511**

GACTTTGCTTGAATGTTTACATTTTCTGCTCGCTGCTCTACATATCACAATATAGTGTTACGTTTTGTAAAAAC  
TTTGGGGTGTGAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA  
TTGGTGCTGGGCTACTAATGACTTCATTAAACCGAGTCTTCCATACAGAATAGTGAGTGCCACAACCTTTGCGTA  
TGTGAAATTTCGTCCTGGTTTACCCACAGTCAACTTACAGAGAAGCCACCAGTGTGATTGCAATGACCTCCGC  
TTAAACAAGGATTCCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT  
GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAACTAGATTTCTCCAAAACAACCTTTACTAACATTAAGGAG  
GTCGGGCTGGCAAACCTAACCAGCTCACAACGCTGCATTTGGAGGAAAATCAGATTACCGAGATGACTGATTAC  
TGTCTACAAGACCTCAGCAACCTTCAAGAAGCTCTACATCAACCACAACCAAATTAGCACTATTTCTGCTCATGCT  
TTTGCAGGCTTAAAAAATCTATTAAAGGCTCCACCTGAACTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT  
GATTCTACACCCAACTTGAAATTTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAACTTCAAA  
CCCCTCGCAAATTTGAGAAGCTTAGTTTTGGCAGGAATGTATCTCACTGATATTCCTGGAAATGCTTTGGTGGGT  
CTGGATAGCCTTGAGAGCCTGTCTTTTATGATAACAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT  
CCAAATTTGAAATTTCTTAGACCTCAACAAAAACCCATTCAAAAATCCAAGAAGGGGACTTCAAAAATATGCTT  
CGGTTAAAGAAGCTGGGAATCAACAATATGGGCGAGCTCGTTTCTGTGACCGCTATGCCCTGGATAACTTGCCT  
GAACTCACAAGCTGGAAGCCACCAATAACCTTAACTCTCTTACATCCACCGCTTGGCTTTCCGAAGTGTCCCT  
GCTCTGGAAAGCTTGATGCTGAACAACAATGCCTTGAATGCCATTTACCAAAGACAGTCGAATCCCTCCCCAAT  
CTGCGTGAGATCAGTATCCATAGCAATCCCCTCAGGTGTGACTGTGTGATCCACTGGATTAACCTCCAACAAAACC  
AACATCCGCTTCATGGAGCCCCTGTCCATGTTCTGTGCCATGCCGCCGAATATAAAGGGCACCAGGTGAAGGAA  
GTTTTAATCCAGGATTCGAGTGAACAGTGCCTCCCAATGATATCTCAGCAGAGCTTCCCAAATCGTTTAAACGTG  
GATATCGGCACGACGGTTTTCTTAGACTGTGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC  
ATTGGAAATAAGATAACTGTGGAAACCTTTTCAGATAAATAACAAGCTAAGTAGCGAAGGTACCTTGAAATATCT  
AACATACAAATTGAAGACTCAGGAAGATACACATGTGTTGCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA  
ACAATTAAGGTTAACGGGACCCTTCTGGATGGTACCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT  
TCCATCTTAGTGCTCTGGAAAGTTAATCCAATGTCATGACGTCAAACCTTAAATGGTCTGCTGCCACCATGAAG  
ATTGATAACCTCACATAACATATACTGCCAGGGTCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG  
CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCCAATATTCATCAGCAGACTCAAAAGTCATGCGTAAATGTC  
ACAACCAAAAATGCCGCTTCGCAGTGGACATCTCTGATCAAGAAACCAGTACAGCCCTTGCTGCAGTAATGGGG  
TCTATGTTTGCCGTCATTAGCCTTGCGTCCATTGCTGTGTACTTTGCCAAAAGATTAAAGAGAAAAAACTACCAC  
CACTCATTAAAAAAGTATATGCAAAAACCTCTTCAATCCCACTAAATGAGCTGTACCCACCACCTCATTAAACCTC  
TGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAAGC  
TATTACATGTGGTAACTCAGAGGATATTTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTTGCTTTATTCTGC  
AAAAGTGAACAAGTTGAAGACTTTTGTATTTTGACTTTGCTAGTTTGTGGCAGAGTGAGAGGACGGGTGGATA  
TTTCAAAATTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT  
TTGGTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTTTATTTTTAGTTGTTGTGCTAAACTCAAT  
AATGCTGTTCTAACTACAGTGCTCAATAAAATGATTAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 512**

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL  
TRIPSNLSSDTQVLLLQSNNIAKTVDELQQLFNLTELDQSNNFTNIKEVGLANLTQLTTLHL  
EENQITEMTDYCLQDLSNLQELYINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS  
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV  
KVPQLALQKVPNLKFLLDNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELT  
KLEATNNPKLSYIHRFAFRSVPALLESMLNNAALNAIYQKTVESLPNLREISIHNSNPLRCDCV  
IHWINSNKTNIREFMEPLSMFCAMPPEYKQHVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT  
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV  
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPH  
ITYTARVPVDVHEYNLTHLQPDYEVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETST  
ALAAVMGSMFAVISLASIAVYFAKRFKRKNYHSLKKYMQKTSSIPLNELYPPLINLWEGDSE  
KDKDGSADTKPTQVDTSRSYYMW

**Important features:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 508-530

**N-glycosylation sites:**Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;  
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

**N-myristoylation sites:**

Amino acids 16-22;224-230;464-470;637-643;698-704

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**FIGURE 513**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
CAGCAAT~~ATG~~CATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG  
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC  
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG  
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCC~~TAA~~ACTGG  
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG  
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA  
CTTGATACACCA

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**FIGURE 514**

MHLARLVGSCSLLLLLGLSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR  
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA  
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN  
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

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**FIGURE 515**

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT  
TTCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA  
CCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG  
AAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG  
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCGGTGTG  
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTCGCCG  
GCCGGCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTGCGCCCGC  
TGCGAGCCCGGCGTCCGGCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTGGCGGGCGC  
GCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCCGCCGCCCGG  
GACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT  
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA  
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCGGGGCGGGT  
GAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAG  
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCAGGG  
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCCGGGGACACCCCGCAGGCGGAAGC  
CCTGGCCGCAGCCGCCAGGACGCGATTGGCCCCGGAACCTCGCGCCCACGCCCGAGCCACCCGA  
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC  
GATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCCTGCCTGTGCACCGAGGAGGGGCC  
GCTGTGCGCGCAGCCGAGTGCCCCGAGGCTGCACCCGCGCTGCATCCACGTCGACACGAGCCA  
GTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC  
TTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTGTGAAGCCAACGGTGAGGTGCT  
ATGCACAGTGTACGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGATCAGTG  
CTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG  
AGAAGTGAAGACTGACGAGTGCACCAATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT  
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCGAGAACACA  
AACTCTGACTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACATC  
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA  
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA  
AATCCTTCTCTAAATAAATGTGCTATTTTACAGTAAGTACACAAAAGTACACTATTATATAT  
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTCCTATAGATGCAGAT  
TAAAAATGCTGTGTTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 516**

MPSSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNELG  
RPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA  
AQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKEKFAPGPSACPCLCTEEGPLCAQ  
PECPR LHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVS PCERCRC EANGEVLCTVS  
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYE EGTWRIERQA  
MCTRHECRQM

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

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**FIGURE 517**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT  
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC  
GGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC  
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG  
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATCTAATC  
CTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG  
GAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACAACCTTCC  
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCATTCTGGT  
CGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAATGAAG  
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG  
TTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCACCACTTTAGATA  
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAACTG  
CGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA  
AAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGACACCAGCAACCCAG  
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG  
CAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA  
ATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTCTAGATCTAACTCTATG  
AATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA  
CATTAaaaaATATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAAAGTTATTAAACAATAA  
TATAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGATTTAAGCAAAGTGCATTTTT  
TCACAGGAGAAATAATCATATTTCGTAATTTCAAAGTTGTATAAAATATTTTCTATTGTAGT  
TCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACAATTTTCATATGCACTAAAAACC  
TAATTTAAATAAAATTTTGGTTCAGGAAAAAA

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**FIGURE 518**

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPSGEPGREKKSNSPKH  
VYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSIKP  
NNVSIVLHAEEPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDKSTG  
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNPAYRE  
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD  
IKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Important features:****Signal peptide:**

amino acids 1-19

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**FIGURE 519**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG  
GATTTGAAAGTTGAGAGCAGCATGTTTTGCCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG  
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT  
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC  
TGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC  
AGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTATGCAATGAT  
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC  
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC  
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAGAGCACAGAA  
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA  
TTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAG  
AATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTG  
AGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA  
ACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG  
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG  
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCT  
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT  
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA  
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG  
AGGTCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA  
GCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT  
GTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCCTCCTGTCTCATT  
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA  
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG  
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGATCAGACCCTCCTGTGGGCAGGG  
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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**FIGURE 520**

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGE  
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV  
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL  
RMSVEYSQSWGHEFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIVLHVS  
PEEPRTLVT PAALRPLVLGQNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTVLVKN  
KKTNPEIKEKPCHEFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWPSLRSDRNNS  
LEKKS GGGMPKTQQAF

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**FIGURE 521**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG  
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA  
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCAGGA  
TGAAGATGGATACATCACCTTAAATATTAAAACCTCGGAAACCAGCTCTCGTCTCCGTTGGCCC  
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT  
TGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGATGAGAA  
TGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA  
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAACTGGAGATA  
TTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAGTAAGCAGTA  
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA  
AGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA  
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGATGGAAAAGGAAA  
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA  
TTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT  
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAAGATATGTATGAATGCATCAGTA  
GCTGAAAAAAAAAAAAA

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**FIGURE 522**

MQDEEDGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYLQ  
DENENRTGTLQQLAKRFCQYVVKQSELKGTFGHKCSPCDTNWRYYGDSYGFRRHNLWEES  
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVKKWEDGSVISENMFEFLEDG  
KGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

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**FIGURE 523**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGC  
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA  
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAAT  
TGTCCCTGTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA  
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG  
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA  
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT  
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTT  
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA  
AAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT  
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA  
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG  
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA  
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA  
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG  
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGT  
CTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATATAATAAATGCATGCTATT  
CAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG  
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA



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**FIGURE 524**

MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYD  
MEHTFYSNGEKKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQI  
KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPT  
LISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG  
IEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

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**FIGURE 525**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC  
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA  
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT  
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACCGAGA  
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC  
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC  
TTTCAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT  
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT  
TAACACGTCAATAAAAAAATAATCTCCAGA

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**FIGURE 526**

MKITGGLLLLCTVVYFCSSSEAAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE  
CHLCTESLKSNQGRVQFLHDGSC

**Important features:**

**Signal peptide:**

amino acids 1-19

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**FIGURE 527**

CGACGATGCTACGACGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTTG  
CTGCGGGCGCTGCTCTCGTCGCTTGGCGGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGCCCT  
CGTCGCTCAGCCCCATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT  
CGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC  
TGGTGCGCCCTCATTCGCCACGGCACCCGCTACCCACACGGTCAAACAGATCCGCAAGCTGAGGC  
AGCTGCACGGGTGTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC  
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTTGGGTACGCGGACTGGATGGACGGGCAGG  
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG  
CCCTTTTTCAGCCGTGAGAACTACGGCCGCTTGGCGCTCATCACCAGTTCCAAGCACCGCTGCA  
TGGATAGCAGCGCCGCCTTCCTGCAGGGGCTGTGGCAGCACTACCACCCTGGCTTGCCGCCGC  
CGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG  
ATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAG  
CCTTCAAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC  
CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTACCTGTTTCATTTGACCTGG  
CAATTTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTGACATAGATGATGCAAAAGGTATTAG  
AAATTTAAATGATCTGAACAATATTGGAAGAGGATATGGGTATACATACTATTAACAGTCGAT  
CCAGCTTGACACCTTGTTTTCAGGATATCTTTCAGCACTTGGACAAAGCAGTTGAACAGAAACAAA  
GGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCAC  
TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAA  
AAATGCATCGGAAGTTCGAAGTGGTCTCATTTGTACCTTATGCCTCGAACCTGATATTTGTGC  
TTTACCCTGTGAAAATGCTAAGACTCCTAAAGAACAATTCCGAGTGCAGATGTTATTAAATG  
AAAAGGTGTTACCTTTGGCTTACTACAAGAACTGTTTTCATTTTATGAAGATCTGAAGAACC  
ACTACAAGGACATCCTTCAGAGTTGTCAAACAGTGAAGAATGTGAATTAGCAAGGGCTAACA  
GTACATCTGATGAACATTGAGTAAGTAACTGAAGAACATTTTTTAATTCTTTAGGAATCTGCAATGAG  
TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG  
TATTTCTGTCTTTTCACAGAAAAACATTGGGTTCCTCTCTGGGTGGACATGAAATGTAAGA  
AAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC  
CCTGCAAATGTTTACAGAAATGAAATTCTTCTACTTATATAAGAAATCTCACACTGAGATAG  
AATTGTGATTTTACATAAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCAT  
CCTTAACTTGATTGAACTGTCTAGGAACCTTACAGATTGTTCTGCAGTTCTCTCTTCTTTCC  
TCAGGTAGGACAGCTCTAGCATTTTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT  
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTTGTAAAAGGAC  
ACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTGGTATTTATTTATGAA  
ATATTTGAACATTTTTTCAATAATTCTTTTACTTCTAGGAAGTCTCAAAGACCATTAA  
ATTATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTAGAATCGAAGTTTTTTCAAATCC  
ATTGCTTAGCTAACTTTTTTCACTTCTGTCACTTGGCTTCGATTTTTTATATTTTCTATTATATG  
AAATGTATCTTTTGGTTGTTTGATTTTTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCA  
AATGCCGTGAAAGTATTTGCTATAATAAAGAAAATTCTTGTGACTTTAAAAAAA

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**FIGURE 528**

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLSG  
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD  
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD  
SSAAFLQGLWQHYHPGLPPPVDADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF  
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDAKVLEY  
LNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL  
SLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK  
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

**Important features:****Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

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**FIGURE 529**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG  
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA  
CGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG  
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGGGCTC  
TTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAAATGGT  
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC  
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTCCCAAGGG  
CAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC  
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT  
GATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCGTAGAA  
AAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCTTA  
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAAACTCTAAACGG  
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGCTCCTCGGAAGTCC  
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACCAGGGCCCAGTCATA  
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG  
GTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA  
ACCAAATGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGTAGCCTTGGAGACCCAGG  
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA  
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGATGAAAAGATGGTATGATTC  
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG  
ATTTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTGCCTTAATGGAGACAATAGCAG  
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA  
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC  
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG  
AAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACTAAAAATATGGGGCAATTGTTAGCCTT  
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT  
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCACTTCATTCTGGACACAGTTGGAT  
CAATACTGATTAAGTAGAAAATCCAAGCTTTGCTTGAGAACTTTTGTAACGTGGAGAGTAAAA  
AGTATCGGTTTTTA

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## **FIGURE 530**

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST  
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASININMQ  
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMILAV  
LYRRKNSKRDTGCTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS  
DKINKSESVVYADIRKN

**Important features:**

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

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**FIGURE 531**

GTGACACTATAGAAGAGCTATGACGTGCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA  
GGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC  
TTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACTGGT  
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCTGCTG.  
GAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCTGGAAC  
CAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC  
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG  
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG  
CACCTGTGCGACCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTGGTG  
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC  
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG  
CGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCAAGGAGCAGAAGTCCTTCTTCGCC  
AAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC  
GGGGGCCAGGGTGGGGGTGGGGGTGGGGTGGTGGTGGGGTAGTGGCCTTTGCTGTGTGCCA  
CCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAA  
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCT  
TGATTGAAATTCAGTCTCACTTGATACGTTATTAGAAACCCAAGGAATGGCTGTCCCATC  
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAACTGTCCCCAGATC  
GACACGCAAAAAAAA



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## **FIGURE 532**

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID  
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEAGG  
YVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP  
PTTAPGPETA AFIERLEMEQAQKAKNPQE QKSFFAKYWMYIIPVVLFLMMSGAPDTGGQGGGG  
GGGGGGGSGLCCVPPSL

**Important features:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243



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## **FIGURE 534**

MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDWC  
CQTHDCCYDHLKTQGCgiYKDNNKSSIHCMdLSQRYCLMAVFNViiYLENEdSE

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

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**FIGURE 535**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG  
AACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC  
CCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT  
TTTTTAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCAT  
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT  
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG  
GGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG  
CTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAA  
AGGATGGTTCATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCC  
ACTGTCTTACTGACAATGCTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA  
GGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTAAGTATATCTGCTGGT  
TGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTAAGTATAATCAATTTAAAGGG  
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT  
TTTAATGGAATACGCAGACTCAAAGAGCTGATTCCTAGTTCCAATAGAATCTCCTATTTTCTT  
AACAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCCTATAATCAGCTGCAT  
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTACATTTACGGTCTAAC  
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACCTTTGGACCTG  
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGCTTTTGGCTGGCATGATCAGACTCAAAGAA  
CTTCAGAACTTTACTTGCACTGGAATAAAATCAGTGTATAGGACAGACCATGTCCTGGACC  
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT  
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT  
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG  
GAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG  
AATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG  
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG  
CCGACGTTTAAGCCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTTTGCCCCCGACG  
GTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCTTTCCATAAA  
ATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG  
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC  
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTAGAT  
TATAAAACCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTAT  
AACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAGC  
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC  
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTCTATA  
ATACTGGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT  
GAAGCTTGAATCCGGTTTAAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAAT  
GTCGCATTTGTTTTAAGATAAACTTCTTTCATAGGTAAAAA

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**FIGURE 536**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC  
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLN  
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTPVRIFQDCRNLELLDLG  
YNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTW  
SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWE  
CSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKP  
TFKPKLPRPKHESKPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVS  
WKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYN  
KSGSRECEV

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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**FIGURE 537**

GGGACTACAAGCCGCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAATGTCTTGCATCATTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTGCTGCTGCAATGACCGCAAGGAAATTTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCCACGGATT  
CCAGAGCCAATCCAGATTTTCGCAATTCTTCTTCCACTTAAACTCTGAAACAGGCACCTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCGAGTACTACTGCATTGCTTCCAATGACGCGAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGCGGAATTATTGGGGGGTTCGGTGTCTTGTCTGCTGACTGGCCCTGA  
TCAGTGTGGGCATCTGCTGTGCATACAGAGCTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAACACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGGCTGAGAGCGCACAGAGCGCACGTCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCGCCGATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCGTGCTGGGCCCTGTGAAGCCAGCATGTTTACCAGTGGTCTGCT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAATTTGGTGTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGTATTTATGAAAAGAAAATTTCTATTAAACTGTAAATATTTGT  
CATACAATGTAAATAACCTATTTTAAAAAAGTTCAACTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAGAGTATTTTACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT  
CACACAAGTTTTCAGCTTTTTCACAAGGGAATCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGTTTGGCCAGGCGCCCCGCTCTAGCTCACTGTTGCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTTTCTTTTAAAGTTGTTTAAATATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAGAAAATGGAT  
CCCACTGTTCTCTTTGCCACAGAGAAAGCACCCAGAGCCACAGGCTCTGTCCGATTTCAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCAT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTATACTTTGACAGCTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA  
GGAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTT  
CCTCCATCATTTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACAGCTCCAGCCTCCT  
TCTTGGTTGTATAGTATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA  
TGGGAACAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGACTAACACACCGTAATTTGGCATTGTGTTAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

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**FIGURE 538**

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP  
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI  
DEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR  
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGGVLVV  
LAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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**FIGURE 539**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAGC  
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA  
CTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTGAACTCCAGCCCCGCACATCCACGCGCGG  
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCTGGGCAGCTGG  
GCTCGGGCGGCGGGAGTAGGGCCCCGAGGGAGGAGGAGGCTGCATATTCTAGAGTCGCGGG  
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGA  
**AG**AGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC  
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG  
CCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTG  
AGGGAGGAGTCCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAAGTTAATAGAGAGCATGTTGC  
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGA  
ATGGAGATGGGCAAACATCTGGTGCCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT  
CCCAGTACCGAAACTGGTACACAGATGAACCTTCTGCGGAAGTGAAAAGTGTGTTGTGATGT  
ATCACCACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCAGTGGAAATGATGACA  
GGTGTAAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCTG  
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG  
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC  
TGGTTGCTTTTGGAACTGTGTTTCCAGATGCTGCATAAAAAGTAAAGGAAGAACAAAACTA  
GTCCAAACAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGT**A**  
**ATA**AACTCATTGACTTGGTTCAGAATTTTGTAACTCTGGATCTGTATAAGGAATGGCATCAG  
AACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAAGATGAACTGTAAGCTCCCCCT  
TGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTTCAATTAAAGAATATGCTGTGCTA  
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA  
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT  
TCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA  
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAAATGAACTGTTCTA  
ATATTTATTTTTATGGCATCTCATTTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC  
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAGTTTGTCTCTCGAA  
ATAATTCATCTTTAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA  
AGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT  
AATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTACTTAAATTAACAGATTTTG  
TAATAATGTAACCTTGTAAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAGT  
GACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTG  
AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTGCGGGTTT  
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC  
CTCTGACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAG  
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAA  
ATGGGTTTGGAAACCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATG  
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGA  
AAGTTGTAACCTCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTG  
TTTCTGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 540**

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADEFKHPCKMAYFHELSSRVSFQEARLACES  
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSACPDLYQWSDGSN  
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP  
VEKPYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRTKT  
SPNQSTLWISKSTRKESGMEV

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89 and 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

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**FIGURE 541**

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
CCACAGCCACTGGGCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTGCTGTGCGAGGCCGGCAGGTGG  
GCGTGAAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTGGCCAGCCGCCACTGGGCCCTGACC  
GGTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCCTCAACGAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
GCCTGGTCTCAACGTCTATAGCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCAATGGTATGGGTCCATG  
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGG  
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTACGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAACATCGCCCCCTCGGGGGTGACCTCAACTGTGTCA  
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTC  
ACAGAGCCATCACACAGAGTGGGGTCAACACACCCAGGGATCATCGACTCTCACCTTGGCCCCCTAGCTCAGA  
AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGTGGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
CAACACCCGTCTTGACCACTGTGGATGTGCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAAATGCCAGGCTTCCAGGAATTCATGGGTGACGTATTTCATCAATGTTCCACCGTCA  
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG  
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCGAGGGTGTCTTTGTGTTTCGAGGTCCCTTCCCTCA  
TGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG  
AACAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG  
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTAGAGCC  
AGGCCTGAACCTTCTTGGCTGGGGCAACCACTCTTCAAGTGGTGGCAGAGTCCAGCAGCGCAGCCCGCCTCTC  
CCCCGTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
ATGTCAAGGCGCCTCCACCTCTGGGGCATTGTACAAGTCTTCCCTCTCCCTGAAGTGCTTTCTGCTTT  
CTTCGTGGTAGGTTCTAGCACATTCTCTAGCTTCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTCTGTCT  
CCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCCTTAACCCCACTCTGTCAACCCACACCAAGGATCGGTGGGA  
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCTGGCCAGAGGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCTGAC  
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTTGGCCCTGCACAAGACAACAGA  
ATCCATCAGGGCCATGAGTGTCAACCCAGACCTGACCTCACCAATTCCAGCCCTGACCTCAGGACGCTGGATG  
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCTCCTCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGGCAGGGGAGGGCATCTGGACCAGGGCATCCGTCGGGCTATTGTACACA  
GAGAAAAGAAGAGACCCACCCACTCGGGTCAAAAAGGTGAAAAGCACCAAGAGGTTTTCAGATGGAAGTGAGAG  
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTGCGCCTCTGCTGGGCTCCCACTTTGGCA  
GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGGCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT  
CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGCGGCCAG  
AGTGAGTTCGGGTGGGCTGGGCTCGGCGGGGCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT  
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGCAGGGCTCGG  
GACCTGCAGCCCTCCATGCCTGACCTCCCCCAGCCCCCTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAG  
CGCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACACCCCAAGGGCTGAGGAGTGCAGGCTGCACAGCGCGGGA  
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
GACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTAATGCACCAATCCACACTCTGTATCTGGCT  
ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
TTGTGTCTAGCTCAGGGATCGTAAACGCAACCAATCAGCACCTGTCAAAAACAGACCACTTGACTCTGTAAAAT  
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
CCCTCGGGTCCCTCCCACGCCGTGGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCCAAAA

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**FIGURE 542**

MERAVRVESGVLVGVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGKGTDRLVNVFLGI  
PFAQPPLGPDREFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV  
LNVYSPAEPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFFSTG  
DEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPVAAGLFHRAI  
TQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT  
VDGTVFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLAISTPVL  
TSLDVPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF  
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMMAQWTHFA  
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA  
QEDL

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 226-245

**N-glycosylation site.**

amino acids 105-109

**N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**Carboxylesterases type-B serine active site.**

amino acids 216-232

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**FIGURE 543**

TGTCGCCTGGCCCTCGCCATGCAGACCCCGGAGCGTCCCCTCCCCGCCGGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGCGCCACGGCCTCTTTCTGAGGAGCCGCCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTGTTGTGGGCAGCGGGCCCGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTCATTGGGGACAGGGACAACCTCTACCGCTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTTGTGTCGGATGAAG  
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTCCAACGCCTCAACCCGGTGTGCGCAACTACAGCATAGACACCTGCAGCCCGTTCGGAGACAACATCAGC  
GGTATGGCCCGTGCCTGACGCCCAAGCAGGCCAATGTTGCCCTCTTCTGACGGGATGCTCTTCACAGCT  
ACTGTTACCGACTTCTAGCCATTGATGCTGTCATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATGGAGTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCTGGCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGTGAGAGAAGCAGTGGACGCTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCCGGCCCGTG  
GTCCTGGCCGTTTTTCCACGCGCCAGCAACAGCATCCCTGCGCTCGGCTGTCTGCGCCTTGACCTGACACAGTG  
GCAGCTGTGTTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCGCGTGCCTGGAGGATCAG  
GTGCTCGACCCCGCCCGGGTGTGCGCAGCCCCCGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTGTCAAGACCCACCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGGACCTGATGAGGCACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCTGGGGCAACCAGACCGTT  
GTCTTCCCTGGGTTCTGAGGCGGGGACGGTCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACTCAGGGACGCT  
GGGCTCAGTGTCTTCTGAGGAGTTTGAAGCTACCGCCGGACAGGTGTGGACGGCCCGCGGTGGCGAGACA  
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGAGCTTCGGGGGGCTGCTGGCTGCCCTCCCCCGCTGCGTGGTC  
CGAGTGCCTGTGGCTCGCTGCCAGAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC  
GGTGGGCCCCCGACGGCTCTGCATCTTCTCAGCCCGGCACAGAGCCGCCTTTGAGCAGGACGTGTCCGGG  
GCCAGCACTCAGGCTTAGGGGACTGCACAGGACTCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTCGTCGGTGGCGGCCTTCGTGGTGGGAGCCGTGGTGTCCGGCTCAGCGTGGGC  
TGGTTCTGTGGCCCTCCGTGAGCGGCGGGAGCTGGCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG  
GGCAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGGTTCCCCCGAGGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTCGAGGGCGGGCCACGACCTGGACTCGGGGCTGCTGCCACGCCCCGAGCAGACGCGCTCGGGCGGACGCGC  
CTGCCCACTCCGACCCCGACCCCCACGCCCTGGGCCCCCGCGCTGGGACCACGGCCACCCCTGCTCCCGGCC  
TCCGTTCTATCCTCCTCCTGCTGCTGGCGCCCGCCGGGCCCCGAGCAGCCCCCGCGCTGGGGAGCCGACC  
CCCGACGGCCGCTCTATGCTGCCCGGCCCGCGCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC  
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCTTGGACCCAGCCTCAGCCGCGGATGGCCTCCCGCG  
CCCTGGAGCCCGCCCCGACGGGACGCTGAGGAGGCCACTGGGCCCCACGCCCCCTCCGGCGCCACCCCTGCGC  
CGCACCCACAGTTCAACAGCGGCGAGGCCCGGCCCTGGGACCGCCACCGCGGCTGCCACGCCCGGCCGGGCACA  
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCCTAGGCGGGGGCCCCCG  
ATGCCCTTGGCAGTGCCAGCCACGGGAACAGGAGCGAGAGCGGTGCCAGAAGCCGGGGCCCGGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACAG  
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTGAGTTTTGGTTTTCTTTGCGGTTTTCTAACC  
AATTGCACAACCTCCGTTCTCGGGGTGGCGGCAGGAGGGAGGCTTGGACGCCGTTGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCCGGGAGGTGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGCGTGTGTGTCAAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGGTTAGGAGTTTGAAC  
CCCCCACTCTGCAGAGGGAAGCGGGACAATGCCGGGTTTCAAGGAGGAGACACGAGGAGGGCCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCAAGGTGGGTGGGGCCCCCTCTGTAA  
ATACGGCCCCAGGTTGGTGGAGAGTCCCATGCCACCCGTCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCCACGCTGGCTGGTGGTCTCTGCTGCTTGGAGTTTGCTCCCCAGCCCCCTCCCCATCAAT  
AAACTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 544**

MQTPRASPPRPALLLLLLLLGGAHGLFPPEPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGAD  
DLNIQRLVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC  
RNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG  
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREIAMEF  
NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGVS LG  
GRPVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTPVPEDQVPRPRPGCC  
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHPWILRTLMRHQLTRVAVDVGAGPWGN  
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQRLLSLELD  
AASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV  
SGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGWVGLRERREL  
ARRKDKEAILAHGAGEAVLSVSR LGERRAQGPGGRGGGGGGAGVPPEALLAPLMQNGWAKAT  
LLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLL PASASSSLLLLAPA  
RAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTGPLDPASAADGLPR  
PWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHL LPYGGADR  
TAPPVP

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 318-339, 598-617

**N-glycosylation sites.**amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation sites.**amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885

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**FIGURE 545**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 546**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPE  
IFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE  
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY  
TLRKISSLANSEFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI  
LLQWMEETE

**Important features:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

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**FIGURE 547**

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGGTTCTCGGCCGGGACAGCA  
GAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTTCGCG  
GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA  
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT  
ATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC  
TTTCTGGCGACAGTTCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG  
AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTTCTATATT  
CAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG  
AAAGTCTCAGCACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT  
GGTCTCTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTAAA  
TTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAAGGGCCGGTTTACCATGAGAAC  
TGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT  
GCTCAGATTTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA  
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGTT  
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGATGCCATACTACTTTCT  
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTGGGAGACTGGCCTTTG  
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCCTGGTGTGGCTCCACAGATTCC  
AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA  
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCCTCCCTGGGAAAGCAAAATTCCTACT  
GCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA  
CACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG  
TATGGTCCCATTGTGAAACATATTTCAATTTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT  
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG  
AAGCAGGATTCCATCTACTATGAACATTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT  
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACTTAAATGGGCGAAAGATCACGATGAA  
GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC  
ATATTCTGTTATTATTTCAAACTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA  
ATCCGAGAGGGCATGAAAAGGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGTACTTGC  
CATAGGAAAAAGACCAAGATGAACTCTGATATGCAAAATAACTTCTATTAGAATAATGGTGC  
TCTGAAGACTCTTCTTAACTAAAAAGAAGAATTTTTTTAAGTATTAATTCATGGACAATATA  
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG  
TACTTTAAAGTACATTTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAA



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**FIGURE 548**

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVLPARYFYIQAVDTSGNKET  
SSPGEKVFQVKVSAPEEQFTRVGVQVLDKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY  
ILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQRQSL  
CHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVN LGDWPLEKKKSNSNIHP  
IFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE  
RLELVKLSRKHP ELIDAAFTNFFFFKH DENLYGPIVKHISFFDFFKH KYQINIDGTVAAYRLP  
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEKLKWAKDHDEEAKKIAKAGQE  
FARNNLMGDDIFCYYFKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 302-306, 414-418

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

**Tyrosine kinase phosphorylation site.**

amino acids 341-348

**N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

**Endoplasmic reticulum targeting sequence.**

amino acids 499-504

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**FIGURE 549**

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTGC  
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC  
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC  
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA  
AGGACTCACCTCCCAAAAATTCCGTGAAGGTTGATGAGCTTTCACCTCTACTCAGTTCCTGAGG  
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC  
ACTATTGCGAGCCATACACAACCTGGTGTGAGGAAACGTACTCCCAAACTAAGCCCAAGATGC  
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT  
TTCCGAGACTTGGTGTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA  
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC  
ACAAGCCATCGTGTTTGCCCAGGTGAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT  
ATATAGTCATAGAAGATTTGTGGAAGGAGAACTTCAAAGCCAGGAAATGTGAAGAATTCAC  
CTGGAACCTAAGTAGAAAACTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA  
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA  
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT  
ACAAGCAAATAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT  
TCTCATGTTGCTATTTATGTACCTAATTAACCAAGTTTAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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## **FIGURE 550**

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES  
ISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL  
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG  
NVKNSPGTK

**Important features:**

**Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195

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